NORTH PACIFIC RESEARCH BOARD
SUBAWARD AGREEMENT

1. Scope of Work

(a) The North Pacific Research Board (NPRB) and the Recipient listed below, jointly and severally agree to the provisions herein and to perform the work described in Appendix 1, which contains a statement of work, schedule, and budget for the following project recommended for approval by NPRB on **September 23, 2021**, and approved by the Secretary of Commerce on **October 14, 2021**:

PROJECT NUMBER:	2110
PROJECT TITLE:	Pacific halibut population genetics
RECIPIENT:	International Pacific Halibut Commission 2320 West Commodore Way Seattle, WA, 98199
RECIPIENT DUNS:	88726997
PRINCIPAL INVESTIGATOR:	Josep Planas Josep.planas@iphc.int
PROJECT PERIOD:	December 1, 2021 – January 31, 2024
TOTAL SUBAWARD AMOUNT:	$193,685 (Uniform Guidance 2.C.F.R Part 200 applies)

(b) This AGREEMENT is a subaward of Federal Award Identifier **NA19NM470069, "North Pacific Research Board 2019-2024"** in the amount of **$13,261,144** (Federal Award Date **October 1, 2019)** to NPRB from the U.S. Department of Commerce/National Oceanic and Atmospheric Administration, Assistance Listing number 11.472 (Unallied Science Program). All funds received under this Federal Award are used for direct costs as NPRB does not claim indirect expenses. This award is considered Research and Development.

(c) The Recipient shall provide to NPRB the time and expertise of the Principal Investigator to perform the Scope of Work contained in **Appendix 1**. Material change to the Scope of Work requires prior approval by NPRB.

(d) The Recipient shall provide full and timely financial and programmatic reporting in compliance with all federal laws, regulations, and OMB Circulars appertaining to funds received by NPRB for the Scope of Work described herein.

(e) The Recipient acknowledges that the Scope of Work comprises professional scientific research and agrees that all such work shall be performed by the named individual(s) and with intellectual integrity and scientific competence equal to or better than the professional community standards applicable to such work.

(f) The Recipient accepts full responsibility for performing the Scope of Work while managing and monitoring the project to a successful conclusion. The Recipient attests that he or she has read, understands, and while performing the Scope of Work, will comply with the North Pacific Research Board's March 2, 2009 Policy on Compliance with Subaward Agreements (**Appendix 2**).

2. Term

The Scope of Work shall be completed during the Project Period identified in Section 1. The NPRB may grant extensions to the Project Period in writing if requested at least 30 days before the conclusion of this Agreement.

3. Payment

(a) For all activities described in the Scope of Work, the Recipient shall be reimbursed in accordance with the budget detail in **Appendix 1** and NPRB Financial Reporting Form set forth in **Appendix 3**, not to exceed the Total Subaward Amount identified in Section 1 above. Costs incurred in a currency other than U.S. dollars shall be reimbursed in U.S. dollars at the average exchange rate for the month of the expenditure.

(b) NPRB may authorize in writing payment in advance for anticipated immediate expenditures to be incurred during the first thirty days of the Scope of Work, if the Recipient submits sufficient justification.

(c) The Recipient shall submit invoices and supporting documentation to NPRB through its fiscal agent, the Seward Associated for the Advancement of Marine Science dba the Alaska SeaLife Center (ASLC), quarterly for expenses incurred during the calendar year (invoices due January 31st, April 30th, July 31st and October 31st). All invoices must be accompanied by a properly completed NPRB Financial Form (**Appendix 3**), and shall itemize costs in compliance with the law and NPRB reporting requirements.

Invoices shall be submitted electronically with signature to:

grants-contracts@alaskasealife.org,

Or be mailed to:

Alaska SeaLife Center
NPRB Fiscal Agent
P.O. Box 1329
Seward, AK 99664-1329

Final invoices shall be marked "Final" and must be submitted no later than 60 days following the conclusion of the Agreement. Failure to submit the final invoice within such period shall constitute a complete waiver of all claims by the Recipient to any amounts not previously invoiced.

(d) 90 percent of all incurred costs authorized and properly reported by the Recipient shall be paid by NPRB within 30 days following receipt of the same amounts by NPRB from the federal funding agency. Payments will be withheld while financial or programmatic reporting is delinquent. The remaining 10 percent shall be paid to the Recipient within thirty days following acceptance of the final programmatic report described in Section 5 below.

(e) Allowable direct costs shall be determined in accordance with the federal cost principles applicable to the Recipient (Uniform Guidance 2.C.F.R Part 200 applies). Allowable indirect costs shall be in accordance with the Negotiated Indirect Cost Agreement in effect on the date of signature of this Agreement. A copy of the Negotiated Indirect Cost Agreement (NICRA) must be provided during the application process.

(f) New subawards $25,000 and greater from the NPRB are subject to pre-award reporting requirements based on the implementation of the Federal Funding Accountability and Transparency Act of 2006 (FFATA). **Appendix 4** (if included) represents the information that is required and must be completed (if applicable) and signed prior to the release of funds.

(g) Reallocation of funds between or among the direct cost categories in the NPRB Financial Reporting Form in **Appendix 3** must be approved in writing by NPRB prior to any such reallocated expenditure occurring, if that reallocation exceeds 10 percent of the total Recipient budget amount. Prior approval by NPRB is required to reallocate funds from direct costs to indirect costs, or vice versa, regardless of amount.

(h) All equipment and supplies over $5,000 purchased with funds pursuant to this Agreement that are not consumed in the Scope of Work and that have a useful life of more than one year from the date of purchase shall remain the property of Recipient. Equipment should be used for continued project work, after which it should be used for other federally funded programs, with the first preference being given to awards from the same funding agency. The Recipient will be responsible for tracking the equipment use after the award ends and will be required to seek disposition instructions when the equipment is no longer of use.

(i) The Recipient has no requirement for reporting any matching or in-kind contribution related to this Scope of Work.

4. Key Personnel

The Recipient shall designate the person identified in Section 1 as the Principal Investigator for the Scope of Work to be performed under this Agreement. This individual is essential to the project and shall not be removed or replaced without the prior written approval of NPRB.

5. Manuscripts, Reports, and Data Provisions

(a) In addition to programmatic reporting required by law, the Recipient shall submit semiannual progress reports and a final programmatic report in accordance with provided templates and guidelines. For projects with multiple partner organizations, only one report is required for the project in its entirety. Reports will be submitted via the Research Workspace account provided to the PI by the NPRB Program Manager. Reports must be in the current template provided in the Workspace account or as downloaded from the NPRB website.

Semi-annual progress reports are due every January 31 and July 31 until the Agreement is completed. Reports are not required for due dates that fall in the first or final six months of the Project Period.

The Recipient shall submit a final programmatic report, a copy of the data and accompanying metadata via the Research Workspace within 60 days of the end of the project period indicated in Section 1. The Recipient will provide responses to all review comments within 30 days.

(b) The Recipient shall strive to submit research results for publication by an appropriate scientific journal and present project results at appropriate scientific conference within one year following the completion date in Section 1. The Recipient shall deliver a reprint of any publications or presentations to NPRB within sixty days of publication or presentation.

(c) All manuscripts and reports pertaining to the Scope of Work shall acknowledge that funds were provided by a subaward through the North Pacific Research Board.

(d) The Recipient is required to immediately notify NPRB of any development that may significantly impact the project supported by this Agreement; in particular, notification is necessary regarding problems, delays, or adverse conditions which may materially impair the ability to meet objectives and milestones. The Recipient should not wait until the next semiannual report to notify NPRB of these types of developments. The notification must describe the action(s) taken or planned as well as any assistance needed to resolve the situation.

(e) NPRB reserves the right to distribute any and all information pertaining to the data and analyses found in and deriving from Recipient reports. NPRB will give appropriate credit to the authors who hold the copyright.

(g) All rights, title, and interests (including patents, copyrights, trademarks and any other intellectual property) created under this Agreement shall be held solely by the Recipient. The Recipient grants to

NPRB a royalty-free, paid-up, non-exclusive, worldwide, and irrevocable license to any copyrightable works of authorship, data, databases, software, photographs, outreach materials, and other information first developed by the Recipient under this Agreement to use, distribute, create derivative works, display, reproduce, translate, and publish for purposes within the mission of NPRB. Such license does not include the right to sell copies of the copyrightable material. Recipient does not warrant or make any representations; NPRB assumes all risk related to the use, or the results of the use, of the work, output, derivative works or related documentation with respect to their accuracy, reliability, or otherwise.

(h) The Recipient and PI agree to transfer all data and metadata to NPRB at the completion of the project according to the following metadata and data transfer policy: i) For projects involving data collection or generation, NPRB requires a copy of the data and associated metadata; ii) For any third-party datasets used in the NPRB-funded project, only the transfer of the metadata associated with the third-party data is required; iii) If third-party data is modified for use in the NPRB funded project, the metadata associated with the third-party data is required in addition to the modified dataset and the associated metadata; iv) transfer requirements for modeling projects will be evaluated on a case by case basis.

6. Audit and Records Retention

(a) The Recipient shall maintain accurate records of all costs incurred in the performance of this Agreement and shall make such records available upon request to representatives of NPRB or the federal funding agency to verify the validity and eligibility of expenses reimbursed under this Agreement. Financial records, supporting documents, and other records pertaining to this Agreement shall be retained and kept available by the Recipient for a period of 3 years from the termination date of this Agreement or, if under audit, for as long as is required to resolve.

(b) The Recipient agrees to comply with the requirements of OMB Uniform Guidance: Cost Principles, Audit, and Administrative Requirements for Federal Awards, Subpart F – Audit Requirements and will provide NPRB with copies of all audit reports regardless of results. In case of noncompliance, the Recipient shall provide copies of responses to auditor's reports and a plan for corrective action.

7. Hold Harmless and Indemnification

Each party to this Agreement agrees to hold harmless the other party from and against any and all claims, liabilities, losses, expenses, fees including attorney's fees, and damages arising from or pertaining to the performance of this Agreement, but only in proportion to and to the extent such claims, liabilities, losses, expenses, fees including attorney's fees, and damages are caused by or result from the negligent or intentional acts or omission of the indemnifying party, its officers, agents or employees.

8. Subcontracting and Assignment

The parties agree that the Recipient is providing the unique services of individual, qualified professionals/scientists and their staff in performance of the research under this agreement. The Recipient shall not assign or subcontract any portion of the Agreement without the prior written consent of NPRB.

9. Project Suspension

If the Recipient fails to comply with the project objectives, the terms and conditions of this Agreement, or the reporting requirements, NPRB may temporarily suspend this Agreement in accordance with **Appendix 2** and follow the procedures contained therein, pending either corrective action by the Recipient or a decision to terminate the Agreement. NPRB may immediately suspend this Agreement without prior notice when it is believed that such action is reasonable to protect the interests of NPRB and the federal government. No costs incurred during a suspension period will be allowable, except those costs approved by NPRB in the suspension notice, or which NPRB deems necessary and not reasonably avoidable.

10. Termination for Cause or Default

NPRB may terminate this Agreement, in whole or in part, in accordance with Appendix 2 and follow the procedures contained therein in the event that the Recipient: fails or refuses to perform any component of the Scope of Work within the time provided, fails to obtain appropriate permits, violates any of the conditions of this Agreement, or if it becomes evident that the Recipient is not conducting the work in accordance with the specifications or with diligence so as to permit delivery on or before the specified delivery date. Delays in delivery beyond the time specified in this Agreement due to causes beyond the control and without the fault or negligence of the Recipient may be excused by NPRB if the Recipient notifies NPRB in writing of the cause of such delay within a reasonable time and requests an extension of the Project Period.

11. Compliance with Law

(a) The Recipient will comply with all federal, state and local laws and regulations in the performance of the Scope of Work and in the performance of the terms and conditions of this Agreement, including but not limited to Department of Commerce Financial Assistance Standard Terms and Conditions, and NOAA Administrative Standard Award Conditions. This award is subject to and the recipient must comply with the Uniform Administrative Requirements, Cost Principles, and Audit Requirements for Federal Awards (Uniform Guidance), which is codified at 2.C.F.R Part 200. In effect as of December 26, 2014, this final guidance is a streamlining of the Federal government's guidance on administrative requirements, cost principles, and audit requirements for Federal awards. It supersedes requirements contained in OMB Circulars, A-21, A-87, A-102, A-110, and A-133.

(b) The Recipient agrees to obtain and to accept full responsibility for the proper administration of all permits and approvals required by law for the performance of the Scope of Work, including vessel safety and inspection.

12. Independent Contractor

The Recipient represents and warrants that it is a contractor independent of NPRB in the performance of the Scope of Work. The Recipient assumes full and sole responsibility for all benefits and protections of its employees whose services are utilized in the execution of this Agreement. Nothing in this Agreement shall be construed as authorizing the Recipient or its employees, agents or assigns to act as an agent or assign of NPRB, and the Recipient shall exercise all diligence to ensure that no third party construes the Recipient as an actual, ostensible or apparent agent of NPRB.

13. Debarment and Suspension Certification

In accepting this Agreement, the Recipient certifies that neither it nor its principals are presently debarred, suspended, proposed for debarment, declared ineligible or voluntarily excluded from participation in this transaction by any federal department or agency. Any change in the debarred or suspended status of the Recipient during the life of this Agreement must be reported immediately to NPRB. The Recipient agrees to incorporate a similar Debarment and Suspension Certification into any subaward that it may enter into as part of this Agreement.

14. Payment of Taxes

The Recipient shall be solely responsible to pay any and all taxes incurred by and through the performance or payments made pursuant to this Agreement.

15. Dispute Resolution

The Recipient agrees to follow the problem resolution procedures contained in **Appendix 2**, and to negotiate diligently in good faith before resorting to a court of law or equity for the resolution of any dispute arising from or pertaining to this Agreement.

16. Applicable Law, Jurisdiction, and Venue

This Agreement shall be governed by the laws of the State of Alaska except to the extent pre-empted by United States federal law (including the International Organizations Immunities Act, 22 U.S.C. Sec. 288 et seq). Jurisdiction for the resolution of any dispute between the parties shall be determined based on applicable taxes.

17. Entire Agreement and Modifications

This **Agreement**, **Appendix 1**, **Appendix 2**, **Appendix 3** and **Appendix 4** represent the entire agreement between the parties, and supersede all prior oral or written agreements, understandings and alleged causes for detrimental reliance regarding any of the terms, conditions or Scope of Work contained in

this Agreement. This Agreement may be amended or modified only in writing and must be executed by both parties. The NPRB Executive Director may authorize the NPRB Program Manager to execute Amendments to this Agreement.

18. Notices

All notices that in any way modify or alter this Agreement shall be sent to the following addresses:

NPRB:
Jo-Ann Mellish, Senior Program Manager
North Pacific Research Board
1007 West 3rd Ave., Suite 100
Anchorage, AK 99501
Phone: (907) 644-6712, Fax: (907) 644-6780
joann.mellish@nprb.org

Authorized Signer:
David T. Wilson
2320 West Commodore Way
Seattle, WA 98199
Phone: (206) 662-1838
david.wilson@iphc.int

19. Authorizing Signatures

North Pacific Research Board Lynn Palensky, Executive Director	Date
David T. Wilson	12/01/2021
Recipient Institution Authorized Signer	Date

Acknowledged and agreed by:

Josep Planas	12/01/2021
Principal Investigator	Date

Summary Page

Proposal No: 2110-2027-2027 **Submitted:** Jun 11, 2021

REVISED Start Date: Dec 2021 **End Date:** Jan 2024

Title: Leveraging multiple genomic approaches to investigate population structure and dynamics of Pacific halibut

Principal Investigator(s):
Dr. Josep V Planas (Lead) , josep.planas@iphc.int, International Pacific Halibut Commission

Category: Fishes and Invertebrates

Abstract: The Pacific halibut (*Hippoglossus stenolepis*) is a key flatfish species in the North Pacific Ocean ecosystem that supports important commercial, recreational and subsistence fisheries and that is managed as a single stock by the International Pacific Halibut Commission. The overarching goal of the present study is to advance our understanding of Pacific halibut population structure and dynamics in a changing climate through the use of genomic approaches to inform fishery management. In particular, we seek to improve our current understanding of stock structure among spawning groups of Pacific halibut in the northeast Pacific Ocean by conducting low coverage whole genome resequencing, a method that allows the characterization of genomic variation at the highest resolution possible and with which we will establish a baseline of Pacific halibut genetic diversity. Subsequently, we will leverage the obtained genomic data to identify markers that display high differentiation among the different genetic baseline datasets. With approximately 500 of the identified genome-derived markers we will develop a high-throughput and high-resolution genomic marker panel (GT-seq). Finally, we will test the utility of the GT-seq panel to address management and conservation issues in Pacific halibut by using it in two proof of concept applications: 1) to conduct a pilot mixed stock analysis to estimate the stock composition of commercial fishery landings from two different geographic areas in Alaska, and 2) to investigate distribution of Pacific halibut in the latitudinal extremes of the species' range in the northeast Pacific Ocean. The results from this study will inform on the delimitation of management units and provide preliminary information on stock composition in the Pacific halibut fishery, as well as provide a tool to monitor changes in distribution associated with climate change.

Links to Prior NPRB Projects: Several NPRB-funded projects have addressed population or stock structure of commercially- and ecologically-important species from a genetic point of view. NPRB #817 examined population structure of Pacific cod in the Bering Sea and Aleutian Islands in relation to oceanographic and landscape features with the use of microsatellites (with Dr. Ingrid Spies, a collaborator in the present proposal, as Principal Investigator). NPRB #908 analyzed the genetic structure of Pacific ocean perch in the Gulf of Alaska with the use of microsatellites. Finally, NPRB #1125 examined stock structure of Arctic Cod in the Arctic region also with the use of microsatellites. To the best of our knowledge, the present proposal would the first to investigate population structure of an important fish species in the Gulf of Alaska and the Bering Sea with the use of genomic approaches, providing an unprecedented level of resolution to stock structure analyses. In addition, the present proposal would leverage recent advances in genomic technology to address for the first time potential shifts in distribution of Pacific halibut in the Bering Sea that may be linked to climate variation.

Management or Ecosystem Implications: The proposed studies in the present proposal have profound implications for the management of Pacific halibut in the northeastern Pacific Ocean. The use of genomic approaches to define population structure will provide an unprecedented level of resolution to significantly improve our current level of understanding of Pacific halibut population structure that may lead to the adoption of changes in the current stock assessment and management structure implemented by the IPHC. Evidence for demographically isolated portions of the stock (e.g. western Aleutian Islands) will support redefining management units and separating specific mortality limits for these separate stocks from stock-wide trends. Furthermore, the genomic high-throughput tools that will be developed in this project (i.e. GT-

seq marker panel) will allow for the estimation of stock composition in fishery samples by the IPHC in order to evaluate exploitation and productivity rates of individual stocks. Finally, the proposed studies on Pacific halibut distribution with the use of the GT-seq marker panel will inform stock assessment on spatial dynamics of the Pacific halibut population, that has historically represented a major source of uncertainty in the Pacific halibut stock assessment. The proposed studies will also provide information on potential shifts in Pacific halibut distribution and provide the ground for future studies on dispersal and movement of Pacific halibut in response to climate variation.

Total Funding Requested From NPRB: $193,685

1. International Pacific Halibut Commission: $193,685

Total Other Support: $111,672

1. International Pacific Halibut Commission: $111,672

Descriptors

Category

Fishes and Invertebrates

Species

Hippoglossus stenolepis

Large Marine Ecosystem(s)

Bering Sea/Aleutian Islands, Gulf of Alaska

Keywords

Pacific halibut, distribution shift, genetic baselines, marker panel, mixed stock analysis, population structure, whole genome sequencing

Contacts

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   International Pacific Halibut Commission
   2320 West Commodore Way, Suite 300, Seattle, Washington, 98199
   Phone: +1 206-662-1838
   david.wilson@iphc.int
2. Dr. Josep V Planas [PI, Lead-PI]
   International Pacific Halibut Commission
   2320 West Commodore Way, Suite 300, Seattle, Washington, 98199-1287
   Phone: +1 206-552-7687
   josep.planas@iphc.int
   - CVs.pdf (pdf)
3. Mr. Keith Jernigan [Grant Manager]
   International Pacific Halibut Commission
   2320 West Commodore Way, Suite 300, Seattle, Washington, 98199
   Phone: +1 206-662-1838
   keith.jernigan@iphc.int
4. Mr. Andrew Jasonowicz [Co-Investigator]
   International Pacific Halibut Commission
   2320 West Commodore Way, Suite 300, Seattle, Washington, 98199-1287
   Phone: +1 206-662-1838
   andy.jasonowicz@iphc.int
5. Dr. Wesley Larson [Collaborator]
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   17109 Pt. Lena Loop Road, Juneau, Alaska, 99801
   Phone: +1 907-789-6000
   wes.larson@noaa.gov
6. Dr. Ingrid Spies [Collaborator]
   AFSC NOAA Fisheries

7600 Sand Point Way NE, Seattle, Washington, 98115
Phone: +1 206-526-4786 Fax: +1 206-526-4786
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7. Mrs. Liz Dawson [Collaborator]
Alaska Fisheries Science Center, NOAA National Marine Fisheries Service
7600 Sand Point Way NE, Seattle, Washington, 98115
Phone: +1 206-526-6121
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CV_Josep V. Planas, PhD

CURRICULUM VITAE

I. PERSONAL INFORMATION

Name: **Josep V. Planas**

Current Position: Biological and Ecosystem Science Branch Manager

Mailing address: International Pacific Halibut Commission, 2320 West Commodore Way, Suite 300, Seattle, WA 98199-1287.

Phone: +1-206-552-7687; *Fax*: +1-206-632-2983

E-mail: josep.planas@iphc.int

Research Gate: https://www.researchgate.net/profile/Josep_Planas2

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Metrics: ***h*-index: 48, RG Score: 39.3**

II. EDUCATION

PH. D. IN FISHERIES. (1993). University of Washington (Seattle, WA).

PH. D. IN BIOLOGICAL SCIENCES. (1989). University of Barcelona (Barcelona, Spain).

MASTER OF ARTS IN ENDOCRINOLOGY. (1988). University of California (Berkeley, CA).

B.SC. IN BIOLOGICAL SCIENCES. (1984). University of Barcelona (Barcelona, Spain).

III. PROFESSIONAL ACTIVITIES

MANAGER, BIOLOGICAL AND ECOSYSTEM SCIENCE BRANCH. (2016-present). International Pacific Halibut Commission (Seattle, WA).

AFFILIATE FACULTY IN MARINE AND ENVIRONMENTAL SCIENCES. (2017-present). Alaska Pacific University (Anchorage, AK).

VISITING ASSOCIATE PROFESSOR. (FEB. 2013-AUG. 2013). School of Aquatic and Fishery Sciences, University of Washington (Seattle, WA).

ASSOCIATE PROFESSOR. (2001-2015). Department of Physiology and Immunology, University of Barcelona (Barcelona, Spain). *Lab website*: http://planaslab.wordpress.com

ASSISTANT PROFESSOR. (1998-2001). Department of Physiology, University of Barcelona (Barcelona, Spain).

POSTDOCTORAL FELLOW. (1996-1998). Department of Physiology, University of Barcelona (Barcelona, Spain).

POSTDOCTORAL FELLOW. (1993-1996). Department of Pharmacology, School of Medicine, University of Washington (Seattle, WA).

IV. MAIN RESEARCH AREAS (KEYWORDS)

FISH PHYSIOLOGY, FISH GENOMICS, FISHERIES

Publication list (selected from last 5 years)

Kroska, A.C., Wolf, N., **Planas, J.V.,** Baker, M.R., Smeltz, T.S., Harris, B.P. Controlled experiments to explore the use of a multi-tissue approach to characterizing stress in wild-caught Pacific halibut (Hippoglossus stenolepis). 2021. Conserv. Physiol. 9(1):coab001; doi:10.1093/conphys/coab001.

Sadorus, L.; Goldstein, E.; Webster, R.; Stockhausen, W.; **Planas, J.V.**; Duffy-Anderson, J. Multiple life-stage connectivity of Pacific halibut (Hippoglossus stenolepis) across the Bering Sea and Gulf of Alaska. Fish. Oceanogr. 2021. 30:174-193. doi: https://doi.org/10.1111/fog.12512

Lomeli, M.J.M., Wakefield, W.W., Herrmann, B., Dykstra, C.L., Simeon, A., Rudy, D.M., **Planas, J.V.** Use of Artificial Illumination to Reduce Pacific Halibut Bycatch in a U.S. West Coast Groundfish Bottom Trawl. Fish. Res. 2021. 233: 105737. doi: 10.1016/j.fishres.2020.105737.

McKenzie, D.; Palstra, A.; **Planas, J.V**.; MacKenzie, S.; Begout, M.; Thorarensen, H.; Vandeputte, M.; Mes, D.; Rey Planellas, S.; De Boeck, G.; Domenici, P.; Skov, P. Aerobic swimming in intensive finfish

aquaculture: applications for production, mitigation and selection. Rev. Aquacul. 2021. 13: 138-155. doi: 10.1111/raq.12467.

Fish, T., Wolf, N., Harris, B.P., **Planas, J.V.** A comprehensive description of oocyte developmental stages in Pacific halibut, Hippoglossus stenolepis. J. Fish Biol. 2020. 97: 1880-1885. doi: 10.1111/jfb.14551

Graziano, M., Benito, R., **Planas J.V.,** Palstra A. P. Swimming exercise to control precocious maturation in male seabass (Dicentrarchus labrax). BMC Dev. Biol. 2018. 18: 10.

Rovira, M., Arrey, G., **Planas, J. V.** Exercise-induced hypertrophic and oxidative signaling pathways and myokine expression in fast skeletal muscle of adult zebrafish. Front. Physiol. 2017. 8:1063. doi: 10.3389/fphys.2017.01063

Antonopoulou, E., Kaitetzidou, E., Castellana, B., Panteli, N., Kyriakis, D., Vraskou, Y., **Planas, J.V.** In vivo effects of lipopolysaccharide on peroxisome proliferator activated receptor expression in juvenile gilthead seabream (*Sparus aurata*). Biology. 2017. 6:36. doi:10.3390/biology6040036.

Pauletto M, Milan M, Huvet A, Corporeau C, Suquet M, **Planas J.V.**, Moreira R, Figueras A, Novoa B, Patarnello T, Bargelloni L. Transcriptomic features of Pecten maximus oocyte quality and maturation. PLoS One. 2017; 12(3):e0172805.

Planas, J.V., Palstra AP, Magnoni LJ. Editorial: Physiological Adaptations to Swimming in Fish. Front Physiol. 2017; 8:59.

Kals, J., Blonk R.J.W., Palstra, A.P., Sobotta, T.K., Mongile, F., Schneider, O., **Planas, J.V.**, Schrama, J.W., Verreth, J.A. Feeding ragworm (*Nereis virens Sars*) to common sole (*Solea solea* L.) alleviates nutritional anaemia and stimulates growth. Aquaculture Research. 2017. 48:752-759.

Boltaña S, Castellana B, Goetz G, Tort L, Teles M, Mulero V, Novoa B, Figueras A, Goetz FW, Gallardo-Escarate C, **Planas, J.V**, Mackenzie S. Extending Immunological Profiling in the Gilthead Sea Bream, Sparus aurata, by Enriched cDNA Library Analysis, Microarray Design and Initial Studies upon the Inflammatory Response to PAMPs. Int J Mol Sci. 2017; 18(2), 317.

Pardo BG, Álvarez-Dios JA, Cao A, Ramilo A, Gómez-Tato A, **Planas, J.V**, Villalba A, Martínez P. Construction of an Ostrea edulis database from genomic and expressed sequence tags (ESTs) obtained from Bonamia ostreae infected haemocytes: Development of an immune-enriched oligo-microarray. Fish Shellfish Immunol. 2016; 59:331-344.

Books and book chapters (last 5 years)

Manchado, M., **Planas, J.V**., Cousin, X., Rebordinos, L., Claros, M.G. Genetic and Genomic Characterization of Soles. In: "The Biology of Sole". Munoz-Cueto, J.A., Mananos-Sanchez, E.L., Sanchez-Vazquez, F.J., eds. CRC Press. ISBN 9781498727839. 2019, pp. 375-394.

Manchado, M., **Planas, J.V**., Cousin, X., Rebordinos, L., Gonzalo Claros, M. Current Status in other Fish Species: Description of current genomic resources for the gilthead seabream (Sparus aurata) and soles (Solea senegalensis and Solea solea). In: "Genomics in Aquaculture". MacKenzie, S., Jentoft, S., eds. Academic Press. ISBN: 978-0-12-8014189. 2016, pp. 195-221.

Rodnick, K., **Planas, J.V**. In: "Biology of Stress in Fish", Fish Physiology Series, Vol. 35. Schreck, C.B., Tort, L., Farrell, A., Brauner, C., eds. Elsevier. ISBN: 978-0-12-802728-8. 2016, pp. 251-294.

Other merits or achievements

Awards:

- Fulbright Scholar. 1986-1988. University of California, Berkeley, CA (USA).
- Kenneth K. Chew Endowed Associate Professorship in Aquaculture. 2013. University of Washington, Seattle, WA (USA)

Member of the *Editorial Board* of the following journals:

- *Fisheries Research (co-Editor of Special Issue on Pacific Halibut) (2020-)..*
- *Fishes (since 2015).*
- *Frontiers in Experimental Endocrinology (*since 2011*).*
- *PLoS* One (Academic Editor since 2011).
- *Reproductive Biology and Endocrinology* (since 2002).
- *Research Journal of Endocrinology and Metabolism (since 2013).*
- *Scientific Reports (since 2017).*

Andrew Jasonowicz
Research Biologist
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Education

M.Sc.	University of Washington, *School of Aquatic and Fishery Sciences* **Thesis:** Genomic Signatures of Natural Selection and population Structure in West Coast and Alaskan Sablefish (*Anoplopoma fimbria*) **Advisor:** Dr. Steven Roberts	*Seattle, WA* *2015*
B.Sc.	Northern Michigan University, *Biology*	*Marquette, MI* *2009*

Professional Experience

International Pacific Halibut Commission Research Biologist	*Seattle, WA* *Aug 2019 - present*
University of Washington, *School of Aquatic and Fishery Sciences* Research Scientist *Affiliate Researcher at NOAA's Northwest Fisheries Science Center*	*Seattle, WA* *May 2015 - Aug 2019*
Michigan Department of Natural Resources, Marquette Fisheries Research Station State Worker	*Marquette, MI* *Apr 2010 - Oct 2010*
University of Illinois, Illinois Natural History Survey, Lake Michigan Biological Station Biological Technician	*Zion, IL* *May 2009 - Nov 2009*
Northern Michigan University Stream Survey Technician	*Marquette, MI* *May 2008 - Aug 2008*

Main Research Areas (Keywords)

Population genomics, Genetics, Fisheries

Peer-Reviewed Publications

Sitar, S., F. Goetz, **A. Jasonowicz**, and M. Seider. 2020. Lipid levels and diet compositions in lake charr ecotypes at Isle Royale in northern Lake Superior. Journal of Great Lakes Research 46(3):569–577. International Association for Great Lakes Research.

Goetz, F. W., **A. J. Jasonowicz**, and S. B. Roberts. 2018. What goes up must come down: Diel vertical migration in the deep-water sablefish (*Anoplopoma fimbria*) revealed by pop-up satellite archival tags. Fisheries Oceanography 27(2):127–142.

Guzmán, J. M., J. A. Luckenbach, M. A. Middleton, K. C. Massee, C. Jensen, F. W. Goetz, **A. J. Jasonowicz**, and P. Swanson. 2017. Reproductive life history of sablefish (*Anoplopoma fimbria*) from the U.S. Washington coast. Plos One 12(9):e0184413.

Jasonowicz, A. J., F. W. Goetz, G. W. Goetz, and K. M. Nichols. 2017. Love the one you're with : genomic evidence of panmixia in the sablefish (*Anoplopoma fimbria*). Canadian Journal of Fisheries and Aquatic Sciences 74(3):377–387.

Goetz, F., S. Sitar, **A. Jasonowicz**, and M. Seider. 2017. Transactions of the American Fisheries Society Reproduction of Lake Trout Morphotypes at Isle Royale in Northern Lake Superior. Transactions of the American Fisheries Society 146(2):268–282.

Roloson, S. D., R. L. Gould, D. R. Barton, F. W. Goetz, **A. J. Jasonowicz**, C. Beierling, and M. R. van den Heuvel. 2016. Factors Influencing Growth Variability in Three Northern Alberta Populations of Yellow Perch (Perca flavescens). Journal of Fisheries Sciences 10(4):43–52.

Cook, M. A., K. C. Massee, T. H. Wade, S. M. Oden, C. Jensen, **A. Jasonowicz**, D. A. Immerman, and F. W. Goetz. 2015. Culture of sablefish (Anoplopoma fimbria) larvae in four experimental tank designs. Aquacultural Engineering 69:43–49.

Goetz, F., **A. Jasonowicz**, R. Johnson, P. Biga, G. Fischer, and S. Sitar. 2014. Physiological differences between lean and siscowet lake trout morphotypes: Are these metabolotypes? Canadian Journal of Fisheries and Aquatic Sciences 71(3):427–435.

Sitar, S. P., **A. J. Jasonowicz**, C. A. Murphy, and F. W. Goetz. 2014. Estimates of Skipped Spawning in Lean and Siscowet Lake Trout in Southern Lake Superior: Implications for Stock Assessment. Transactions of the American Fisheries Society 143(3):660–672.

Background

The concept of a stock is fundamental to the management and conservation of marine species (Begg and Waldman, 1999).Under this concept, managers define semi-discrete boundaries to fish populations in order to make decisions regarding management units (Begg et al., 1999).Developing management strategies that recognize and conserve population structure can support productive fisheries and contribute to long term sustainability (Schindler et al., 2010; Cadrin, 2020). However, defining and identifying stock structure in marine fisheries is often a challenging and complex task, but doing so will result in higher yield and reduced probability of unintended overfishing (Carvalho and Hauser, 1994; Spies and Punt, 2015; Spies et al., 2015; Cadrin, 2020).

Genetic techniques have been widely used to define stock structure for a number of species and with incredible advances in genomic technology, genomic methods promise to offer increased power and affordability for a multitude of applications in fisheries research and management (Bernatchez et al., 2017). Current genomic technologies now enable researchers to examine entire genomes at unprecedented resolution. While genetic techniques previously employed in fisheries management generally use a small number of markers (~10-100), whole-genome scale approaches can now be conducted with lower cost and provide orders of magnitude more data (millions of markers) (Therkildsen and Palumbi, 2017; Clucas et al., 2019).The high resolution data that whole-genome resequencing (WGR) generates allows to scan the genome for a variety of genetic variations that may be useful in describing population structure and local adaptations (Fuentes-Pardo and Ruzzante, 2017). With this significant advantage of WGR over other currently-used genomic methods (e.g. RAD-seq), the genome can be surveyed to detect neutral mutations (neutral variation) and mutations under natural selection (adaptive variation), and to identify structural variations, such as chromosomal inversions (Fuentes-Pardo and Ruzzante, 2017). Variations associated with chromosomal inversions and mutations potentially under selection may contribute significantly to genetic stock structure in marine fishes. Recent studies utilizing genomic technologies have found adaptive and structural variation to be associated with spatial structure (Clucas et al., 2019; Longo et al., 2020) and other attributes of stock structure that are of interest to fishery managers, such as spawn timing (Petrou et al., 2021).Therefore, genomic tools can aid in the identification of stock structure and in the delineation of biological stock units that are used for proper management resulting in increased fishery yield (Spies et al., 2015). Genomic tools may also be developed to aid in the estimation of stock specific harvest rates among various fisheries. Unfortunately, while genomic data and tools derived from genomic approaches can have direct applications in fisheries management, they are not often incorporated into management strategies (Bernatchez et al., 2017).

The Pacific halibut (*Hippoglossus stenolepis*) supports important commercial, recreational and subsistence fisheries throughout the North Pacific Ocean. The Pacific halibut stock is currently modeled and managed as a single stock in the northeast Pacific Ocean by the International Pacific Halibut Commission (IPHC) (Stewart and Hicks, 2021).The rationale behind this management approach is based on 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 northeast Pacific Ocean population of Pacific halibut by allozyme (Grant et al., 1984) and small-scale microsatellite analyses (Bentzen et al., 1998; Nielsen et al., 2010).However, results from a more recent study using a larger number of microsatellites detected genetic population structure in the western Aleutian Islands (Drinan et al., 2016). These findings were attributed to limited movement of adults and exchange of larvae between the western Aleutian Islands 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, the results from this study were confounded by (1) the use of a relatively limited set of microsatellite markers that only allowed resolving small levels of genetic differentiation, and (2) the inclusion of genetic samples collected outside of the spawning season (winter) which may not accurately represent local spawning groups, but rather a mixture of spawning groups on the feeding grounds, for a subset of the examined geographic areas, including the Aleutian Islands. Therefore, the limitations from this study have motivated the use of higher resolution genomic techniques and

the incorporation of samples only from known spawning groups.

Genomic approaches, as demonstrated in other commercially and ecologically important fish species (salmonids: Larson et al., 2014; Atlantic silverside: Therkildsen and Palumbi, 2017; cod: Clucas et al., 2019; Spies et al., 2020), show tremendous promise to address key ecological and biological questions related to Pacific halibut (e.g. population structure and dynamics, genetic basis of important life-history traits, environmental responses, local adaptation, etc.) at an unprecedented level of resolution. Importantly, they can also inform Pacific halibut management by defining management units and estimating levels of adaptive divergence and connectivity among them, by identifying the population of origin of individuals, etc. (Bernatchez et al., 2017). The recent generation of a reference genome for Pacific halibut (Jasonowicz et al., in preparation) allows for the application of genome-based approaches (WGR) to investigate stock structure, establish genetic baselines and ascertain the source populations of individuals in order to understand the composition of harvested stocks and climate effects on Pacific halibut distribution. Therefore, the proposed study seeks to improve our current understanding of stock structure among spawning groups of Pacific halibut in the northeast Pacific Ocean using methods that characterize genomic variation at the highest resolution possible. Additionally, we propose to leverage the genomic information obtained to develop and validate more cost-effective and high-throughput tools (GT-seq panel of high-resolution markers) that can be used to advance management of the Pacific halibut resource and address important ecological questions (Figure 1A).

This proposal directly addresses 2021 RFP's issues of particular ("understanding distribution, movement, and stock structure of important commercial fishes") and general ("spatial variation in stock structure and distribution patterns"; "direct and indirect effects of climate on fishes") interest.

Objectives

1. Investigate fine scale Pacific halibut population structure in the northeast Pacific Ocean using low-coverage whole genome resequencing: characterization of neutral and adaptive variation at very high resolution among spawning groups leading to the identification of millions of genome-derived genetic markers.
2. Develop a high-throughput genetic marker panel consisting of a selection of genome-derived, high-resolution markers identified in Objective 1: development and validation of a Genotyping-in-Thousands by Sequencing (GT-seq) marker panel for Pacific halibut.
3. Provide a proof of concept for the utility of the GT-seq panel developed in Objective 2 in addressing two specific issues related to Pacific halibut population dynamics: a) stock composition of commercial fishery landings, and b) analyses of distribution of Pacific halibut in the latitudinal extremes of the species' range in the northeast Pacific Ocean.

Design and Approach

In order to accomplish the above-stated specific objectives, this proposal will capitalize on (1) the available extensive collection of genetic samples (Table 1), (2) the recent generation of a complete chromosome-level assembly of the Pacific halibut genome, and (3) the demonstrable expertise of the proposing team in the development and application of population genomics methods in fisheries ecology and management.

The above-stated specific objectives are paired with the following hypotheses:

Hypothesis 1: Low-coverage whole genome resequencing will provide increased resolution of population structure in Pacific halibut in the northeast Pacific Ocean.

Hypothesis 2: Leveraging the low-coverage whole genome dataset will lead to the identification of hundreds of high-resolution markers that will be used for the development and validation of a GT-seq marker panel for Pacific halibut.

Hypothesis 3: The developed GT-seq panel will provide information on stock composition in two different areas in Alaska and on the geographic origin of Pacific halibut from the latitudinal extremes in the northeast Pacific Ocean.

The studies to be conducted in this proposal are distributed among three different tasks that relate directly to each of the three specified objectives:

Task 1. Defining population structure of Pacific halibut by low-coverage whole genome resequencing (lcWGR).

In order to resolve the question of population structure in Pacific halibut and aid in the identification of genetic baselines from spawning groups, genetic samples were collected in the Central and Western Aleutian Islands during the spawning season (January 2020) by the IPHC. These samples represent a valuable addition to an existing collection of samples obtained during the spawning season from other geographic areas and that now comprise a wide range across the northeast Pacific Ocean (i.e. British Columbia, Central Gulf of Alaska, Bering Sea, Central and Western Aleutian Islands). Therefore, this enables the re-examination of genetic structure of Pacific halibut using samples exclusively collected from spawning groups. This project will use a low-coverage whole genome resequencing (lcWGR) approach (Figure 1B) that involves the sequencing of multiple barcoded individuals from various spawning groups at a low genome sequencing depth (2-4x). This approach relies on the availability of the reference Pacific halibut genome recently generated by the proposing team (chromosome-level annotated assembly; RefSeq Assembly No. GCF_013339905.1), allows for the analysis of a large number of samples per population and, most importantly, produces the highest marker density of currently available genomic methods. Overall, the lcWGR approach provides unmatched genomic resolution when assessing neutral and functional genetic variation at a wide range of levels, from single nucleotide differences (SNPs) to structural variations (Fuentes-Pardo and Ruzzante, 2017), and has been successfully applied in other fish species (Clucas et al., 2019; Therkildsen and Palumbi, 2017). Therefore, lcWGR will provide, on one hand, a novel and high-resolution perspective to improve our knowledge of the genomic structure of the Pacific halibut population and, on the other hand, a large dataset of neutral and putatively adaptive genetic markers that will be used in downstream, high-throughput applications (Tasks 2 and 3).

Sample collections

All the genetic samples (i.e. fin clips) required for conducting this task have been collected (Figure 2A,B; Table 1).The available samples from Pacific halibut collected during the spawning season (i.e. winter) correspond to the following geographic areas and dates of collection:

- British Columbia (Haida Gwaii; 1999, 2004, 2007)
- Central Gulf of Alaska (Portlock region; 1999, 2004, 2007, 2018)
- Bering Sea (Pribilof Canyon; 2004, 2007)
- Central Aleutian Islands (east of Amchitka Pass; 2007, 2020)
- Western Aleutian Islands (west of Amchitka Pass; 2020)

The above collection locations correspond to known spawning grounds for Pacific halibut (St-Pierre, 1984).Additionally, temporal replicates at many of these locations will be used to evaluate the stability of genetic structure over time, ensuring confidence in the results (Waples, 1998).

Methodology

Library preparation and sequencing

Fifty samples from each of these collections will be analyzed, totaling 600 individuals. High-quality genomic DNA will be extracted and purified (Qiagen), libraries for lcWGR will be prepared according to published protocols (e.g. Therkildsen and Palumbi, 2017; Clucas et al., 2019) and sequenced on Illumina's NovaSeq platform. Based on an initial sequencing run consisting of 36 individuals, we estimate that sequencing can be carried out in 3 lanes to achieve 2-4x sequencing coverage per individual on Illumina's NovaSeq S4 platform. While low sequencing coverage introduces uncertainty to individual genotype calls, simulation studies have shown that sequencing many individuals at low depth gives more accurate estimates of population parameters than sequencing fewer individuals at depths required to call genotypes with a high degree of confidence (Fumagalli et al., 2013; Lou et al., 2021).Additionally, individual based methods that take into account genotype uncertainty by handling genotype likelihoods directly can still produce reliable results (Skotte et al. 2013; Meisner and Albrechtsen 2018).

Raw sequence reads will be mapped to the recently sequenced Pacific halibut genome (Jasonowicz et al., in preparation) using Minimap2 (Li, 2018).Having a reference genome available is a major benefit to this study as constructing one is quite expensive and time consuming. Furthermore, the Pacific halibut genome has been annotated (https://www.ncbi.nlm.nih.gov/genome/gdv/browser/genome/?id=GCF_013339905.1) so that the locations of genes are known, enabling the functional significance of mutations located in protein coding regions to be inferred. Samtools (Li et al., 2009) will be used to filter out alignments with a mapping quality score less than 20 (99% probability of a correct alignment) and reads that align to multiple locations in the genome. Polymerase chain reaction (PCR) duplicates will be removed using Picard (https://broadinstitute.github.io/picard) and overlapping read pairs will be clipped using Bamutil (Jun et al., 2015).Local realignment will be performed using GATK (Van der Auwera and O'Connor, 2020) to improve alignments around insertion/deletion elements (Figure 1C).

Population Structure

The software ANGSD (Korneliussen et al., 2014) will be used detect SNPs throughout the Pacific halibut genome. ANGSD is designed to accommodate low coverage data by accounting for the uncertainty associated with low-coverage genotypes in a probabilistic framework by utilizing genotype likelihoods directly. ANGSD will also be used to estimate measures of genetic diversity (allele frequencies and heterozygosity) for each sample collection. Measures of genetic differentiation (F_{ST}) will be estimated among the sample collections to examine levels of divergence between them and test for patterns of isolation by distance. In addition to population based analyses, patterns of population structure will be analyzed using individual based methods developed for low-coverage data such as admixture analysis (Skotte et al., 2013) and principal components analysis (Meisner and Albrechtsen, 2018).Individual based analyses complement traditional population genetic analyses and have the ability to identify cryptic patterns of population structure because population groups do not need to be defined a priori. Additionally, genome-wide selection scans will be used to identify genomic regions showing signals of divergent selection. SNPs in regions of the genome showing signatures of selection may offer more power to resolve population structure in highly migratory marine fish (Grewe et al., 2015; Anderson et al., 2019).F_{ST} and PCA based methods will be used to identify regions of the genome showing signals of selection. Pairwise F_{ST} will be estimated in 10kb genomic windows for all population pairs using ANGSD (Korneliussen et al., 2014) and PCAngsd (Meisner et al., 2021) will be used to for PCA based selection scans. Additionally, to detect structural variation (i.e. chromosomal inversions) present in these populations we will use *ngsLD* (Fox et al., 2019) to investigate patterns of linkage disequilibrium on each chromosome in the Pacific halibut genome assembly for each population, as summarized in Figure 1C.

Deliverables

1.**Establishment of a baseline of Pacific halibut genetic diversity**. The genomic data produced will represent a detailed baseline of Pacific halibut genetic structure and diversity at neutral and adaptive markers over a large geographical scale (Gulf of Alaska, Aleutian Islands and Bering Sea) and over a broad temporal scale (last 30 years).

2.**Delineation of fine-scale Pacific halibut stock structure**. The next generation sequencing approach (i.e. lcWGR) used will provide high resolution population structure in the sampled geographic areas at an unprecedented level that will inform on the delimitation of management units.

Task 2. Development of a high-throughput genetic marker panel (GT-seq) for Pacific halibut

The application of genomic approaches to address management and conservation issues in exploited species may involve, as described in Objective 1, the analysis of fine population structure to assist in the delineation of management units. In particular, the lcWGR resequencing approach conducted in Task 1 will result in the identification of a high number of genetic markers (both neutral and putatively adaptive) with which to explore genomic diversity at an unprecedented level in Pacific halibut. However, for the purpose of addressing additional important issues related to the management and conservation of the species involving large number of individuals (e.g. distribution changes, population assignments, sex identification, etc.), more cost-effective and high-throughput genotyping methods involving the use of a subset of genome-derived genetic markers are needed (Fuentes-Pardo and Ruzzante, 2017). One of the most cost-effective, rapid and user-friendly methods currently available is an amplicon sequencing method termed Genotyping-in-Thousands by Sequencing (GT-seq). GT-seq is based on a highly-multiplexed PCR strategy to amplify a few hundred (~500) genetic markers followed by high-throughput sequencing (Campbell et al., 2015; Meek and Larson, 2019) and is a subject of expertise for project participant Dr. Larson. This powerful method allows genotyping thousands of individuals at hundreds of high-resolution markers and has been extensively used in management and conservation studies to conduct mixed stock and parentage analyses (Barclay et al., 2019; Bootsma et al., 2020; Campbell et al., 2015; Janowitz-Koch et al., 2019). Therefore, here we propose to leverage the lcWGR dataset generated in Task 1 in order to design a GT-seq panel for Pacific halibut (Figure 1A) containing approximately 500 markers validated for their ability to accurately discriminate among spawning groups. Recent research has shown that utilizing multi-SNP haplotypes improves the accuracy of population assignments compared to bi-allelic SNPs alone (McKinney et al., 2017). Therefore, we plan to incorporate haplotype information where possible to take advantage of this improved accuracy. This panel will then be used in studies assigning individuals to populations of origin to investigate the stock composition of commercial landings and potential distribution shifts (Objective 3). Furthermore, this marker panel may prove useful in future investigations of dispersal and seasonal migration of Pacific halibut.

Sample collections

For this task, we will select 96 samples from the set of samples used to define the genetic baseline in Task 1 (Table 1).

Methodology

Identification of high-resolution markers for the GT-seq panel

To select a set of markers that can accurately discriminate among spawning stocks, training and holdout procedures will be used to accurately assess the discriminatory power of the panel (Anderson et al., 2010; Waples, 1998).Briefly, individuals from each spawning stock will be split into two parts, training and holdout. The individuals in the training set will be used to calculate statistics such as F_{ST} (Weir and Cockerham 1984) and allele frequencies. Markers will be selected based on these statistics and used to assign the set of holdout individuals back to their stock of origin. The discriminatory power of various marker panels will be assessed

using the R packages *AssignPOP* (Chen et al., 2018) and *Rubias* (Moran and Anderson 2019) as they both implement training and holdout routines. Initially we will select 600 markers to initiate development of the GT-seq panel with the assumption that some markers will be lost following PCR optimization. In addition to genomic markers derived from Task 1, two additional markers corresponding to sex-linked loci identified previously for females (Drinan et al., 2018) and currently used for sex identification in Pacific halibut, will be included in the construction of the GT-seq panel. This will allow us to derive sex information on all genotyped fish and continue to inform the Pacific halibut annual stock assessment on sex ratio data of the commercial catch (Stewart and Hicks, 2021).

Construction and performance test of the GT-seq panel

GT-seq uses highly multiplexed PCR to amplify targeted regions of the genome and then sequence only those regions using high-throughput sequencing (e.g. Illumina) (Campbell et al., 2015). A major benefit of GT-seq over other panel development methods is its cost effectiveness: as additional samples are added to the project, the per-sample cost declines exponentially due to savings in sequencing costs (see Figure 6 in Campbell et al., 2015). This aspect makes it very attractive for high-throughput applications that require genotypes from large numbers of individuals (e.g. mixed-stock analysis, genetic tagging and monitoring, etc.).

GT-seq consists of four main steps: 1) PCR amplify the targeted regions, 2) ligate barcodes to identify amplicons from each individual, 3) normalize the amount of DNA for each sample, 4) pool samples and sequence. Initial panel development will be carried out using 96 samples selected from the set of samples used to define the genetic baseline in Task 1 (Table 1). An initial sequencing run on an Illumina MiSeq platform will be carried out with the 600 discriminatory markers identified using cross validation methods. Sequence coverage at each marker will be analyzed using the scripts provided by Campbell et al. (2015) (located at: https://github.com/GTseq/GTseq-Pipeline/). Markers will be discarded at this point if they show unusually high or low levels of sequence coverage. A second round of GT-seq will be carried out with the retained markers (we expect to retain ~550 markers) using the same 96 samples. This will allow for another round of marker selection and quality control. We expect to retain at least 500 markers after this round. Comparisons of the genotypes across the two sequencing runs and to the lcWGR data will enable us to examine discrepancy rates and ensure quality of the panel.

Deliverables

1.**Identification of high-resolution genomic markers**. Genome-derived markers that display high differentiation among the different genetic baseline datasets will be identified and selected.

2.**Development of a genome-derived marker panel: GT-seq panel containing a minimum of 500 high-resolution markers**. The developed and validated GT-seq marker panel will represent a valuable tool to be practically applied in studies directly informing Pacific halibut management.

Task 3. Proof of concept application of the GT-seq panel for studies on Pacific halibut population dynamics.

In this task, we will test the GT-seq panel in two proof of concept applications that have direct implications for management of Pacific halibut.

On one hand, we will conduct pilot mixed stock analyses (MSA) to infer stock composition from Pacific halibut harvested in two different geographic regions in Alaska. Given that Pacific halibut is a highly migratory species that is harvested during the non-reproductive season, fishery samples are likely composed of individuals from different geographic origins (i.e. different spawning groups). Therefore, reliable estimates of stock composition in fishery samples are required for sound management practices as stock-specific harvest information will assist in estimating exploitation and productivity rates of individual stocks for sustainability and conservation

purposes (Beacham et al., 2009; Larson et al., 2014). The resulting information from these preliminary studies will inform and set the stage for future MSA studies aimed at producing reliable estimates of stock composition in the Pacific halibut fishery in the northeast Pacific Ocean area that is currently managed by the IPHC.

On the other hand, we will determine the geographic origin (i.e. source population) of Pacific halibut in the latitudinal extremes of the species' range to investigate possible changes in distribution. Ecosystem changes in the Bering Sea (BS) driven by variable climate conditions have included shifts in the distribution of important commercial fish species. The warming of the eastern BS and, in particular, the reduction in the cold pool along the shelf areas has been linked to changes in the distribution of gadid and flatfish species (Hollowed et al., 2013; Stevenson and Lauth, 2019). Among these species, Pacific cod (*Gadus microcephalus*) is the best documented with recent evidence of a northern shift in distribution, from the eastern to the northern portion of the BS. Importantly, the recently observed parallel decrease in Pacific cod biomass in the eastern BS and the increase in Pacific cod biomass in the northern BS (Thompson, 2018) has been attributed to the movement of fish originating from spawning populations in the eastern to the northern BS consistent with a northward summer feeding migration, as demonstrated by an important genetic study conducted by Dr. Spies, a project participant (Spies et al., 2019). For Pacific halibut, there is also evidence for a northward shift in distribution within the BS, with the eastern region of the BS traditionally considered for management purposes to represent the northern limit of Pacific halibut distribution in the northeastern Pacific Ocean. A recent IPHC study has shown that the estimated geographical center of Pacific halibut biomass in the eastern BS has shifted northward since 2012 (Webster et al., 2020; Figure 3A). Furthermore, spatiotemporal modeling of survey data (combining calibrated data from NMFS BS shelf trawl survey and northern expansions, ADFG trawl survey in Norton Sound and IPHC's Fishery-Independent Setline Survey), has shown a significant decrease in density index estimates (weight and number per unit effort) in the BS area south of 60°N coupled with an increase north of 60°N since 2013 (Webster et al., 2020; Figure 3B). Therefore, an important question that these studies will address is whether Pacific halibut north of 60°N can be assigned to the baseline genetic groups identified in Task 1 and support the notion of a northern shift in distribution likely caused by changing conditions in the BS. Similarly, population assignments of Pacific halibut from the southernmost limit of its distribution (i.e. California, US) will inform on the distribution of the species in the opposite latitudinal extreme in the northeastern Pacific Ocean. In order to further understand the genetic characteristics of Pacific halibut in the latitudinal extremes of its distribution in the northeast Pacific Ocean, in the present project we will compare these collections to the baseline genetic groups identified in the proposed genomic analysis of population structure (Task 1) with the use of the developed GT-seq panel (Task 2). The results obtained will allow us to answer questions related to the possible geographic origin of these fish at the latitudinal extremes of the Pacific halibut population in the northeast Pacific Ocean and investigate possible changes in distribution.

Sample collections

All the genetic samples (i.e. fin clips) required for conducting this task are available (Figures 2A,C,D; Table 1).

- Fin clips from aged commercial samples collected in 2019. The IPHC has been collecting genetic samples from the commercial fishery since 2017 as part of a monitoring program to determine the sex ratio of the Pacific halibut commercial fishery landings. For this task, we will select 640 individual aged samples from commercial landings in IPHC Regulatory Areas 3A and 4B (N = 320 per area) (Figure 2A; Table 1), corresponding to two geographic areas with evidence of genetic structure (Drinan et al., 2016) and different demographics, with IPHC Regulatory Area 4B showing higher proportion of male Pacific halibut and a greater frequency of older fish (>25 yrs) (Stewart and Webster, 2021).
- Fin clips collected north of 60^{o}N from NOAA trawl surveys (2017-2019) in the Bering Sea (N = 337) (Figure 2C).
- Fin clips from Pacific halibut caught by recreational fishermen between 40 ^{o}N and 42 ^{o}N in northern California were collected in the summer of 2013 (N = 270) (Figure 2D).

Methodology

Individual genotypes will be obtained using the GT-seq panel developed in Task 2. Since in Task 2 we will have genotyped 96 samples from the collection used to define the genetic baseline (Task 1), the remaining 504 samples in the genetic baseline will re-genotyped using the GT-seq panel developed in Task 2 to ensure compatibility and facilitate direct comparisons of the lcWGR data with this dataset. We estimate that sequencing can be carried out in 3 lanes on Illumina's HiSeq 4000 platform. Mixed stock analysis will then be used to ascertain the population of origin for each individual. Two complementary methods will be used for this: *AssignPOP* (Chen et al. 2018), which utilizes supervised machine-learning classification models to assign individuals to a set of reference populations, and *Rubias* (Moran and Anderson, 2019), which is based on the conditional genetic stock identification (GSI) model, will also be used to estimate the proportions of each stock represented in the sample collections. Individual population assignments can also be assessed using *Rubias* and testing can be implemented to determine if individuals originate from a population that is not included in the set of reference populations (i.e. if fish caught in the Bering Sea originate from a spawning group not included in the genetic baseline).

Deliverables

1.**Application of a GT-seq panel to examine the proportion of the different genetic baseline groups contributing to a mixed-fishery sample.** Demonstration of the use of the developed GT-seq panel to determine the stock composition of commercial fishery landings from two different geographic areas.

2.**Examination of the geographic origin of Pacific halibut from the latitudinal extremes of its geographic distribution**. Evidence will be provided regarding a potential northern shift of the Pacific halibut distribution.

Preliminary data

The Pacific halibut genome (GenBank accession JABBIT000000000) recently generated by the IPHC has a size of 594 Mb and contains 24 chromosome-size scaffolds covering 98.6% of the complete assembly with a N50 scaffold length of 25 Mb at a coverage of 91x, and with 97.6% complete BUSCOs (RefSeq Assembly No. GCF_013339905.1). The Pacific halibut genome has been annotated by NCBI (https://www.ncbi.nlm.nih.gov/genome/annotation_euk/Hippoglossus_stenolepis/100/) with the use of transcriptomic data generated by the IPHC (https://www.ncbi.nlm.nih.gov/bioproject/PRJNA634339).

An initial sequencing run of 36 samples from the collection detailed in Table 1 was conducted using the Illumina HiSeq 4000 (2x150 bp paired end reads) platform (Novogene, Sacramento, CA).This sequencing run was carried out to ensure that the library preparation methods were successful and to begin developing a bioinformatics pipeline for processing the raw sequence data into analysis ready sequence alignments. Preliminary results indicate that an average of 26.5 million (range = 21.8 - 42.9 million) raw sequencing reads per sample were obtained from this sequencing run. The alignment of the reads to the Pacific halibut genome and quality filtering steps resulted in an average of 60% (range = 54% - 69%) of the raw reads being retained per sample and used for SNP calling. Individual genomic coverages for the quality filtered alignments were on average 3.2x (range = 2.6x – 5x).A total of 5,051,577 SNPs were identified using the GATK model implemented in ANGSD (v0.934) (Korneliussen et al. 2014).The annotation of the Pacific halibut genome was used to determine the number of SNPs present in protein coding regions of the genome (Figure 4).

Figure 1. (A) Flow diagram of activities and deliverables. (B) Schematic representation of the low-coverage whole genome resequencing strategy (adapted from Fuentes-Pardo and Ruzzante, 2017). (C) Bioinformatics workflow and downstream analyses.

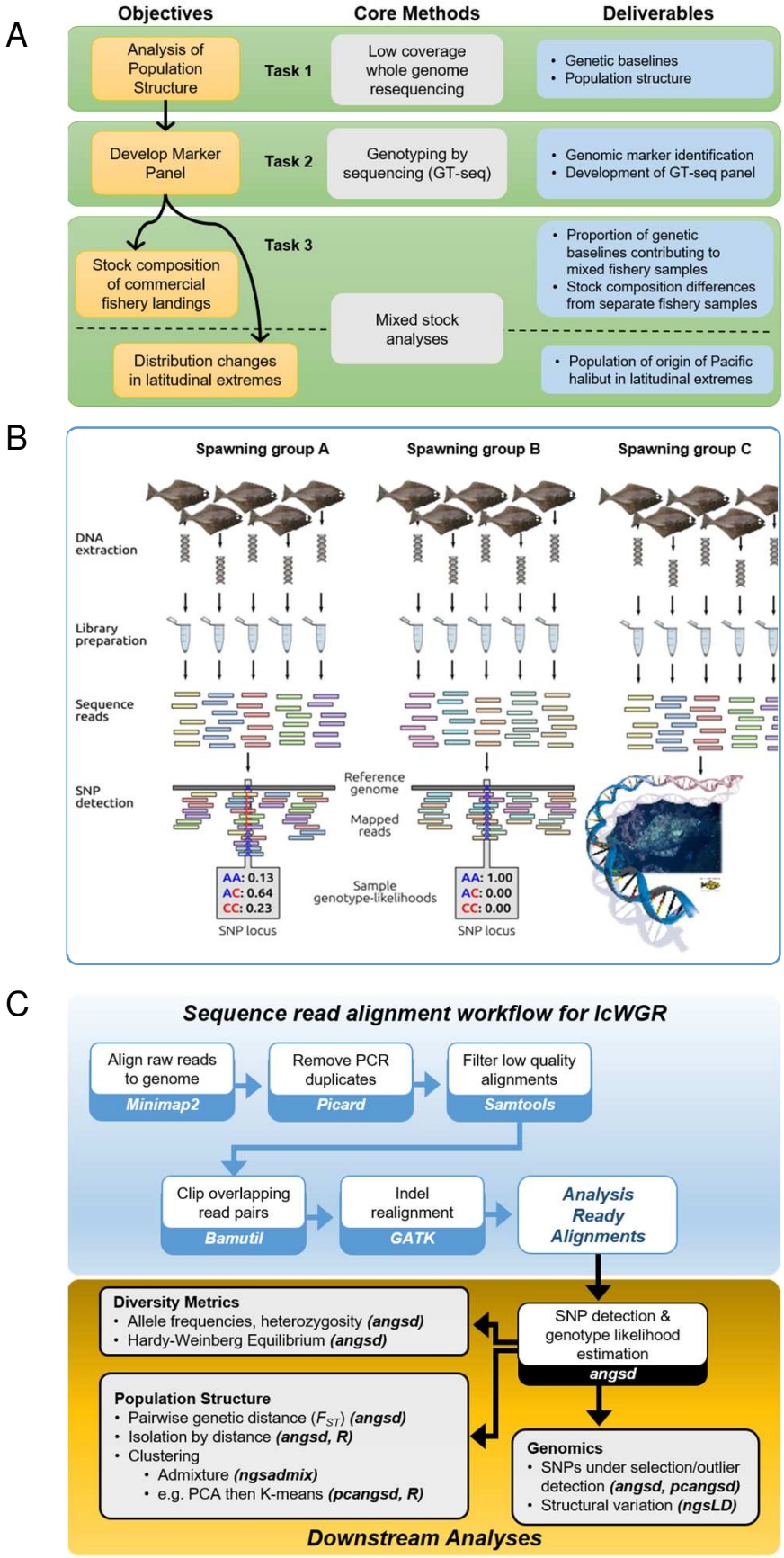


Figure 2. (A) Map of IPHC Regulatory Areas within Convention waters. (B) Map of collection of samples from spawning groups (red: western Aleutian Islands; green: central Aleutian Islands; purple: Bering Sea; yellow: central Gulf of Alaska; blue and orange: Haida Gwaii). (C) Map of collection of samples in the Bering Sea north of 60°N. Red dots indicate the NMFS trawl survey stations. (D) Map of collection of samples from the California recreational fishery.

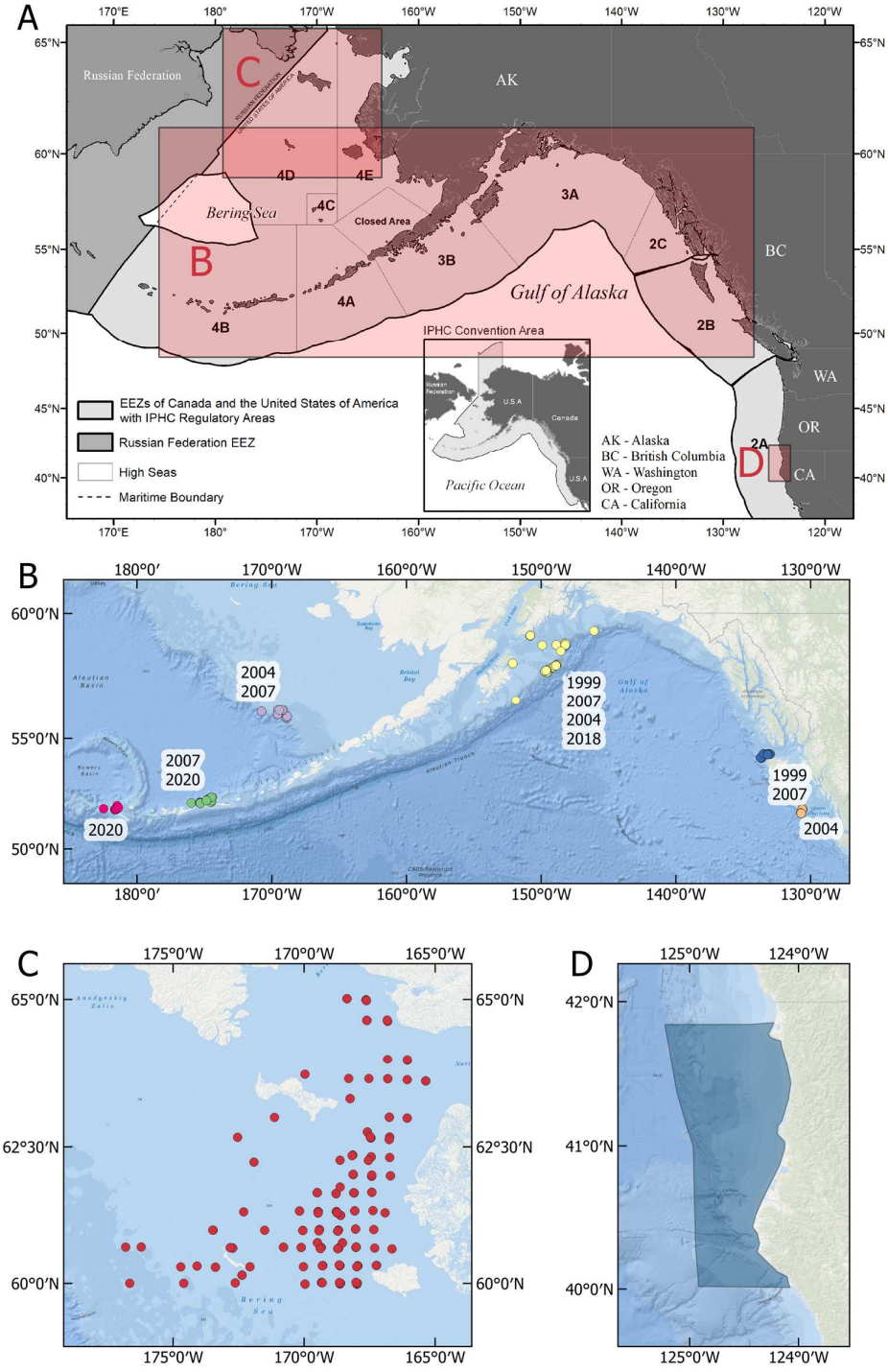
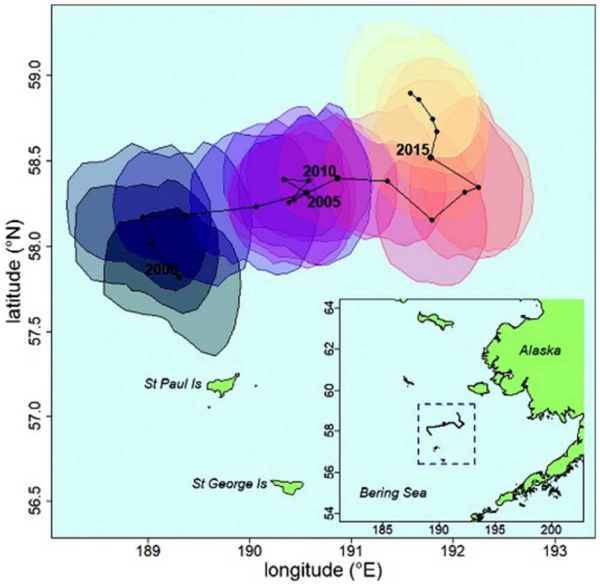


Figure 3. (A) Change in the estimated center of biomass of Pacific halibut in the eastern Bering Sea from 2000 until 2019. (B) Weight Per Unit Effort (WPUE) for Pacific halibut in the Bering Sea (1993-2019) north (red line) and south (blue line) of 60°N. Taken from Webster et al., 2020.

A



B

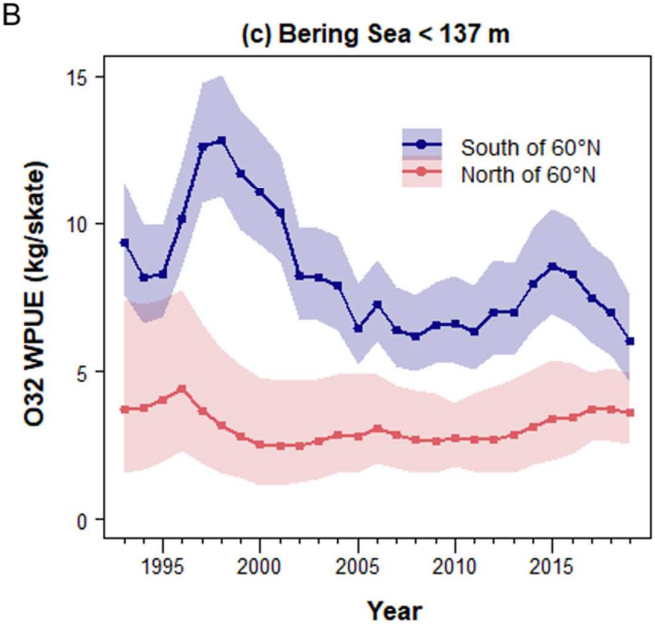


Figure 4. Bar plot showing the number of SNPs detected on each chromosome of the Pacific halibut reference genome using lcWGR data generated from a preliminary sequencing run. Red bars indicate the number of SNPs found in known protein coding regions (CDS) of the genome and blue bars indicate the total number of SNPs detected.

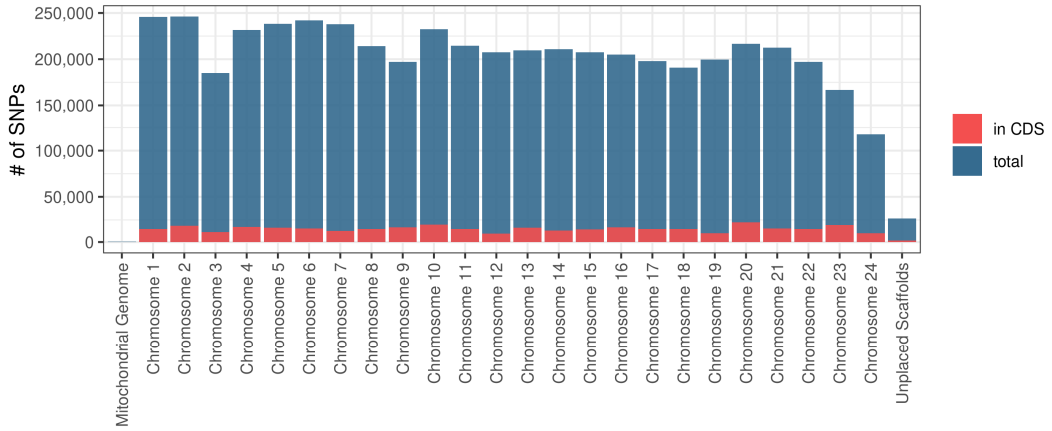


Table 1. Summary of sample collections

Region	*Year*	*Season*	*N*	*Purpose*	*Task(s)*	*Source*
Western Aleutian Islands	2020	Winter	50	Baseline	1	IPHC
Central Aleutian Islands	2007	Winter	50	Baseline	1	IPHC
	2020	Winter	50	Baseline	1	IPHC
Bering Sea	2004	Winter	50	Baseline	1	IPHC
	2007	Winter	50	Baseline	1, 2	IPHC
Gulf of Alaska	1999	Winter	50	Baseline	1	IPHC
	2004	Winter	50	Baseline	1	IPHC
	2007	Winter	50	Baseline	1	IPHC
	2018	Winter	50	Baseline	1	IPHC
Haida Gwaii	1999	Winter	50	Baseline	1	IPHC
	2004	Winter	50	Baseline	1	IPHC
	2007	Winter	50	Baseline	1, 2	IPHC
Commercial Fishery IPHC Regulatory Area 3A	2019	Commercial season#	320	GT-seq	3	IPHC
Commercial Fishery IPHC Regulatory Area 4B	2019	Commercial season	320	GT-seq	3	IPHC
NMFS Bering Sea Trawl Survey*	2017	Summer	71	GT-seq	3	IPHC/NOAA
	2018	Summer	74	GT-seq	3	IPHC/NOAA
	2019	Summer	181	GT-seq	3	IPHC/NOAA
California Recreational Fishery	2013	Summer	270	GT-seq	3	IPHC/NOAA

*Samples collected north of 60ºN.
#The commercial season for Pacific halibut in 2019 was 15 March – 14 November, 2019

Management or Ecosystem Implication

The proposed studies in the present proposal have profound implications for the management of Pacific halibut in the northeastern Pacific Ocean. The use of genomic approaches to define population structure will provide an unprecedented level of resolution to significantly improve our current level of understanding of Pacific halibut population structure that may lead to the adoption of changes in the current stock assessment and management structure implemented by the IPHC. Evidence for demographically isolated portions of the stock (e.g. western Aleutian Islands) will support redefining management units and separating specific mortality limits for these separate stocks from stock-wide trends. Furthermore, the genomic high-throughput tools that will be developed in this project (i.e. GT-seq marker panel) will allow for the estimation of stock composition in fishery samples by the IPHC in order to evaluate exploitation and productivity rates of individual stocks. Finally, the proposed studies on Pacific halibut distribution with the use of the GT-seq marker panel will inform stock assessment on spatial dynamics of the Pacific halibut population, that has historically represented a major source of uncertainty in the Pacific halibut stock assessment. The proposed studies will also provide information on potential shifts in Pacific halibut distribution and provide the ground for future studies on dispersal and movement of Pacific halibut in response to climate variation.

Engagement Strategy

Given the great economic and societal importance of the Pacific halibut fishery for Alaska and the West Coast of the US, the IPHC has a long history of working together with communities and stakeholders. On an annual basis, contacts between communities and stakeholders and the IPHC take place formally in the framework of advisory bodies to the IPHC that include the Conference Board, the Processors Advisory Group, the Management Strategy Advisory Board and the Research Advisory Board. In addition to these meetings where communities and stakeholders discuss with IPHC scientists key aspects of the Pacific halibut fishery and biology, the IPHC interacts locally with communities and stakeholders during the fishing season in ports throughout Alaska that host IPHC field staff. For the purpose of the proposed project, the research plans and results related to our proposed studies on Pacific halibut stock structure and distribution, as assessed by assigning individuals to populations of origin, will be formally presented to IPHC's advisory bodies and feed-back and comment will be requested. Reports on the presentation and discussion of the proposed research to the community and stakeholders will be produced and made publicly available in the IPHC website (https://www.iphc.int). In addition, results of the proposed project with be presented to the general public in simple and easy to understand posters in IPHC-attended events such as ComFish Alaska, Pacific Marine Expo and Fisherman’s Fall Festival in Seattle, WA, and through local newspaper and radio medias (particularly in Pribilof and western Aleutian Islands). It is noteworthy that the present proposal has received formal support from stakeholder groups in St. Paul, AK in the Pribilof Island area (Central Bering Sea Fishermen's Association), in Adak, AK in the Western Aleutian Island area (Adak Community Development Corporation and the City of Adak) and in the northwest California area (Humboldt Area Saltwater Anglers) that are invested in the Pacific halibut resource and that have direct and explicit interest in the results of the proposed study (see attached letters of support). Dissemination and outreach activities will be particularly directed to those areas in the form of news releases and presentations to stakeholder groups, including a presentation to the City council of Adak on the implications of the proposed research for Pacific halibut management in that area and a presentation in St. Paul, AK on the implications of potential shifts in Pacific halibut distribution in the Bering Sea. The results from this project will be written as manuscripts for submission to peer-reviewed journals, such as Molecular Ecology Resources, Evolutionary Applications, Canadian Journal of Fisheries and Aquatic Sciences, etc., and will be disseminated at selected scientific conferences such as the Alaska Marine Science Symposium, the Western Groundfish Conference, the Wakefield Fisheries Symposium and the American Fisheries Society annual meeting.

Links to Prior NPRB Projects Section

Several NPRB-funded projects have addressed population or stock structure of commercially- and ecologically-important species from a genetic point of view. NPRB #817 examined population structure of Pacific cod in the Bering Sea and Aleutian Islands in relation to oceanographic and landscape features with the use of microsatellites (with Dr. Ingrid Spies, a collaborator in the present proposal, as Principal Investigator). NPRB #908 analyzed the genetic structure of Pacific ocean perch in the Gulf of Alaska with the use of microsatellites. Finally, NPRB #1125 examined stock structure of Arctic Cod in the Arctic region also with the use of microsatellites. To the best of our knowledge, the present proposal would the first to investigate population structure of an important fish species in the Gulf of Alaska and the Bering Sea with the use of genomic approaches, providing an unprecedented level of resolution to stock structure analyses. In addition, the present proposal would leverage recent advances in genomic technology to address for the first time potential shifts in distribution of Pacific halibut in the Bering Sea that may be linked to climate variation.

Project Management

The proposing team is composed of researchers with considerable expertise in conducting population genetics and genomics studies in commercially exploited fish stocks in the northeastern Pacific Ocean and in applying the resulting information in fisheries management. Therefore, the proposing team is well suited to successfully address the questions proposed here.

Primary responsibility for the work proposed herein will be by Dr. Josep Planas (Principal Investigator, IPHC), with the help of project co-Investigator Andrew Jasonowicz (IPHC), and project collaborators Dr. Wes Larson (AFSC-NOAA Fisheries, Juneau, AK), Dr. Ingrid Spies (AFSC-NOAA Fisheries, Seattle, WA) and Liz Dawson (AFSC-NOAA Fisheries, Seattle, WA). Briefly:

Principal Investigator (PI):

Dr. **Josep Planas** is Manager of the Biological and Ecosystems Science Branch at IPHC. Dr. Planas has extensive experience in fish biological research, with particular emphasis in the development and application of genomic tools in physiological and ecological research in commercially important fish species. Dr. Planas has participated in leading and managerial roles in a number of research projects, both at national (including as PI on NPRB #1704 and #2009) and international levels. As PI, Dr. Planas will be responsible for project coordination, administration, reporting and publication, and will work directly with project collaborators in the execution of the work proposed here.

Co-Investigator:

Andrew Jasonowicz is currently Research Biologist at the IPHC. Mr. Jasonowicz has expertise in population genomics and bioinformatics. As part of his MSc thesis work at the University of Washington, Mr. Jasonowicz conducted a comprehensive genomic study on the population structure of sablefish off the West Coast of the United States and Alaska. In addition, Mr. Jasonowicz contributed to studies on the migratory behavior of sablefish off the West Coast of the United States in collaboration with the Northwest Fisheries Science Center-Manchester Research Station. At the IPHC, Mr. Jasonowicz's work has focused on the development of genomic resources for Pacific halibut, including the reference transcriptome and the reference chromosome-level genome assembly, and the development of bioinformatics pipelines for genomic analyses. For this project, Mr. Jasonowicz will be responsible for conducting the proposed lcWGR effort to investigate population structure, bioinformatic analyses and proof of concept application of the GT-seq marker panel.

Collaborators:

Dr. **Wes Larson** is the Genetics Program Manager at the Alaska Fisheries Science center. Dr. Larson has an

extensive background leveraging genetic tools to inform management of marine and freshwater fishes. Dr. Larson received his BS from the University of California-Santa Cruz and his PhD from the University of Washington. His PhD focused on applying genomic tools to study local adaptations and inform management of Pacific salmon in Alaska. In particular, he investigated genomic differentiation of Chinook salmon from western Alaska and genetic divergence of different ecotypes of sockeye salmon in Bristol Bay. More recently, Dr. Larson was the Assistant Unit Leader of the USGS Wisconsin Cooperative Fishery Research Unit, where he led a genetics research program in Wisconsin with the goal of conducting research to inform fisheries management. He is especially interested in the development of high-resolution marker panels for fisheries management and has developed more than five of these panels in both marine and freshwater species. For this project, Dr. Larson will assist in the development, validation and implementation of the proposed GT-seq marker panel.

Dr. **Ingrid Spies** is a Research Fisheries Biologist at the Alaska Fisheries Science Center in Seattle, WA. Her research interests include using genetic data to inform fisheries management and stock assessment. She has worked in fisheries genetics since 2000 and as a stock assessment scientist since 2008. She has participated in research cruises in all the large marine ecosystems in Alaska and is the lead stock assessment author for the Bering Sea and Aleutian Islands Yellowfin Sole assessment and will be lead author for the Gulf of Alaska Pacific cod assessment in 2022. She has recently completed two publications based on NPRB #1404 which examined genetic differentiation among skates from nursery sites along the Bering Sea shelf. For this project, she will assist in population assignment of Pacific halibut to examine shifts in distribution and mixed-stock fisheries.

Liz Dawson is a Fisheries Biologist at the Alaska Fisheries Science Center in Seattle, WA. Mrs. Dawson helps coordinate and participates in the standardized, annual bottom trawl surveys in the Eastern and Northern Bering Sea. In 2015, Mrs. Dawson completed her MSc work at Humboldt State University studying age, growth, and maturity of Pacific halibut recreationally caught in waters off Northern California. During the data collection portion of her graduate work in Northern California, Mrs. Dawson collected Pacific halibut tissue samples with the goal to one day compare them to Pacific halibut samples from the northern extreme of their range. Mrs. Dawson will assist with data analyses and publications that emanate from this study.

Coordination and collaboration plans:

Communication among the proposing team members will consist in virtual meetings (online platforms) every two months, starting at month 1, for planning purposes and discuss progress and eventualities. At the beginning of year 2 of the project (months 13 or 14), an in-person project meeting will take place in Seattle, WA (travel for Dr. Larsen included in the proposed budget) to review progress during year 1 and plan research activities and publication, dissemination and outreach activities for year 2. For initiating Objective 2, Mr. Jasonowicz will travel to Dr. Larsen's laboratory in Juneau, AK for 1 week to work on the development of the GT-seq marker panel (Task 2).

Dissemination of results:

The results from this project will be written as manuscripts for submission to peer-reviewed journals, such as Molecular Ecology Resources, Evolutionary Applications, Canadian Journal of Fisheries and Aquatic Sciences, etc., and will be disseminated at selected scientific conferences such as the Alaska Marine Science Symposium, the Western Groundfish Conference, the Wakefield Fisheries Symposium and the American Fisheries Society annual meeting.

Leveraging multiple genomic approaches to investigate population structure and dynamics of Pacific halibut
February, 2022 – January, 2024

	Responsible Party	2022				2023				2024
		Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4	Q1
Alaska Marine Science Symposyum	**Jasonowicz, Planas**	X				X				X
Final Report	**Planas**									X
Data and Metadata Transfer	**Planas**									X
Progress Report	**Planas**	X		X		X		X		X
Objective# 1 Investigate fine scale Pacific halibut population structure in the northeast Pacific Ocean using low-coverage whole genome resequencing	**Jasonowicz**, Planas			X						
Objective# 2 Develop a high-throughput genetic marker panel consisting of a selection of genome-derived, high-resolution markers identified in Objective 1.	Jasonowicz, Planas, **Larson**					X				
Objective# 3 Provide a proof of concept for the utility of the GT-seq panel developed in Objective 2 in addressing two specific issues related to Pacific halibut population dynamics.	**Jasonowicz**, Planas, **Larson**, **Spies**, Dawson							X		
Virtual project meetings. Every two (2) months using online platforms with all project participants.	**Jasonowicz, Planas, Larson, Spies, Dawson**	X	X	X	X	X	X	X	X	X
In-person project meeting. Meeting in Seattle, WA with all project participants.	**Jasonowicz, Planas, Larson, Spies, Dawson**					X				
Publication #1. Genomic analysis of population structure in Pacific halibut in the Northeastern Pacific Ocean	Jasonowicz, **Planas**					X				
Publication #2. Analysis of potential shifts in distribution of the Pacific halibut population with the use of a GT-seq marker panel	Jasonowicz, **Planas, Larson, Spies**, Dawson						X			X
Outreach activities. Produce news releases in media outlets, conduct stakeholder meetings (virtual) in St. Paul, AK, Adak, AK, Eureka, CA.	**Jasonowicz**, **Planas**, Larson, Spies, **Dawson**							X		X

Budget

No	Institution	Requesting Funds	Other Support
1	International Pacific Halibut Commission	193,685	111,672

1. Dr. David T. Wilson [Authorized Organizational Representative]
   International Pacific Halibut Commission
2. Dr. Josep V Planas [PI, Lead-PI]
   International Pacific Halibut Commission
3. Mr. Keith Jernigan [Grant Manager]
   International Pacific Halibut Commission

APPENDIX 1

BUDGET DETAIL

PROJECT SHORT TITLE	Pacific halibut population genomics
PRINCIPAL INVESTIGATOR	Josep V. Planas
ORGANIZATION	International Pacific Halibut Commission

CATEGORIES	NPRB Year 1	NPRB Year 2	NPRB TOTAL	DESCRIPTION **Instructions:** Provide sufficient description for each line item to reconcile each amount shown. Add/remove rows as necessary. Enter amounts to the nearest whole dollar only. **Ensure all formula cells are correct before submitting.**
1. Salaries	**46,762**	**47,931**	**94,693**	**Unit effort and rate applied must be shown for each individual.**
Andrew Jasonowicz	36,277	37,184	73,461	1120 hours (7 mos.) per year are requested for Mr. Jasonowicz (at $32.39/hour, and annual inflation increase of 2.5%), to conduct sample DNA purification, library preparation, genomic data analyses, GT-seq panel development, testing and its application Tasks 3 and 4, manuscript drafting.
Josep Planas	10,485	10,747	21,232	160 hours (1 month) per year are requested for Dr. Planas (at $65.53/hour, and annual inflation increase of 2.5%), to oversee project development and ensure deliverables.
2. Fringe benfits	**15,586**	**15,975**	**31,561**	**Fringe rate applied must be shown for each individual.**
Andrew Jasonowicz	11,738	12,031	23,769	1120 hours (7 mos.) per year are requested for Mr. Jasonowicz (at $10.48/hour, and annual inflation increase of 2.5%), to conduct sample DNA purification, library preparation, genomic data analyses, GT-seq panel development, testing and its application Tasks 3 and 4, manuscript drafting.
Josep Planas	3,848	3,944	7,792	160 hours (1 month) per year are requested for Dr. Planas (at $24.05/hour, and annual inflation increase of 2.5%), to oversee project development and ensure deliverables
3. Travel	**3,100**	**3,825**	**6,925**	**NOAA approval must be obtained through NPRB PRIOR TO foreign travel on funded projects. Allow minimum of 3 months.**
Foreign	0	0	0	
	0	0	0	
Domestic	3,100	3,825	6,925	
Airfare (Seattle-Anchorage)	500	0	500	Travel to AMSS 2023 (Mr. Jasonowicz). Air travel for 1 person ($500/person)
Hotel Anchorage	450	0	450	Travel to AMSS 2023 (Mr. Jasonowicz). ($150/night x 3 nights x 1 person)
Per diem Anchorage	375	0	375	Travel to AMSS 2023 (Mr. Jasonowicz). Meals and incidentals (Department of Defense) for 1 person ($125/day x 3 days x 1 person)
Airfare (Seattle-Anchorage)	0	1,000	1,000	Travel to AMSS 2024 for 2 presenters (Mr. Jasonowicz, 1 other project participant TBD). Air travel for 2 people ($500/person)
Hotel Anchorage	0	900	900	Travel to AMSS 2024 for 2 presenters (Mr. Jasonowicz, 1 other project participant TBD). ($150/night x 3 nights x 2 people)
Per diem Anchorage	0	750	750	Travel to AMSS 2024 for 2 presenters(Mr. Jasonowicz, 1 other project participant TBD). Meals and incidentals (Department of Defense) for 2 presenters ($125/day x 3 days x 2 people)
Airfare (Seattle-Juneau)	400	0	400	Travel to Auke Bay Laboratories for GT-seq panel development (Mr. Jasonowicz). Air travel for one person ($400/person)
Hotel Juneau	750	0	750	Travel to Auke Bay Laboratories for GT-seq panel development (Mr. Jasonowicz). ($150/night x 5 days x 1 person)
Per diem Juneau	625	0	625	Travel to Auke Bay Laboratories for GT-seq panel development (Mr. Jasonowicz). Meals and incidentals (Department of Defense) ($125/day x 5 days x 1 person)
Airfare (Juneau-Seattle)	0	400	400	Travel to Seattle for project meeting (Dr. Larson). Air travel for 1 person ($400/person)
Hotel Seattle	0	400	400	Travel to Seattle for project meeting (Dr. Larson). ($200/night x 2 days x 1 person)
Per diem Seattle	0	375	375	Travel to Seattle for project meeting (Dr. Larson). Meals and incidentals (Department of Defense) ($125/day 3 days x 1 person)
4. Equipment (>$5,000)	**0**	**0**	**0**	**Individual items that fit in the 'Equipment' category usually have a cost greater than $5K and a useful life of more than 1 year.**
	0	0	0	
5. Supplies (<$5,000)	**10,100**	**16,000**	**26,100**	**Add lines for additional items or categories of items needed to complete the research project.**
Genomics reagents	7,100	6,000	13,100	Qiagen DNA purification kits (2@$1,324/kit), clean up and small fragment removal ($1,200), library construction kits for lcWGR (2@$1,008/kit) , Kappa library amplification kit ($525), Unique dual indexes set ($672), primers for GT-seq panel development and testing (600 @$10/pair)
GT-seq processing costs	0	6,000	6,000	1,500 samples @$4 per sample (as detailed in Meek and Larson, 2019)
General laboratory supplies	3,000	4,000	7,000	Pipette tips, plastic, plates, tubes, etc.
6. Contractual	**9,199**	**7,150**	**16,349**	**List each contract for individuals or businesses and what work or service will be provided.**
Sequencing costs	5,949	3,900	9,849	Novogene sequencing costs: 1. Novaseq platform at $5,949/lane; 1 lane needed to complete sequencing of 600 libraries; 2. Three lanes of HiSeq400 platform at $1,300/lane.
Cloud computing services	3,250	3,250	6,500	Images of Azure Virtual Machine Costs

BUDGET DETAIL

PROJECT SHORT TITLE	Pacific halibut population genomics
PRINCIPAL INVESTIGATOR	Josep V. Planas
ORGANIZATION	International Pacific Halibut Commission

7. Other Expenses	**150**	**300**	**450**	**Include items which may not fit into another category such as postage, shipping, honoraria.**
AMSS Registration Fees	150	300	450	Registration fees for AMSS 2023 (1 person; Jasonowicz) and AMSS 2024 (2 persons; Jasonowicz, project participant TBD)
8. Total Direct Costs	**84,897**	**91,181**	**176,078**	
9. Modified Total Direct Costs	**84,897**	**91,181**	**176,078**	**Total base amount to which indirect costs are applied.**
10. Indirect Costs	**8,489**	**9,118**	**17,607**	NPRB allows organizations without a NICRA to claim 10% of total direct costs as indirect costs. Therefore, the IPHC is requesting 10% of indirect costs.
11. TOTAL FUNDING REQUEST	**93,386**	**100,299**	**193,685**	

W170°

N57°

Central Bering Sea Fishermen's Association

P.O. Box 288 | Saint Paul Island, Alaska 99660 | Phone: 907.546.2597 | Fax: 907.546.2450 | cbsfa.com

June 10, 2021

Dr. David T. Wilson, Executive Director
International Pacific Halibut Commission
2320 West Commodore Way
Seattle, WA 98199

Dear Dr. Wilson:

Central Bering Sea Fishermen's Association (CBSFA) would like to express the support of our group and our community for the IPHC research proposal being submitted to the North Pacific Research Board entitled "Leveraging multiple genomic approaches to investigate population structure and dynamics of Pacific halibut in the northeast Pacific Ocean."

We believe this research will provide important information on stock structure and distribution of Pacific halibut to inform management of the Pacific halibut fishery.

CBSFA is the management organization for St. Paul Island under the Western Alaska Community Development Quota Program (CDQ). Through the CDQ Program, which was created in 1992, the Federal government awarded various species of fish, including Pacific halibut, from the Bering Sea and Aleutian Islands (BSAI) commercial fisheries to six CDQ groups including CBSFA. Pursuant to the CDQ Program Statute (16 U.S.C 1855(i)(1)), the CDQ groups manage these allocations to promote social and economic development in their respective regions

CBSFA is actively engaged in the directed halibut fishery in IPHC Area 4CDE (Bering Sea); in addition to fishing CDQ halibut, a number of our residents also hold halibut IFQ. From a historic, cultural, subsistence, and commercial perspective, halibut is a critically important species to the mostly Unangan (Aleut) residents of St. Paul. CBSFA has a direct interest in ensuring that Pacific halibut stocks are well understood, and equitably utilized among user groups. This includes a community and corporate commitment to reducing the use of halibut as bycatch in trawl fisheries.

CBSFA has also been closely involved in the management of halibut, and we are proud that our members have long served on the advisory panels to the IPHC, as well as on the Commission itself.

The Pacific halibut (*Hippoglossus stenolepis*) is a key flatfish species in the North Pacific Ocean ecosystem that supports important commercial, recreational and subsistence fisheries and that is managed as a single stock by the International Pacific Halibut Commission. The goal of the

present study is to advance understanding of Pacific halibut population structure and dynamics in a changing climate through the use of genomic approaches to inform fishery management. This is particularly important to the users of halibut.

IPHC seeks to improve current understanding of stock structure among spawning groups of Pacific halibut in the northeast Pacific Ocean. They plan to 1) to conduct a pilot mixed stock analysis to estimate the stock composition of commercial fishery landings from two different geographic areas in Alaska, and 2) to investigate distribution and movement patterns of Pacific halibut in the latitudinal extremes of the species' range in the northeast Pacific Ocean. The results from this study will inform on the delimitation of management units and provide preliminary information on stock composition in the Pacific halibut fishery as well as provide a tool to monitor changes in Pacific halibut distribution associated with climate change.

We are very supportive of the NPRB funding this essential research. Thank you for your consideration.

Sincerely,

Phillip Lestenkof, President
Central Bering Sea Fishermen's Association

Adak Community Development Corporation

PO Box 1943 Adak, Alaska 99546
(907) 592-2335

June 3rd 2021

Dr. David T. Wilson, Executive Director,
International Pacific Halibut Commission,
2320 West Commodore Way, Seattle, WA 98199

Re: Pacific Halibut Genomic Research

Dr. Wilson/ Josep Planas,

I am writing you today on behalf of Adak Community Development Corporation.

ACDC supports your grant application to the North Pacific Research Board (NPRB) to delineate population structure of Pacific halibut in the Gulf of Alaska, Aleutian Islands and Bering Sea with the use of genomic approaches, in partnership with the Alaska Fisheries Science

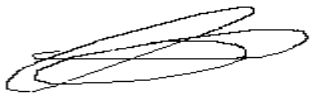
ACDC has had a long standing interest in determining whether the population of Pacific halibut in Regulatory Area 4B represents a separate component of the Pacific halibut stock, and whether it should be managed differently from the rest of the coastwide stock.

We understand that the project will include genomic analyses; and the results are expected to contribute to improved fisheries science and management policy.

ACDC supports long-term, science-based management measures and this project appears to be in alignment with that philosophy.

We wish you every success and we look forward to learning the results.

Sincerely



dave fraser
ACDC

CITY OF ADAK, ALASKA

VIA ELECTRONIC MAIL

June 3, 2021

Dr. David Wilson
Executive Director
International Pacific Halibut Commission
2320 West Commodore Way
Seattle, WA 98199

RE: Pacific Halibut Genomic Research

Dear Dr. Wilson:

On behalf of the City of Adak, Alaska I am pleased to provide a letter of support in regard to the International Pacific Halibut Commission's grant application to the North Pacific Research Board.

In conjunction with the Adak Community Development Corporation (ACDC), the community quota entity designated by the City, we have a long-standing interest in the topic of this grant application. The results of this project, to delineate population structure of Pacific Halibut are necessary in this time of reduced biomass. The City is very interested in the objectives related to Regulatory Area 4B as we support ACDC and other's view that the population of Pacific halibut in the area represents a separate component of the stock. The results, substantiated by research, could have significant management impacts to not only our area, but to the way the stock is overall managed.

Similar to ACDC, the City is very supportive of long-term, science based management measures as we both operate with future generations in mind. This project appears to be aligned with that viewpoint and as such is something we can support.

Please reach out if we can be of assistance as this project advances and we look forward to the results of the study.

Sincerely,

Layton J. Lockett
City Manager

CITY OF ADAK, ALASKA
100 Mechanical Street, Suite B122 • Adak, Alaska 99546
Post Office Box 2011 • Adak, Alaska 99546 • Tel: 907.592.4500 • Fax: 907.592.4262
www.adak-ak.us

Humboldt Area Saltwater Anglers Inc.
P.O. Box 6191, Eureka, CA 95502
Email: hasa6191@gmail.com
FEIN #61-1575751

19 May 2021

Dear NPRB Review Board:

Humboldt Area Saltwater Anglers, Inc. (HASA) is a 501(c)(4) recreational sport fishing group based in northwest California with over 300 members. We have represented saltwater anglers since 2008. We have been actively engaged in saltwater sportfish management over the years, with the goal of providing a long-term sustainable saltwater fishery for our current constituents and future generations. HASA continues to support important science and economic studies to better inform Pacific halibut management in California. The Pacific halibut fishery off the Northern California coast is an increasingly important component of our overall fishery resource.

Accordingly, we would like to express our support for the proposed research project studying Pacific halibut population genomics in the northeast Pacific Ocean. This project has the potential to help us understand the origins of Pacific halibut caught off the Northern California coast and whether they are closely related to the Pacific halibut found in more northern waters. We believe this is important to understand and would directly impact sustainable management decisions related to Pacific halibut.

Thank you for your consideration.

Sincerely,

Larry De Ridder

Larry De Ridder, President
Humboldt Area Saltwater Anglers, Inc.

Criteria

- Fields of Expertise
    - Biological Science
        - Genetics
        - Population Biology
    - Socio/Economic
        - Resource Management
- Professional Activity
    - Field Research & Data Collection
    - Research Program Administration
    - Fishery Management
    - Laboratory Research
- Ecosystems
    - Marine – Benthic
- Ecosystem Components
    - Fish
        - Species Groups
            - Halibut
        - Specific Research Issues
            - Population Structure, Dynamics, & Modeling
            - Genetics and Stock Identification
            - Distribution and Abundance
- Geographic Regions
    - Bering Sea
    - Aleutian Islands
    - Gulf of Alaska
- Technological Expertise/Lab Methods
    - Laboratory Methods
        - Genetic Analysis
- Modeling
    - Modeling method(s)
        - Inference (i.e. function fitting, Bayesian)
    - Modeling type(s)
        - Population
        - Distribution
- Management/Policy/Social
    - Harvest Strategies
    - Commercial Fisheries
    - Coastal Management
    - International Fisheries

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North Pacific Research Board Policy
Compliance with Subaward Agreements

(Adopted March 2009 and revised September 2021)

Purpose

The North Pacific Research Board (NPRB) supports marine research activities in the North Pacific based on highly competitive requests for proposals. Projects are funded through NPRB subawards with subrecipients who agree to comply with subaward provisions and all applicable federal laws and perform the work in the research plan (Statement of Work). The research plan is the primary basis for selecting proposals by NPRB. It identifies hypotheses, conceptual approach, experimental design, and timelines and measurable milestones used to monitor progress based on periodic financial reports, semi-annual progress reports, and a final report. When approved and subsequently attached as an Appendix 1 to the subaward, it becomes the primary basis for evaluating success or failure of the project.

In funding many research projects at institutions across the U.S. and beyond since 2002, NPRB has been fortunate to have supported many very capable principal investigators who have managed their projects successfully. The Board wishes to maintain that high success rate and intends to continue working closely with subrecipients toward successful completion of individual projects.

There are, however, the rare occasions when a project is not progressing satisfactorily. This may happen for a variety of legitimate reasons, for example, bad weather, absence of animals, equipment failures in remote locations, natural disasters, or other factors that may be outside the control of the principal investigators. NPRB fully understands there is risk inherent in conducting scientific research, especially in remote locations, and intends to work closely with subrecipients to bring about a reasonable and acceptable conclusion to those projects.

The procedures herein cover such inadvertence, but this policy is aimed more squarely at situations where principal investigators diverge from their research plan, fail to manage, or report properly, or fail to meet other subaward provisions, without prior approval of NPRB. This policy describes steps that NPRB will take to address such deficiencies. Its provisions are derived mainly from a close reading of the Code of Federal Regulations Title 2, Part 200, Subpart D (2 CFR 200), the NOAA Research Terms and Conditions Overlay to the Uniform Administrate Requirements, Cost Principles, and Audit Requirements for Federal Awards, and the US Department of Commerce Financial Assistance Standard Terms and Conditions (DOC). Part 180 – OMB Guidelines on Government wide Debarment and Suspension also is referenced.

Guiding Principles

In general, NPRB will strive to adhere to two guiding principles in taking steps to resolve issues that may arise with research projects. The first guiding principle will be to identify performance problems as early as possible so the subrecipient, working with NPRB, has the opportunity to resolve problems before the situation worsens. NPRB will review progress reports to assess performance. It must be noted, however, that NPRB does not have the primary responsibility for detecting emerging issues. 2 CFR §200.329 (e) requires subrecipients to immediately notify NPRB, as the awarding agency in this case, of developments that have a significant impact on the subaward-supported activities, including any problems, delays, or adverse conditions which may materially impair the ability to meet the objectives of the subaward.

The second guiding principle will be to strive to resolve problems at the lowest point of potential failure, normally at the principal investigator level. Working with the principal investigators, and then the grants managers as appropriate, NPRB will strive to resolve issues at the staff level before elevating the situation to higher authority at the subrecipient or NPRB, as provided for in this policy.

Non-compliance

In agreeing to the subaward provisions, the subrecipient accepts full responsibility for managing and monitoring its NPRB-funded project to a successful conclusion (§200.329 (a)). Subrecipients must report performance in accordance with subaward provisions, which at a minimum, require brief information on each of the following: a comparison of actual accomplishments to stated goals and objectives, research findings and quantitative data as appropriate, reasons why established goals were not met, if appropriate, and any cost overruns (§200.329 (c.2.iii)). It has been NPRB's experience that when problems occur, they generally involve: (1) incomplete or late finance, progress, and final reports; (2) non-achievement of objectives or milestones or pursuit of new ones without prior approval; or (3) incomplete reporting of data or metadata. These problems, as well as any other occasion when subaward provisions are not followed without prior approval of NPRB, may be viewed as instances of non-compliance.

Problem Resolution

Successful completion of individual research projects is of paramount importance. NPRB will proceed in good faith to work with recipients and their respective principal investigators and grants managers to resolve potential issues early and at the lowest level necessary in accordance with the two guiding principles stated above. To facilitate resolution, subrecipients are reminded that they are required to:

- Report deviations from budget and program plans and request prior NPRB approval for any change in scope or objective, even if there is no associated budget revision (§200.308(b)).
- Immediately notify NPRB of any development that may significantly impact their subaward supported activities, particularly problems, delays, or adverse conditions which may materially impair the ability to meet their objectives and milestones. The notification must describe the action taken or contemplated and any assistance needed to resolve the situation (§200.329(e)).

<u>Staff Resolution</u>

Problems and issues will be resolved to the extent possible through communication between NPRB Program staff and the principal investigators. If the issue cannot be resolved, the NPRB Executive Director will review the situation and notify the subrecipient, normally through the grants manager, in writing of the circumstances, the nature of the problem, citing the specific deficiency, and the status and outcomes of direct negotiation with the principal investigators to date. A copy of the written communication will be provided to the principal investigator(s). The subrecipient will be requested to respond in writing within 30 calendar days of the date of such communication, describing the steps and schedule for correcting the deficiency (§200.332 (c.2)). If the prospective actions are deemed satisfactory by the Executive Director, the grants manager will be notified of that decision in writing.

Elevation to NPRB

If deficiencies remain unresolved, or the subrecipient has not provided a satisfactory response within the 30-day period or requests to elevate the decision to the Board, the Executive Director will refer the matter in a written report to the NPRB Executive Committee. The report will present the facts as understood, describe the situation and deficiencies, provide responses from the subrecipient, and recommend remedial action as appropriate.

The subrecipient will be notified in writing of this elevation. Upon notification, the subrecipient will have up to 15 calendar days to provide additional information. The NPRB Executive Committee then will review the report and any additional information and take action as appropriate. All actions will be taken by unanimous vote of the members eligible to vote in accordance with NPRB recusal policies. Following a decision, the NPRB Executive Committee will formally notify the subrecipient by certified mail, with copies to the principal investigator(s). The full Board will be informed of the actions taken at their next regularly scheduled meeting.

Mediation

If the above procedures fail to resolve the situation, NPRB or the subaward recipient may request formal mediation. In that event, the subaward recipient and NPRB agree to participate in at least two hours of mediation with an independent, professional mediator, with both parties agreeing to share equally in the costs of the mediation. The costs will not include costs incurred by a party for representation by counsel at the mediation. Mediation involves each side of the dispute sitting down with an impartial person, the mediator, to attempt to reach a voluntary settlement. Mediation involves no formal court procedures or rules of evidence, and the mediator does not have the power to render a binding decision or force an agreement on the parties.

Suspension without Prior Notice

NPRB may temporarily withdraw its sponsorship under a subaward, pending corrective action by the subrecipient or a decision to terminate the subaward, if the subrecipient has failed to comply with the project objectives, the terms and conditions of the subaward, or reporting requirements (§200.339 (d)). Action by NPRB to suspend an award normally will be taken only after the grants manager has been informed by NPRB of the proposed action and provided an opportunity for hearing, appeal, or other administrative proceeding to which the subrecipient is entitled (§200.342) or the steps described above have been taken, and there has been an opportunity to correct the problem(s).

The Executive Director may immediately suspend a subaward without prior notice when it is believed that such action is reasonable to protect the interests of NPRB and the federal government. No costs incurred during a suspension period will be allowable, except those costs approved by NPRB in the suspension notice, or which, in the opinion of NPRB, are necessary and not reasonably avoidable (§200.343).

The Executive Director then will send a follow-up notice of suspension to the subrecipient (normally the grants manager), with a copy to the principal investigator(s), setting forth the reasons for suspension and its effective date. The NPRB Executive Director will inform the NPRB Executive Committee of any such action and provide a written report fully describing the situation, the need for immediate suspension, and

the conditions under which the suspension may be lifted. The NPRB Executive Committee will meet as appropriate to determine the next steps for resolving the situation.

Remedies

After carefully reviewing the situation and responses from the subrecipient, NPRB will consider taking action as appropriate. NPRB may impose temporary special subaward conditions in accordance with §200.339. These actions include:

1. Temporarily withhold cash payments pending correction of the deficiency.
2. Disallow all or part of the cost of the activity or action not in compliance.
3. Wholly or partly suspend or terminate the current award.
4. Recommend the suspension or debarment as authorized under 2 CFR part 180 to the Federal awarding agency.
5. Withhold further awards for the project or program.
6. Take other remedies that may be legally available.

NPRB also may prohibit participation by an individual as a principal investigator, co-investigator or collaborator on new projects for a specified time and under specified conditions until problems are deemed to be resolved by NPRB. Failure to provide required reports within the period specified in the subaward could delay NPRB review and processing of pending proposals for all identified principal investigators and co-PIs on a given subaward. NPRB also may call for a full audit of expenses for the subaward in question and other subawards to the institution as appropriate.

Remedial actions will stay in effect until all issues identified in writing have been fully resolved to the satisfaction of NPRB. NPRB reserves the right to terminate a subaward if it has attempted to resolve issues under the guidance provided in this policy but has failed to do so. In cases of termination, NPRB will adhere closely to requirements set out in §200.340.

Research Misconduct

Research misconduct means fabrication, falsification, or plagiarism in proposing or performing research funded by NPRB, reviewing research proposals submitted to NPRB, or in reporting research results funded by NPRB. In determining if misconduct has occurred and is taking action, NPRB will adhere as closely as possible to procedures described in the Administrative Standard Award Conditions for the National Oceanic and Atmospheric Administration Financial Assistance Awards U.S. Department of Commerce for investigating scientific integrity or scientific and research misconduct.

Debarment and Suspension

This policy does not refer to debarment or suspension as covered by Part 180 – OMB Guidelines to Agencies on Government-wide Debarment and Suspension (Non-procurement), in Federal regulations at 70 FR 51865, August 31, 2005, and Executive Orders 12549 and 12689. Under those regulations, certain parties who are debarred, suspended or otherwise excluded may not be participants or principals in Federal assistance awards and subawards, and in certain contracts under those awards and subawards (§200.332 (d.4)). NPRB is not defined as a Federal agency pursuant to §180.15, and thus can only make recommendations to the Secretary of Commerce regarding debarment and suspension. The above

procedures and remedies do not preclude a subrecipient from being subject to debarment and suspension.

Notification

This policy was approved by NPRB on March 2, 2009 and revised on Sept 22, 2021. Subrecipients will be notified of this policy during each NPRB request for proposals and must acknowledge and agree to it when accepting subawards. Current and past subawards are covered by their subaward provisions and all applicable Federal law.

Appendix 3 to NPRB Agreement

NPRB Financial Reporting Form

NPRB Project #: 2110

Fiscal Agent Project #: F9110-00

Date of Invoice:

Institution Project #:

Institution Name: International Pacific Halibut Commission

Remittance Address: 2320 West Commodore Way, Suite 300, Seattle, WA 98199

Invoicing Contact Info: **Name:** Keith Jernigan **Phone:** 206-624-1838

Email: secretariat@iphc.int

Project Title: Leveraging multiple genomic approaches to investigate population structure and dynamics of Pacific halibut

Principal Investigator(s): Dr. Josep V Planas - josep.planas@iphc.int

Period of Performance: 12/1/21 **to** 1/31/24

This Invoice Period: **to**

Current Invoice Details:

Cost Categories	Approved funds by category	Previously reported expenses	Expenses this invoice	Cumulative expenses with this invoice	Total funds remaining after this invoice
a. Personnel Salaries	$ 94,693.00	$ -	$ -	$ -	$ 94,693.00
b. Fringe Benefits	$ 31,561.00	$ -	$ -	$ -	$ 31,561.00
c. Travel	$ 6,925.00	$ -	$ -	$ -	$ 6,925.00
d. Equipment	$ -	$ -	$ -	$ -	$ -
e. Supplies	$ 26,100.00	$ -	$ -	$ -	$ 26,100.00
f. Contractual / Consultants	$ 16,349.00	$ -	$ -	$ -	$ 16,349.00
h. Other	$ 450.00	$ -	$ -	$ -	$ 450.00
i. Total Direct Charges	$ 176,078.00	$ -	$ -	$ -	$ 176,078.00
j. Indirect - 10%	$ 17,607.00	$ -	$ -	$ -	$ 17,607.00
k. TOTAL COSTS	$ 193,685.00	$ -	$ -	$ -	$ 193,685.00

Signed: **Dated:**

Subaward Details

Indirect Rate: 10% (MTDC = $176,078)

MTDC Exclusions: None

Connected to Other Subawards: None

Notes: None

Submission Instructions:

1. Please sign and email a PDF version of this form with appropriate backup to: grants-contracts@alaskasealife.org

2. Submission of a properly completed NPRB Financial Reporting Form for expenses incurred during each calendar quarter is due by the following deadlines:

Expenses Incurred During Calendar Quarter	Deadline for Submission
October 1 - December 31	January 31
January 1 - March 31	April 30
April 1 - June 30	July 31
July 1 - September 30	October 31

3. Please refer to section 3 of the NPRB subaward agreement or Appendix 2 NPRB compliance policy for more information on billing and allowable costs.

(Form Revised 2021)

Invoice Notes:

NPRB Fiscal Agent Use:

a.	5115	F9110-00	$ -
b.	5315	F9110-00	$ -
c.	5790	F9110-00	$ -
d.	6510	F9110-00	$ -
e.	6110	F9110-00	$ -
f.	7120	F9110-00	$ -
h.	8190	F9110-00	$ -
j.	9210	F9110-00	$ -
			$ -

FFATA Requirements for Subawards

New subawards from the North Pacific Research Board (NPRB) are subject to pre-award reporting requirements based on the implementation of the Federal Funding Accountability and Transparency Act of 2006 (FFATA). The Alaska SeaLife Center, fiscal agent for NPRB, is required to report information about all first-tier subawards, including executive compensation information for certain subaward recipients. Please provide the following information so that we can proceed with processing subawards to your organization.

NPRB Project Number: 2010 (F9110-00) Award Amount: $193,685

Project Title: Leveraging multiple genomic approaches to investigate population structure and dynamics of Pacific halibut

Legal Name of Subrecipient: International Pacific Halibut Commission

DUNS Number of Subrecipient: 088726997 (UEI: TWG2J3J9GQN1)

Principal Place of Performance (POP): IPHC

POP City: Seattle POP State: WA POP Zip+4: 98199-1287

POP Country: US POP Congressional District: 7th

In your preceding completed fiscal year, did the organization associated with this DUNS number receive:

- 80 percent or more of its annual gross revenues in U.S. federal contracts, subcontracts, loans, grants, subgrants, and/or cooperative agreements?

-AND-

- $25,000,000 or more in annual gross revenues from U.S. federal contracts, subcontracts, loans, grants, subgrants, and/or cooperative agreements?

Yes _____ No ✔ If **NO**, stop here, sign the form and return to us.

If **YES**, does the public have access to information about the compensation of the executives in your organization through periodic reports filed under section 13(a) or 15(d) of the Securities Exchange Act of 1934 (15 U.S.C. 78m(a), 78o(d)) or section 6104 of the Internal Revenue Code of 1986?

Yes _____ No _____ If **YES**, stop here, sign the form and return to us.

If **NO**, complete the compensation information on the second page of this form, sign the form and return to us.

Please return the completed form to grants-contracts@alaskasealife.org, fax to 907-224-6320, or mail to Grants & Contracts, Alaska SeaLife Center, P.O. Box 1329, Seward AK 99664-1329.

I certify that the information provided on this form is correct for the organization I represent.

Signature: David T. Wilson Date: 12/01/2021

Printed Name: Dr. David T. Wilson Title: Executive Director

Address: 2320 West Commodore Way, SEattle WA 98199

Phone: 206-6341838 Email: secretariat@iphc.int

FOR NRPB/ASLC USE ONLY					
Date of Award Execution:		**FFATA Report Month:**		**Date submitted in FSRS:**	

If the previous page indicated that compensation information is required, please complete the table below with the names and total compensation for the five most highly compensated executives in your organization. "Executive" means officers, managing partners, or any other employees in management positions.

Your organization is defined as the legal entity to which the DUNS number on this form belongs.

Compensation should be for the preceding completed fiscal year in US whole dollars. Total compensation means the cash and noncash dollar value earned by the executive during the recipient's or subrecipient's preceding fiscal year and includes the following (for more information see 17 CFR 229.402(c)(2)):

i. Salary and bonus.
ii. Awards of stock, stock options, and stock appreciation rights. Use the dollar amount recognized for financial statement reporting purposes with respect to the fiscal year in accordance with the Statement of Financial Accounting Standards No. 123 (Revised 2004) (FAS 123R), Shared Based Payments.
iii. Earnings for services under non-equity incentive plans. This does not include group life, health, hospitalization or medical reimbursement plans that do not discriminate in favor of executives, and are available generally to all salaried employees.
iv. Change in pension value. This is the change in present value of defined benefit and actuarial pension plans.
v. Above-market earnings on deferred compensation which is not tax-qualified.
vi. Other compensation, if the aggregate value of all such other compensation (e.g. severance, termination payments, value of life insurance paid on behalf of the employee, perquisites or property) for the executive exceeds $10,000.

	Name	**Total Compensation Amount**
1		$
2		$
3		$
4		$
5		$

Form Rev. September 2013