

The background of the slide is a composite image. On the left, a large catfish is shown in mid-air, its mouth open and hooked by a metal wire. The fish is dark with a lighter underbelly. On the right, a gloved hand in a blue nitrile glove holds a long, thin metal rod. Below the hand, a white cylindrical water sampling device is visible, angled downwards. The entire scene is set against a backdrop of blue water and distant hills under a clear sky.

Biological and Ecosystem Science Program :

Current and Future Research Activities

**SRB Meeting
June 21, 2016**

Josep V. Planas
Program Manager

Personal background

- **Personal information:**

- Born in Barcelona, Spain (Spanish citizen)

- **Education:**

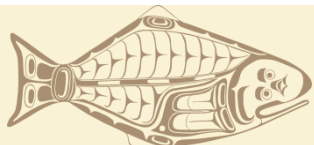
- BSc in Biology, University of Barcelona, Spain (1984)
- MA in Zoology, University of California, Berkeley (1988)
- PhD in Biology, University of Barcelona, Spain (1989)
- PhD in Fisheries, University of Washington, Seattle (1993)



- **Professional experience:**

- Postdoctoral Fellow, University of Washington, Seattle (1993-1996)
- Postdoctoral Fellow, University of Barcelona, Spain (1996-1998)
- Assistant Professor, University of Barcelona, Spain (1998-2001)
- Associate Professor, University of Barcelona, Spain (2001- 2015)

- **Expertise in fish physiology and genomics**

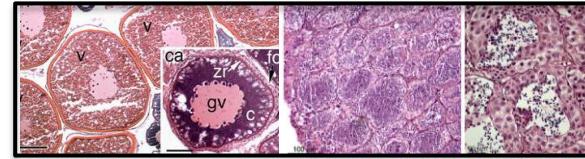


Personal background

Scientific areas of expertise in fish biology:

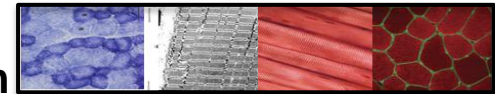
- *Reproductive physiology*

- Gametogenesis
- Final maturation and ovulation



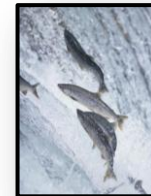
- *Growth and metabolism*

- Regulation of carbohydrate and lipid metabolism
- Muscle growth characteristics



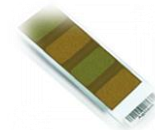
- *Swimming physiology*

- Skeletal and cardiac muscle adaptations
- Swimming performance



- *Fish genomics*

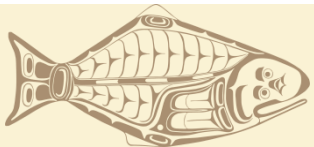
- Development of genomic resources for flatfish
- Application of genomic tools to flatfish biology



Biological research activities at IPHC



- **What are the current objectives?**
 - Identify and address critical knowledge gaps in the biology of the Pacific halibut
 - Understand the influence of environmental conditions on halibut biology
 - Apply resulting knowledge to reduce uncertainty in current stock assessment models
- **What have been traditionally the main research activities at IPHC?**
 - Migration. Adult movement across regulatory areas and to identify spawning grounds.
 - Size and age structure of the population by body measurements and otolith ageing.
 - Oceanographic monitoring.



Current biological research activities

Reproduction

NEW

Gonadal staging

Sex identification:

Commercial marking

NEW

Genetic reproductive markers

NEW

Genetic sexing

NEW

NEW IN
2016

Migration

Archival tags

PAT tags

Wire tags

Early Life History

NEW

Growth-age models
(Increment data)

Genetic growth markers

NEW

Condition factor development

NEW

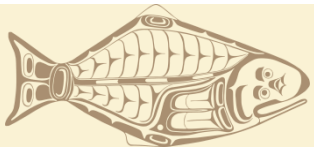
Growth

Oceanographic monitoring

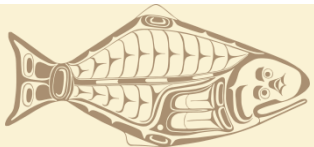
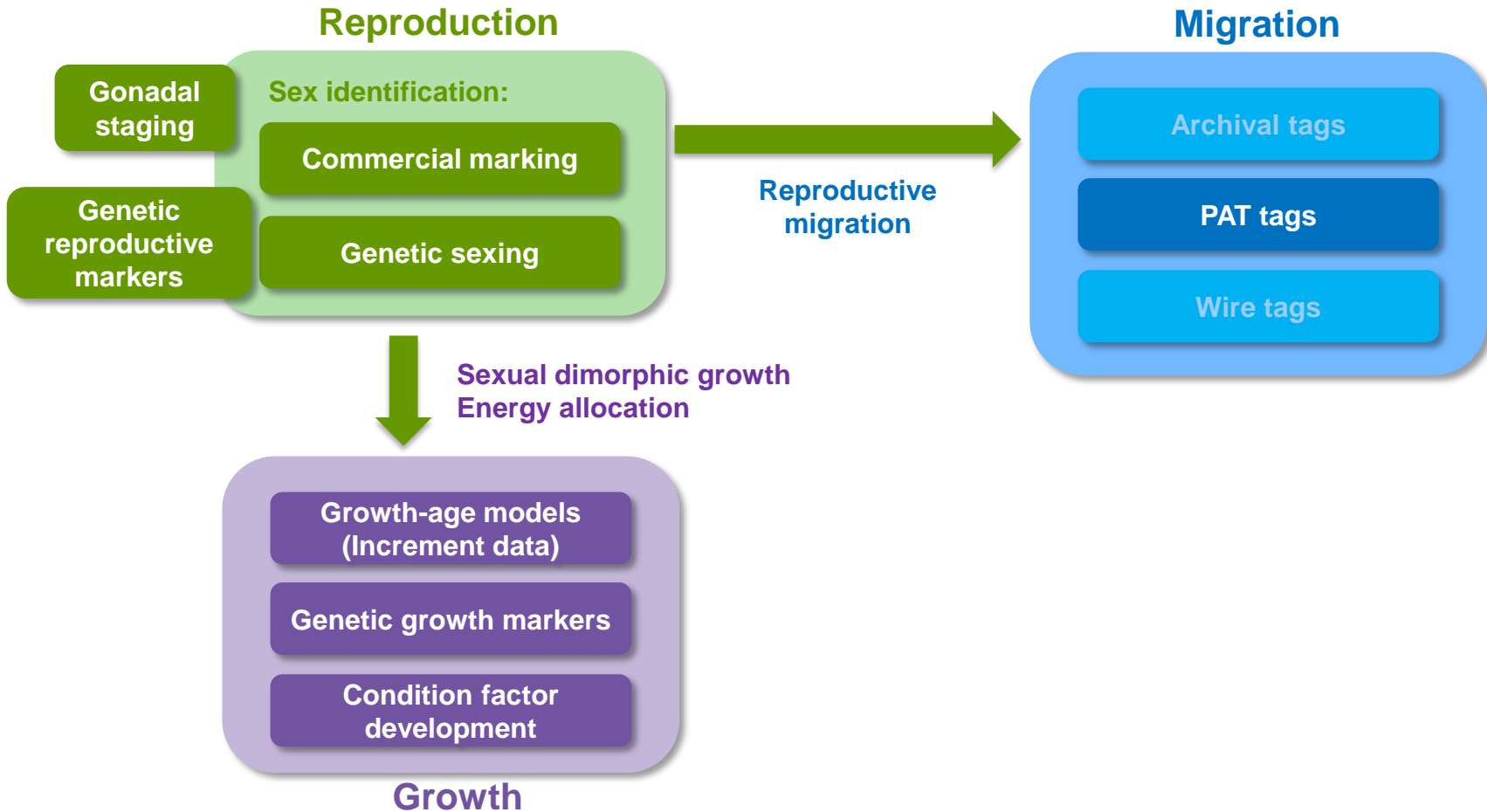
Mercury contamination

Ichthyophorus infection

Oceanographic/environmental monitoring and effects



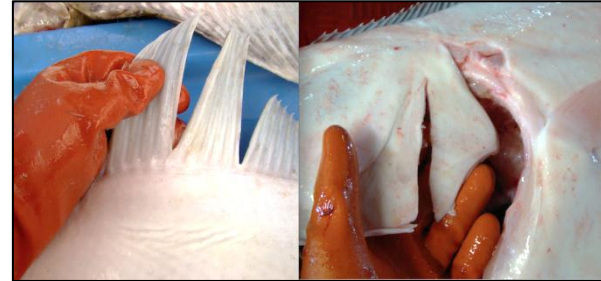
Reproduction studies



Reproduction: ongoing studies

- We need to know the sex of extracted fish

- Commercial marking at sea

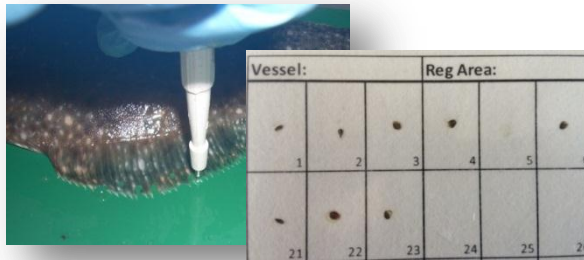


Dorsal Cut (Female) Gill Plate Cut (Male)

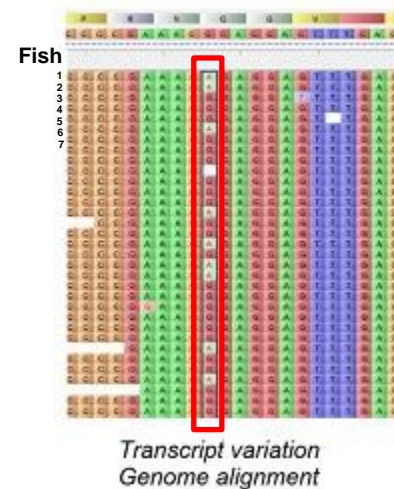
Ongoing

- Identification of genetic markers for sex: **Single Nucleotide Polymorphisms (SNPs)**

Fin clips



→ DNA extraction → DNA sequencing



Ongoing

**We are mining for SNPs associated with sex
(male vs female genetic signatures)**



Reproduction: ongoing studies

Gonadal staging

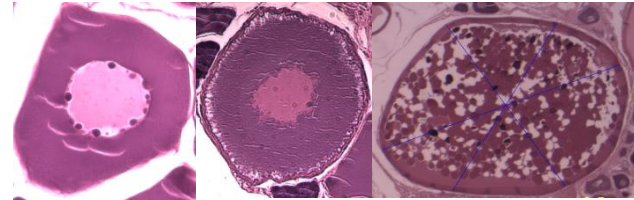
Sex identification:

Commercial marking

Genetic reproductive markers

Genetic sexing

- Pilot study on ovarian staging: summer and winter samples



Ongoing

- Identification of *molecular markers* of ovarian and testicular function

- Identification of sex marker genes
- Identification of maturation marker genes



RNA sequencing

Ongoing

3. De novo Transcriptome Assembly Stats

Sample ID	Total trinity 'genes'	Total trinity transcripts	Percent GC	Contig N50	Median contig length	Average contig	Total assembled bases
R116-pool3	48,573	60,084	48.89	2,494	582	1,240.16	74,513,854
R116-pool4	74,363	87,644	47.10	2,004	489	1,014.53	88,917,698

OVARY
TESTIS

5.1 Mapping statistics

Sample ID	Danio rerio	uniprot	est others	total	unmapped	Danio%	uniprot%	est others%	unmapped%
R116-pool3	18,426	4,259	37,267	60,084	132	30.67%	7.09%	62.02%	0.22%
R116-pool4	23,644	5,539	58,303	87,644	158	26.98%	6.32%	66.52%	0.18%

OVARY
TESTIS



Reproduction: proposed studies

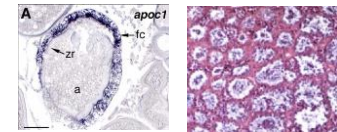
There are important knowledge gaps on the reproductive biology of the species

- Knowledge on reproductive development, maturation, fecundity, sex determination, environmental and hormonal control of reproduction, etc.
- Scientific-based criteria to identify reproductive status and potential.
- Updated estimates of age and size at maturation.
- Information on skipped spawning.

1. Characterization of the annual reproductive cycle

Objective: Understand temporal changes in reproductive development throughout an entire annual reproductive cycle.

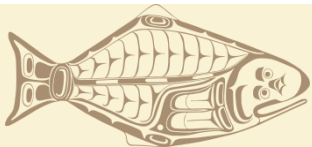
- Histological assessment of gonadal development and maturation.
- Hormonal profiling (blood sex steroids) of the reproductive cycle.
- Gene expression (transcriptome) profiling of the reproductive axis.
- Gonadosomatic index (GSI) determinations throughout the reproductive cycle.
- Ultrasound monitoring of gonadal development and maturation.



2. Sex determination mechanisms

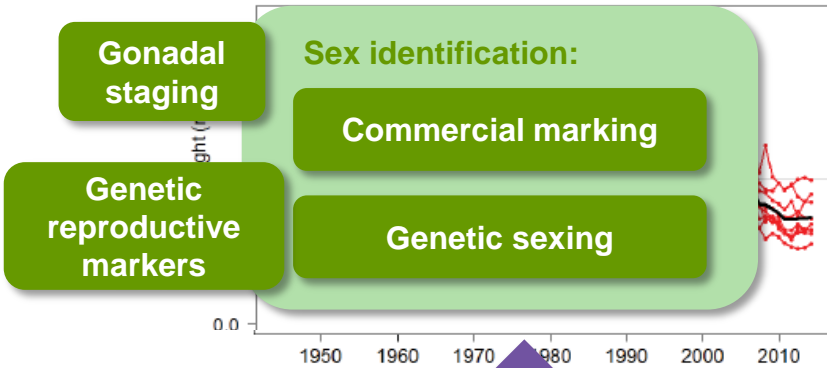
Objective: Understand the sex determination mechanism(s) in Pacific halibut.

- Identification of sex determining mechanism(s) and its onset during early development.
- Identification of environmental influences (temperature) on sex determination.
- Evaluate possible consequences on sex ratios at the population level.

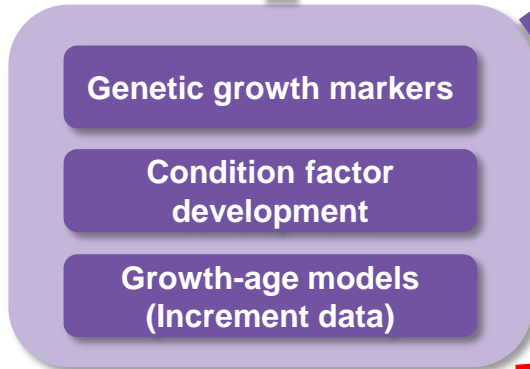


Growth studies

Reproduction



Reproductive performance
Skipped spawning



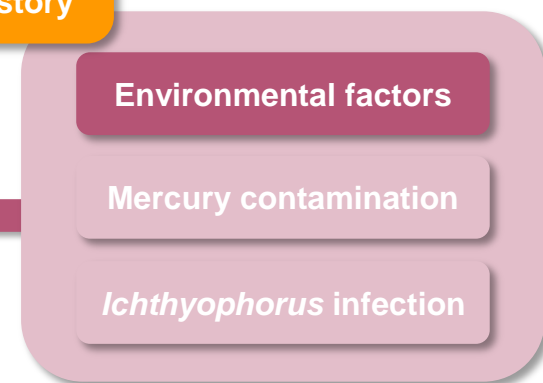
Growth

Fitness

Migration



Early Life History



Other factors:
Density, resource competition, etc

Oceanographic/environmental monitoring and effects



Growth studies: ongoing studies

- Identification of *molecular markers* for growth



RNA sequencing

Ongoing

3. De novo Transcriptome Assembly Stats

Sample ID	Total trinity 'genes'	Total trinity transcripts	Percent GC	Contig N50	Median contig length	Average contig	Total assembled bases
R116-pool1	37,161	39,638	47.76	1,198	385	721.49	28,598,382
R116-pool2	38,143	40,814	46.02	1,096	398	691.85	28,237,340
R116-pool5	70,693	86,561	47.17	2,104	495	1,051.87	91,050,930

WHITE MUSCLE
LIVER
RED MUSCLE

5.1 Mapping statistics

Sample ID	Danio rerio	uniprot	est others	total	unmapped	Danio%	uniprot%	est others%	unmapped%
R116-pool1	13,873	2,661	23,066	39,638	38	35.00%	6.71%	58.19%	0.10%
R116-pool2	13,233	2,547	24,998	40,814	36	32.42%	6.24%	61.25%	0.09%
R116-pool5	25,341	5,579	55,466	86,561	175	29.28%	6.45%	64.08%	0.20%

WHITE MUSCLE
LIVER
RED MUSCLE

- *Condition factor* development: comprehensive set of measures on the physiological condition of fish

- Length/weight relationships (Fulton's k, etc.).
- Morphometric/shape analyses.
- Energy levels (fat content, metabolite levels, energy-sensing molecules).
- Assessment of muscle quality characteristics (muscle fiber composition).



Genetic growth markers

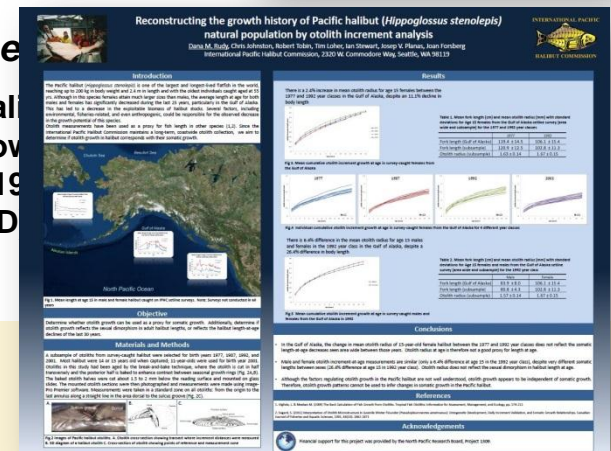
Condition factor development

Growth-age models (Increment data)

Growth

- *Otolith growth increment*

- Assessment of the value as a proxy for somatic growth classes (1977, 1987, 1997) areas (2B, 3A and 4CD)



Growth: proposed studies

Little is known regarding what factors influence growth in this species

- Knowledge on growth processes and environmental effects.
- Improved understanding in the possible role of growth alterations in the observed decrease in size at age.

1. Extensive catalogue of molecular markers for growth

Objective: Identify and validate molecular growth-related markers for growth studies.

- Identification of expressed sequences from skeletal muscle (white and red) and liver.
- Develop molecular assays to quantify gene expression of growth markers in relevant tissues.

2. Evaluation of growth patterns and effects of environmental influences

Objective: Identify molecular and biochemical profiles characteristic of specific growth patterns and evaluate potential effects of environmental influences.

- Evaluation of different growth trajectories in the wild.

In BS NMFS trawl survey in 2016:

- - 75 fish <40 cm length
- - 75 fish 40-60 cm length
- - 75 fish 60-80 cm length



Characterization of molecular and biochemical growth markers in liver and muscle samples from age-matched individuals

- Establishment of different growth trajectories in juvenile fish in captivity.

- *Feeding/fasting*

Fed



Fasted



- *Manipulating growth rates (ration, density, the compensation, etc.)*

Low rate



Normal rate

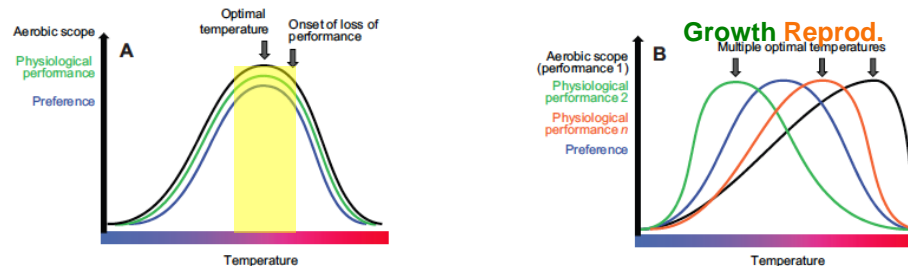


Growth: proposed studies

2. Evaluation of growth patterns and effects of environmental influences (cont.)

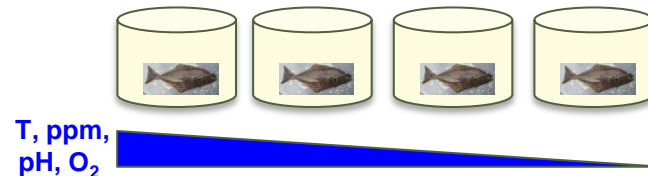
- Understand the basis of the **sexual dimorphic growth** in the Pacific halibut.
- Investigate the effects of **environmental factors** on growth performance.
 - Effects of **temperature, salinity, dissolved oxygen and water pH** on growth.
 - Identify the optimal environmental conditions for growth.

- e.g. Temperature:**
- Is there a relationship between growth rates and T changes?
 - What is the **optimal T range** for growth?
 - What is the relationship between **aerobic scope**, temperature and optimal growth?



- Is growth affected by changes in salinity, dissolved O₂ (hypoxia), water pH?

a) Evaluate growth after exposure to different environmental conditions



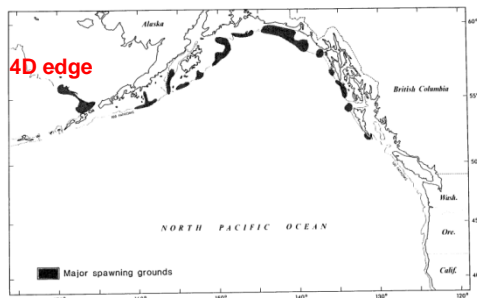
b) In the wild, correlate size at age with environmental levels and individual history



Migration: ongoing studies

- **Adult migration studied by tagging**

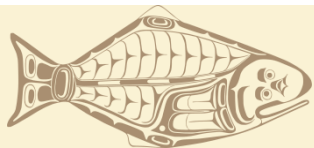
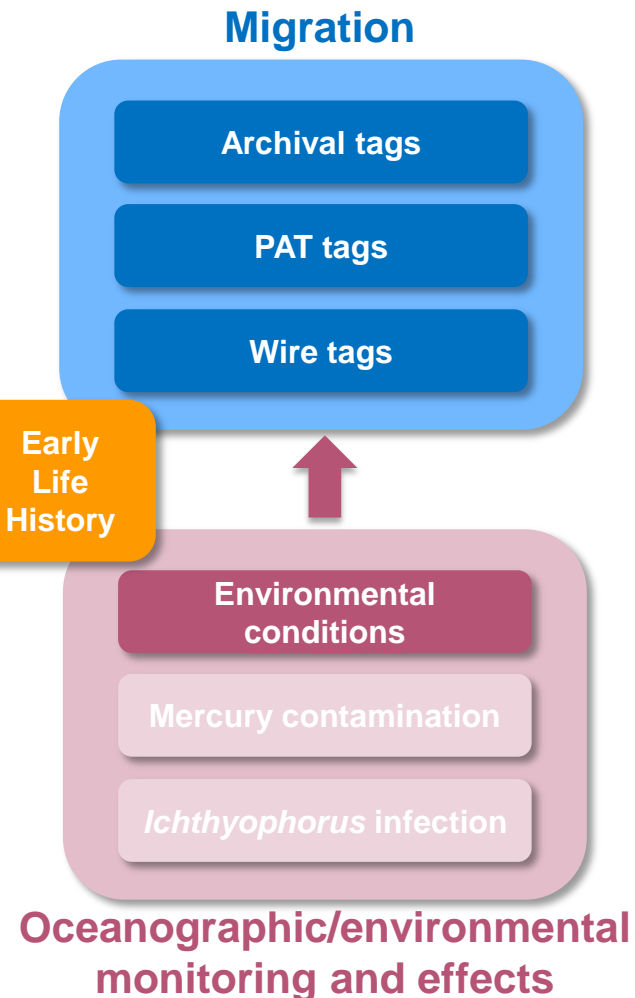
- Wire tags
- PAT satellite tags



June-July 2016: 32 females
(16 ♀ 1 year release program)
(16 ♀ 3 month release program)

- **Bycatch survival as assessed by accelerometer tags**

June-July 2016: 100 fish (60 day release program)



Migration: proposed studies

- Improve our understanding on larval, juvenile and reproductive migration patterns.
- Incorporate additional sources of biological information on migratory patterns.

1. Towards a more comprehensive view on migration

Objective: Combine current tagging efforts with genetic and otolith and tissue composition analyses.

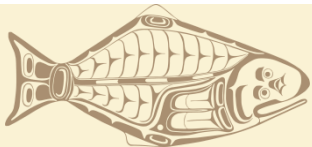
- Collect fin clips for genetic analyses on migration patterns and individual origin determination.
- Otolith microchemical and stable isotope analyses and tissue stable isotope analyses.
- Reproductive monitoring of PAT-tagged adult females: blood endocrine reproductive parameters, ovarian tissue biopsies and ultrasound for ovarian staging.

2. Larval migration and connectivity

Objective: Understand the mechanisms of larval connectivity between the GOA and the BS.

- Collect data from the NMFS ichthyoplankton survey and map larval distribution over time and space.
- Collect larval samples from the survey to conduct genetic analyses.

Collaboration with Janet Duffy-Anderson (NOAA, AFSC)



Migration: proposed studies

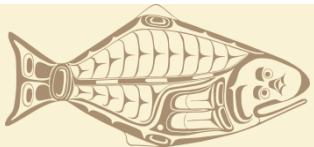
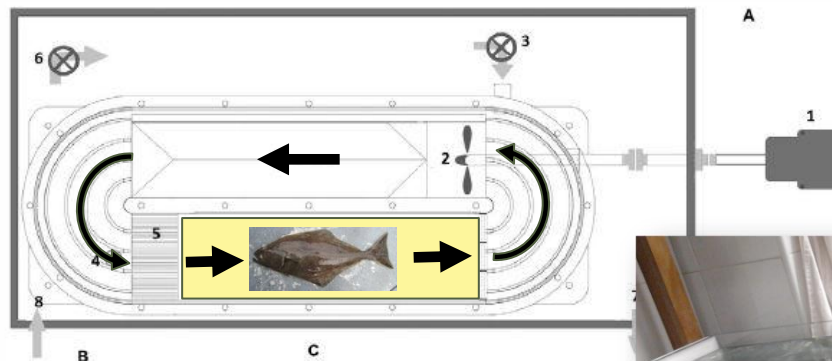
3. Swimming and migratory performance

Objective: Evaluate swimming and migratory performance of juvenile Pacific halibut by swim testing.

Measure of fitness

- Swimming capacity (optimal or maximal sustainable swimming speed; U_{opt} , U_{max}).
- Aerobic scope (respirometry/ O_2 consumption): measure of aerobic performance.
- Biochemical, cellular and molecular indicators of swimming performance in skeletal and cardiac muscle
- Drag effects of PATs.

Swim tunnel:



Genetics and genomics: proposed studies

- Improve our knowledge on the genetic composition of the population
- Establish genomic resources for the species

1. Population genetic studies

Objective: Genetic characterization of Pacific halibut throughout its distribution range

- Characterization of population structure by RAD sequencing and SNP analysis.
- Identification of genetic signatures of geographical population groups

2. Sequencing of the Pacific halibut genome

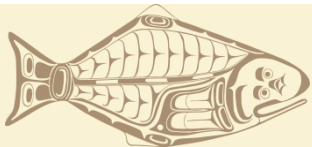
Objective: Genome sequencing at sufficient coverage

- Identify genomic regions and genes responsible for temporal and spatial adaptive characteristics.
- Genome-wide association studies to try to understand the genetic basis of growth, reproductive performance, migratory behaviour and performance, etc.
- Provide genomic resolution to genetic markers (from RAD tag seq or RNAseq).
- Link genotype and phenotype.
- Identify genetic, evolutionary changes in response to environmental and anthropogenic influences.
- Eco-evolutionary dynamics. Spatio-temporal population genomics.

3. Characterization of the Pacific halibut epigenome

Objective: Identify epigenetic effects of environmental and anthropogenic factors on the genome

- Identification of genomic regions potentially subjected to epigenetic regulation, allowing for rapid phenotypic changes and adaptive responses to environmental and anthropogenic influences.
- Complement transcriptomic information on growth and reproductive performance.
- Identification of genetic signatures of geographical population groups



Temporal chart of activities

2016	2017	2018	2019	2020	2021
	Annual reproductive cycle				
	Sex determination mechanisms				
	Population genetic structure				
	Genome sequencing				
		Genome-wide association studies			
	Epigenome characterization				
	Growth transcriptome				
	Growth-related patterns				
	Regulation of growth by environmental factors				
	Comprehensive studies on migration				
	Larval migration and connectivity				
	Tagging sublegal halibut				
	Reproductive monitoring of PAT-tagged adults				





**Thank you for your
attention!**

