Northwest **Power** and **Conservation** Council

September 28, 2022

MEMORANDUM

TO: **Fish and Wildlife Committee Members**

FROM: **Maureen Hess**

SUBJECT: **Update on genetic monitoring tools**

BACKGROUND:

Presenters: Dr. Shawn Narum – Senior Scientist/Lead Geneticist, Columbia River Inter-Tribal Fish Commission
Dr. Jon Hess – Senior Fisheries Geneticist, Columbia River Inter-Tribal Fish Commission
Matt Campbell - Fisheries Genetics Program Coordinator, Idaho Department of Fish and Game

Summary: Presenters will update the Committee on genetic monitoring tools and applications that provide critical information to assist fisheries management and conservation efforts in the Columbia River Basin, with particular emphasis on the value that parentage-based tagging and genetic stock identification tools provide to the region.

Relevance: Genetic monitoring tools and their applications address multiple areas of the 2014 Columbia River Basin Fish and Wildlife Program and the 2020 Addendum, in particular: the Adaptive Management section of the Program (Part 4) and the Fish Propagation Including Hatchery Programs Strategy.

Workplan: Fish and Wildlife Division Workplan; Program Implementation and Performance

Background: In 2009, CRITFC and IDFG staff first presented to NPCC the concept of using genetic tools to monitor distinct stocks of salmonids in the Columbia River Basin. The overarching goal was to monitor stock-specific abundance, run-timing, and harvest to contribute to fisheries management and rebuilding fish runs in the Columbia River Basin. Two BPA funded projects (CRITFC 2008-907-00; IDFG 2010-031-00) enabled this concept to be developed into ongoing studies to identify stock of origin of salmonids at fixed locations (Bonneville Dam and Lower Granite Dam) or intercepted in mainstem fisheries. An update on progress was delivered to the NPCC Fish Tagging Forum in 2012 that summarized the development of genetic resources, empirical testing/demonstration, and results for long-term status and trend monitoring of steelhead and Chinook Salmon stocks. The concepts described initially in 2009, and efforts to improve and expand these genetic tools since then, have evolved into a broadly implemented genetic monitoring program for salmonids in the Columbia River Basin. This includes use of two powerful approaches to identify hatchery-origin fish with Parentage Based Tagging (PBT) and natural-origin fish with Genetic Stock Identification (GSI).

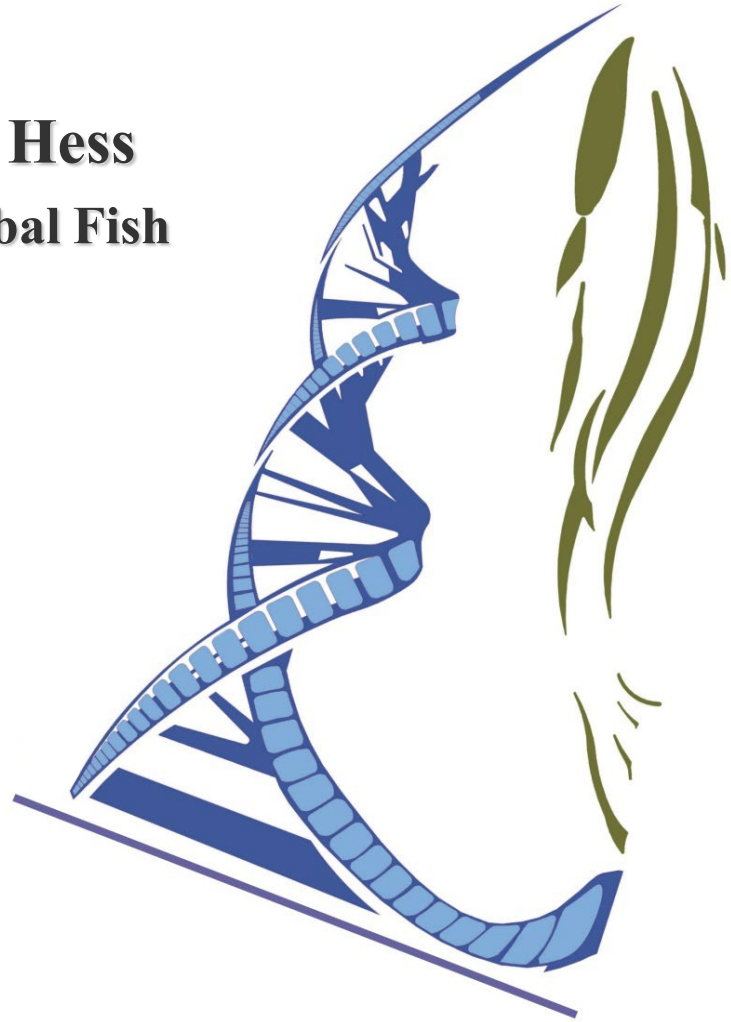
More Info:

- Project #2008-907-00 – Genetic Assessment of Columbia River Stocks
- Project #2010-031-00 – IDFG Genetic Monitoring of Snake River Salmon and Steelhead stocks
- Fish Tagging Forum

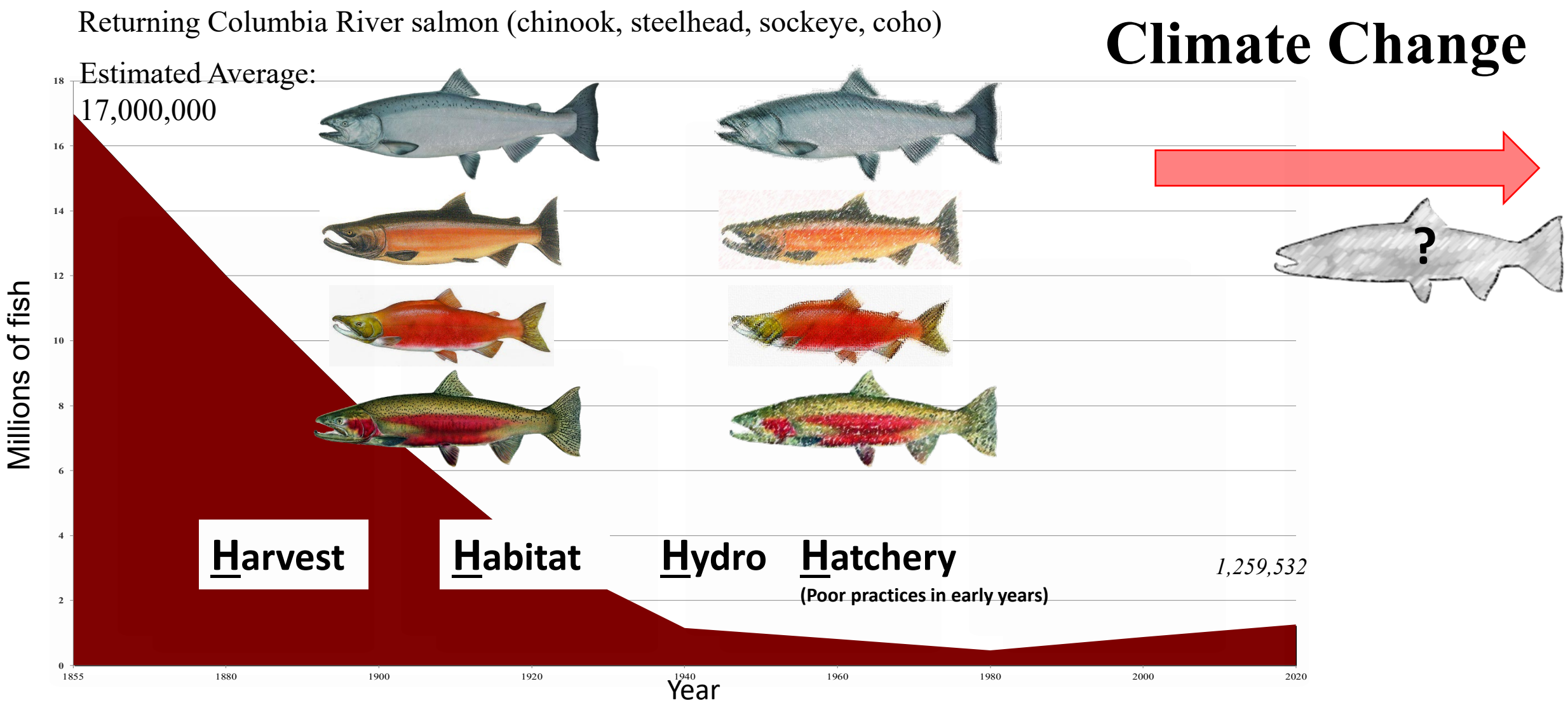
Genetic Monitoring of Salmonids in the Columbia River Basin

Shawn Narum & Jon Hess
Columbia River Inter-Tribal Fish Commission (CRITFC)

Matt Campbell
Idaho Department of Fish & Game (IDFG)



Genetic Monitoring & Research to Support Recovery of Fisheries

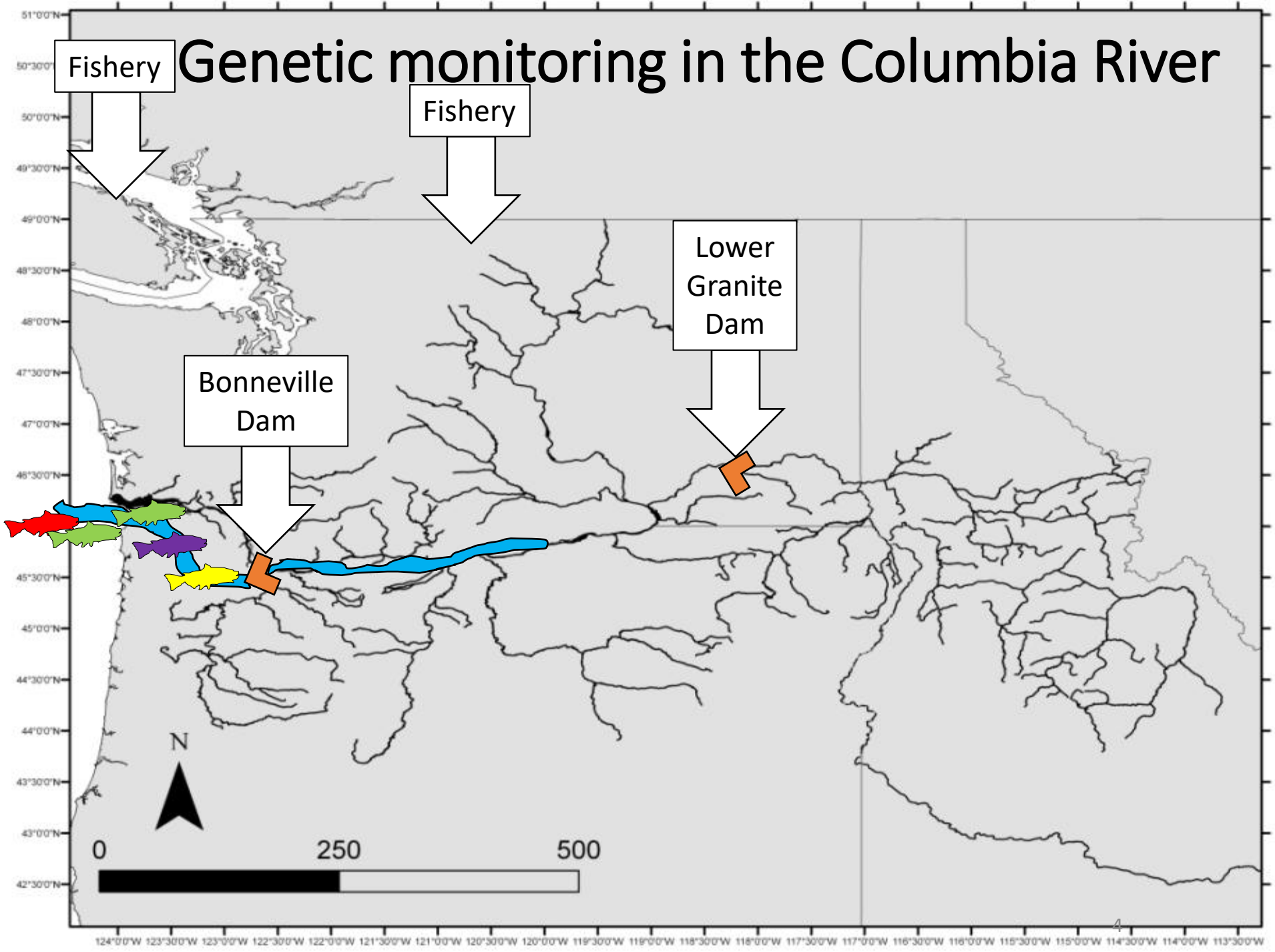


1855: NPCC historical run extrapolation estimate; 1880-1920 data points extrapolated from Columbia River cannery output; 1940-present: dam counts and river mouth estimates

Applied Genetics Research in Salmonids

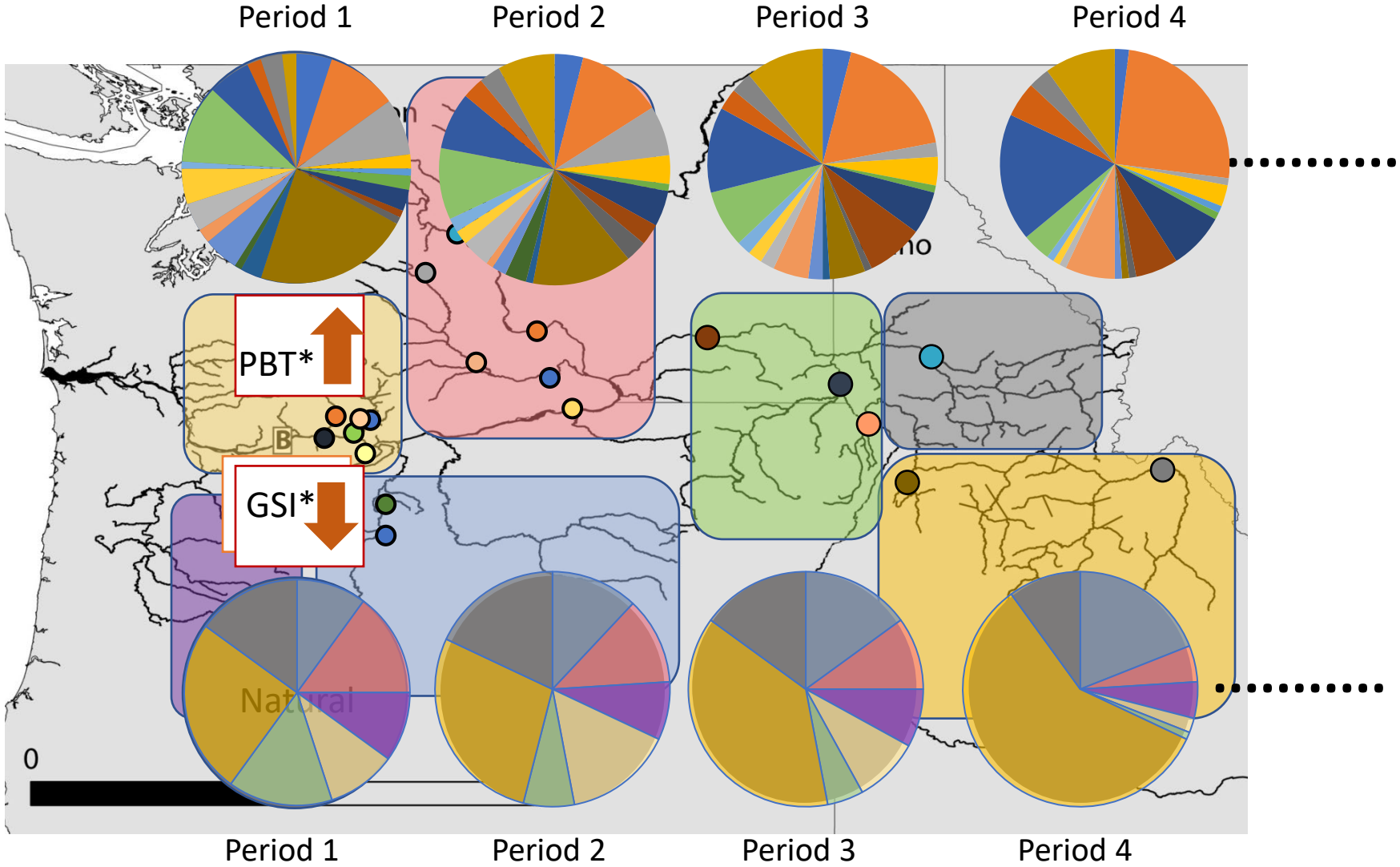
- Genetic monitoring of distinct stocks
  - Return timing and abundance of stocks (hatchery & natural)
  - Estimating harvest of stocks (hatchery & natural)
- Effects of hatchery programs on wild stocks
  - Estimate fitness with genetic pedigrees
  - Monitor effects on heritable phenotypic variation
- Maintain adaptive genetic variation
  - Adaptation to local environments
  - Genomic basis for diverse phenotypic traits

Genetic monitoring in the Columbia River



Bonneville Dam:

In-season estimates of abundance/timing at Bonneville Dam for specific stocks of Chinook, steelhead, sockeye; biweekly reports sent to co-managers



*PBT = Parentage Based Tagging

*GSI = Genetic Stock Identification

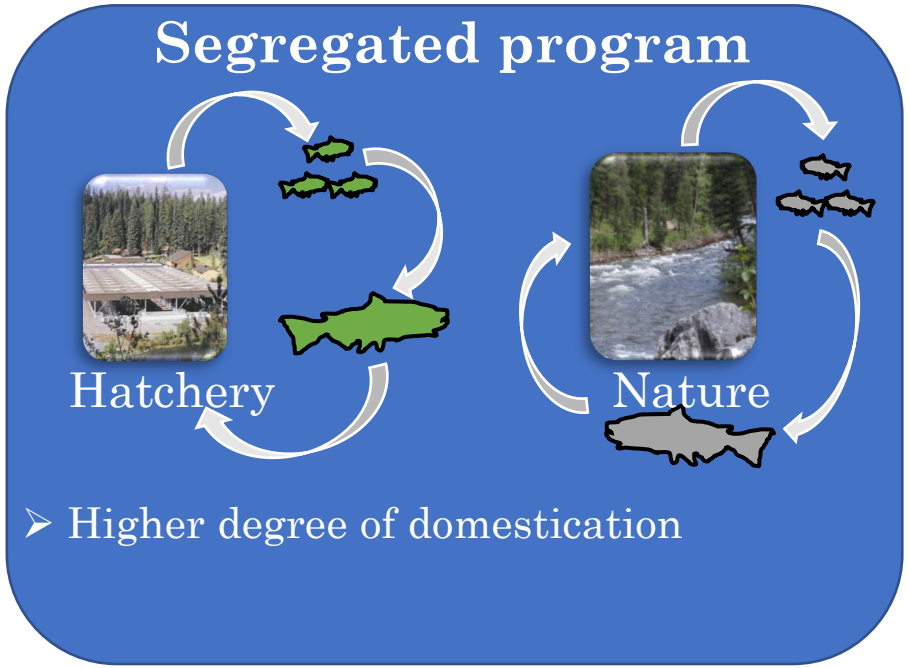
Areas of Applied Research in Salmonids

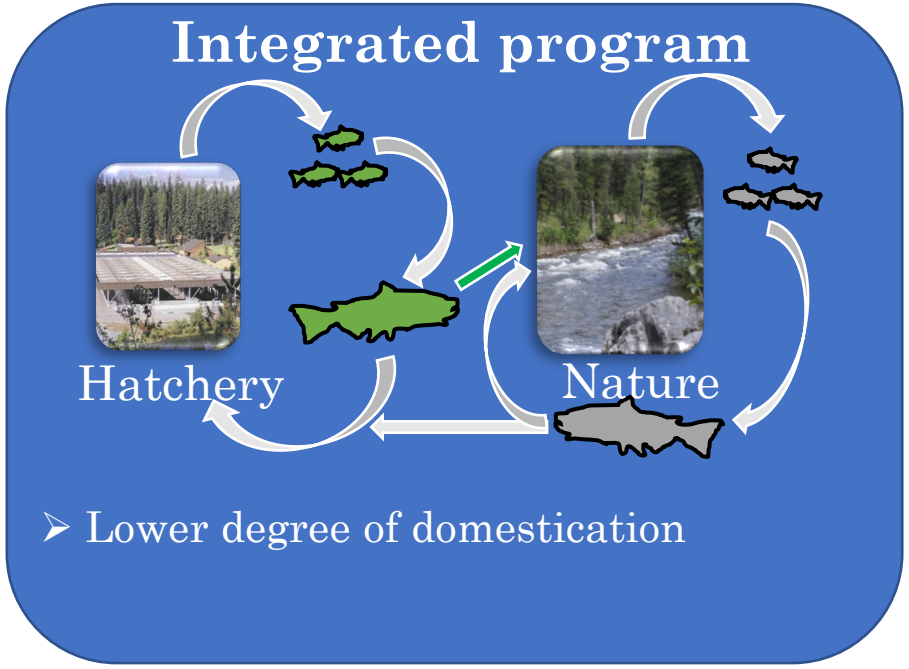
- Genetic monitoring of distinct stocks
  - Return timing and abundance of stocks
  - Estimating harvest of stocks
- **Effects of hatchery programs on wild stocks**
  - Pedigrees to estimate fitness
  - Track heritable phenotypic variation
- Maintain adaptive genetic variation
  - Adaptation to local environments
  - Genomic basis for diverse phenotypic traits

Types of Hatchery Programs

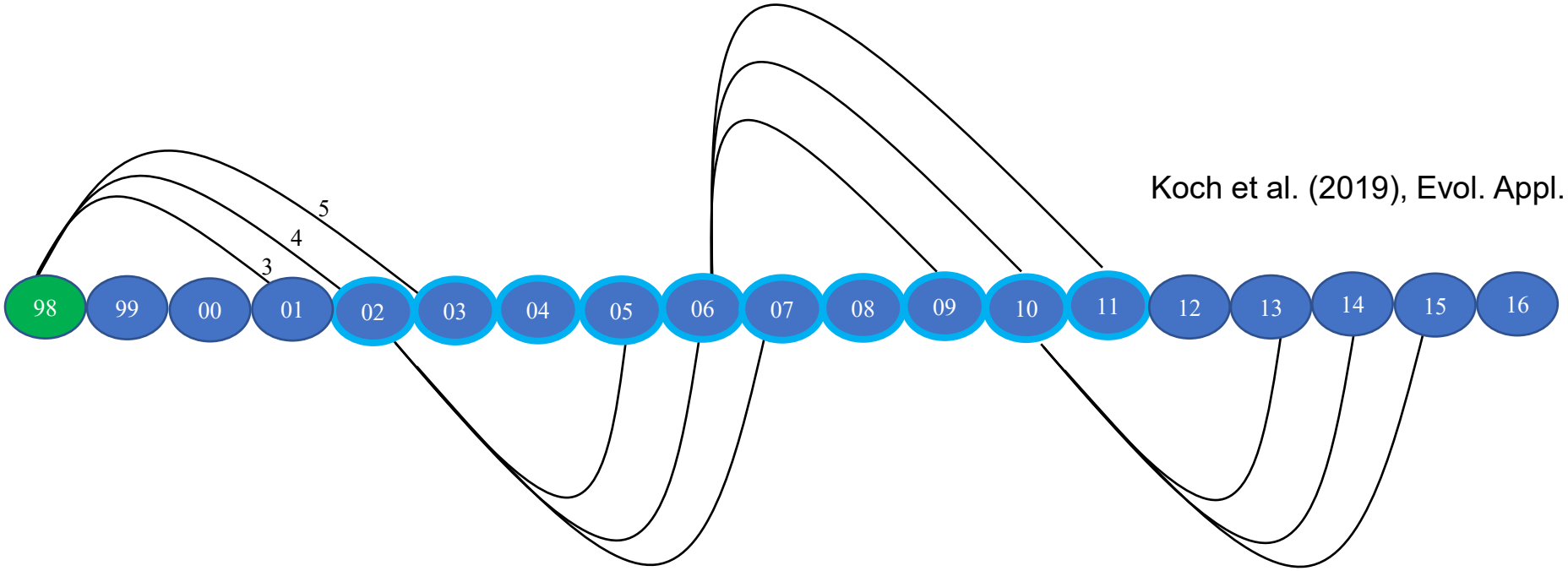
- Harvest augmentation – Fish for harvest (segregated)
- Supplementation – Prevent extirpation, rebuild natural production (integrated)
- Reintroduction – Restore extirpated populations (outside stocks)

Effects of hatchery programs on wild/natural stocks?





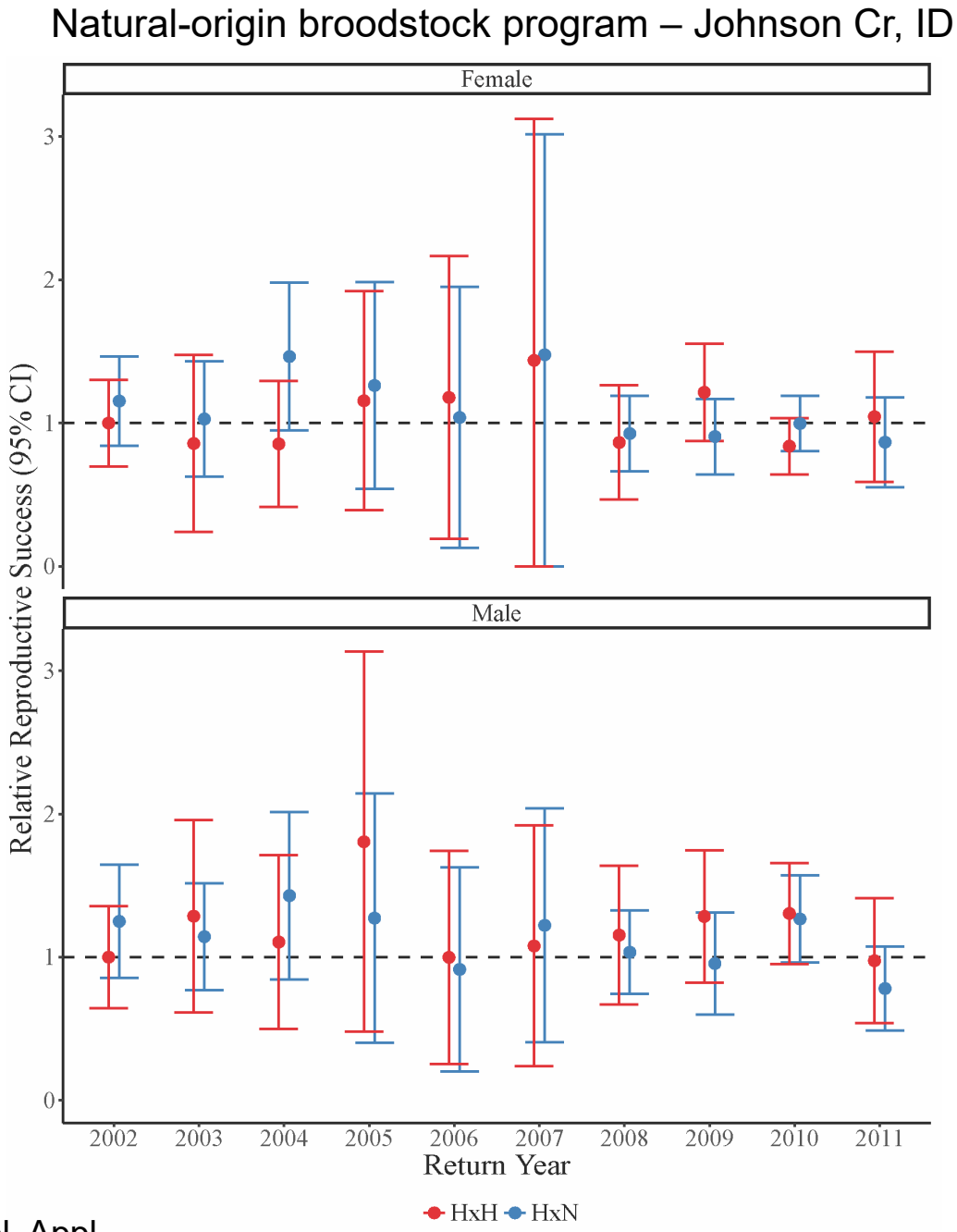
Pedigree Analyses to Track Offspring & Fitness



- Tissue sample collected from parents (non-lethal) to identify offspring
- Samples genotyped for parentage analyses

Effects of Hatchery on Natural Population

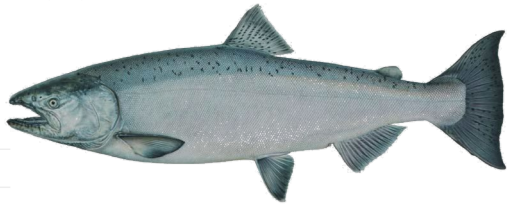
- Key Question: Is reproductive success reduced when hatchery origin fish mate with natural fish?
- Supplementation with highly integrated broodstock may have limited effects on natural populations (e.g., Johnson Cr.)
- Other recent studies suggest NOR broodstock may reduce negative effects (e.g., Waters et al 2015; Ford et al. 2016)



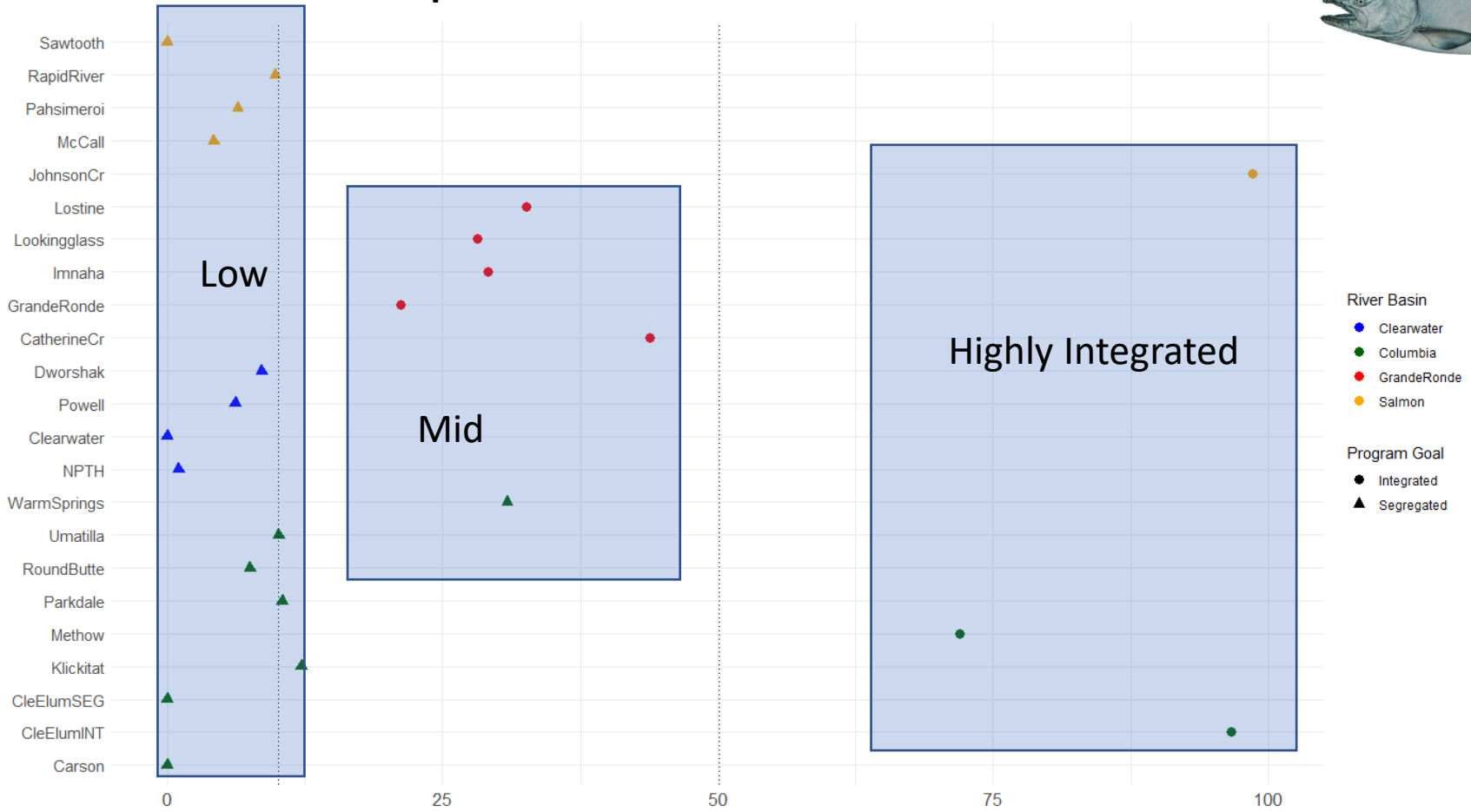
Koch et al. (2019), Evol. Appl.

Integrated vs. Segregated Programs

- Integrated programs may have low risk to natural populations
- Few programs with high percent of natural origin broodstock



Example of 23 Chinook Hatcheries in Columbia R.



Horn et al. 2022 revised, NAJFM

Areas of Applied Research in Salmonids

- Genetic monitoring of distinct stocks
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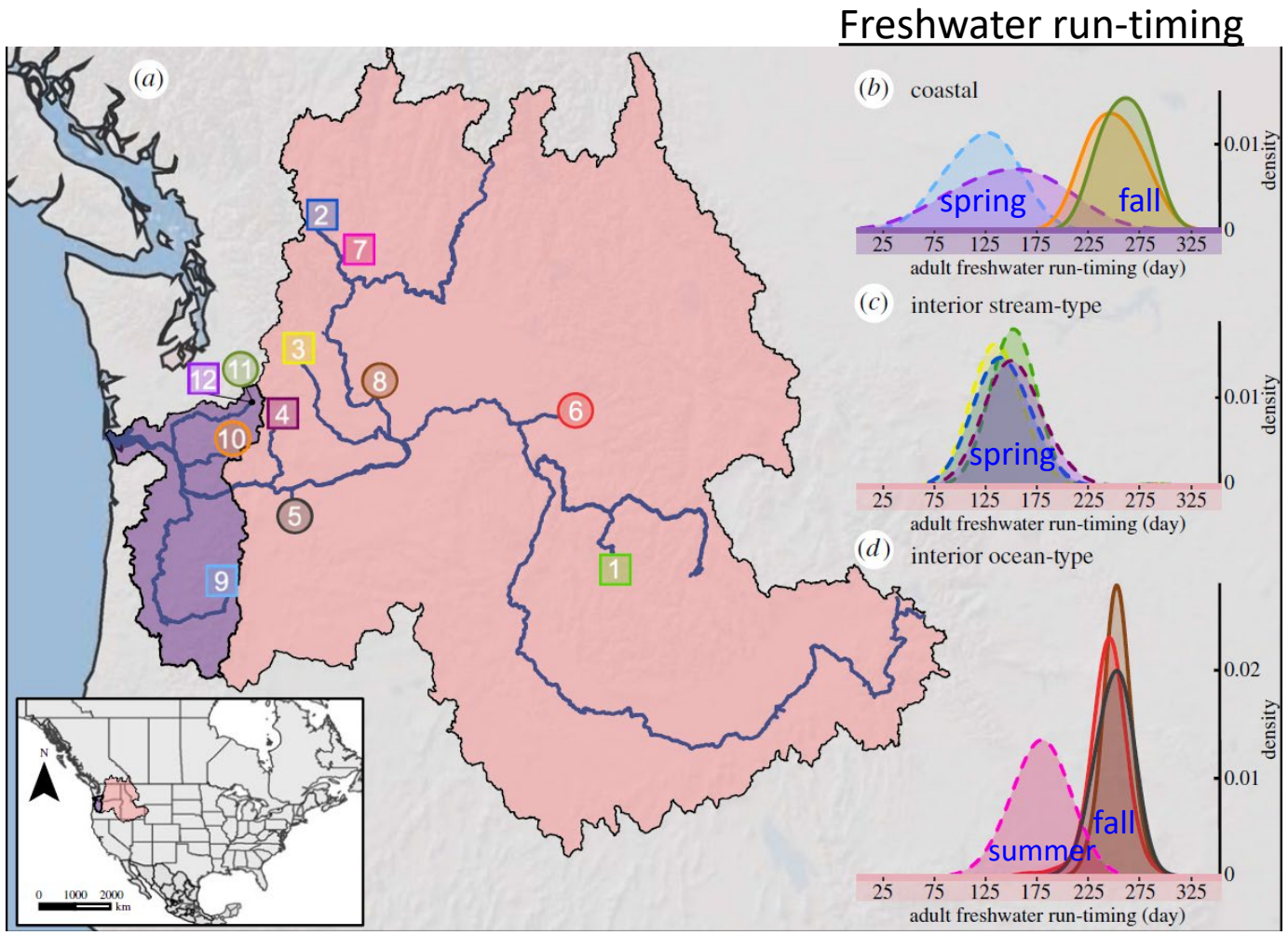
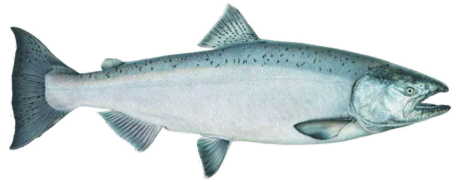
- **Maintain adaptive genetic variation**
  - Adaptation to local environments
  - Genomic basis for diverse phenotypic traits

Genome Scans for Phenotypic Traits

Run-timing for three major lineages of Chinook in Columbia R.

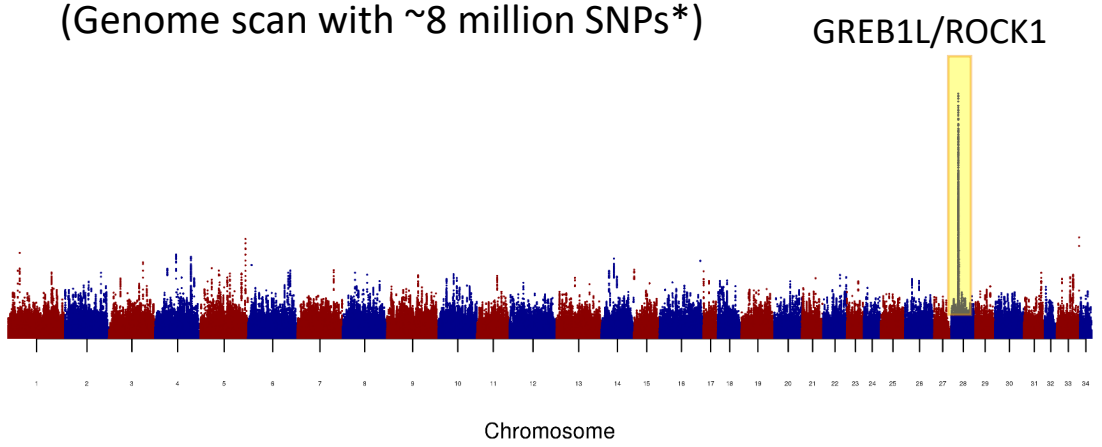




Chinook salmon

Adult Migration Timing (early vs. late)

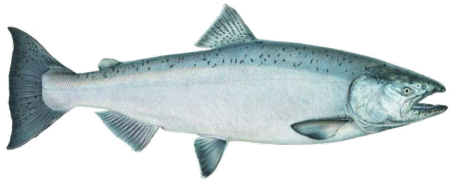
(Genome scan with ~8 million SNPs*)



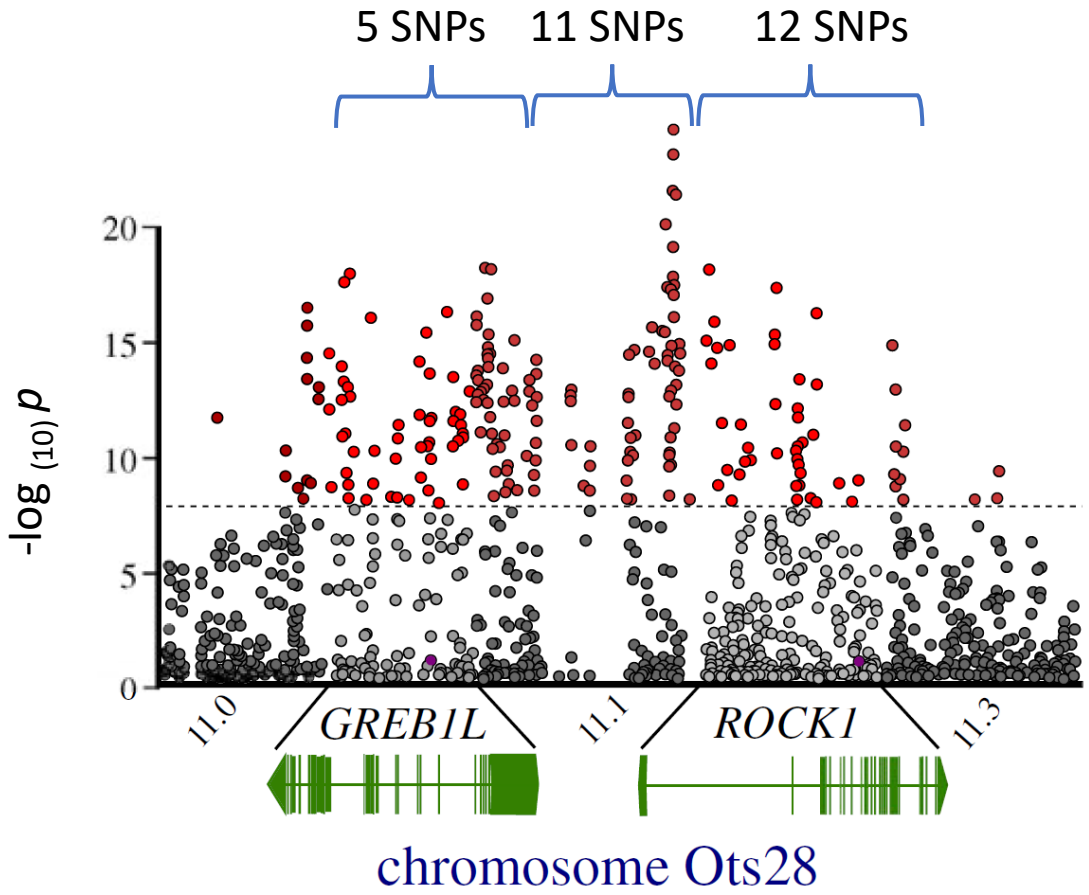
Narum et al. 2018; Proc. B

*SNP = single nucleotide polymorphism

Markers to Validate Association

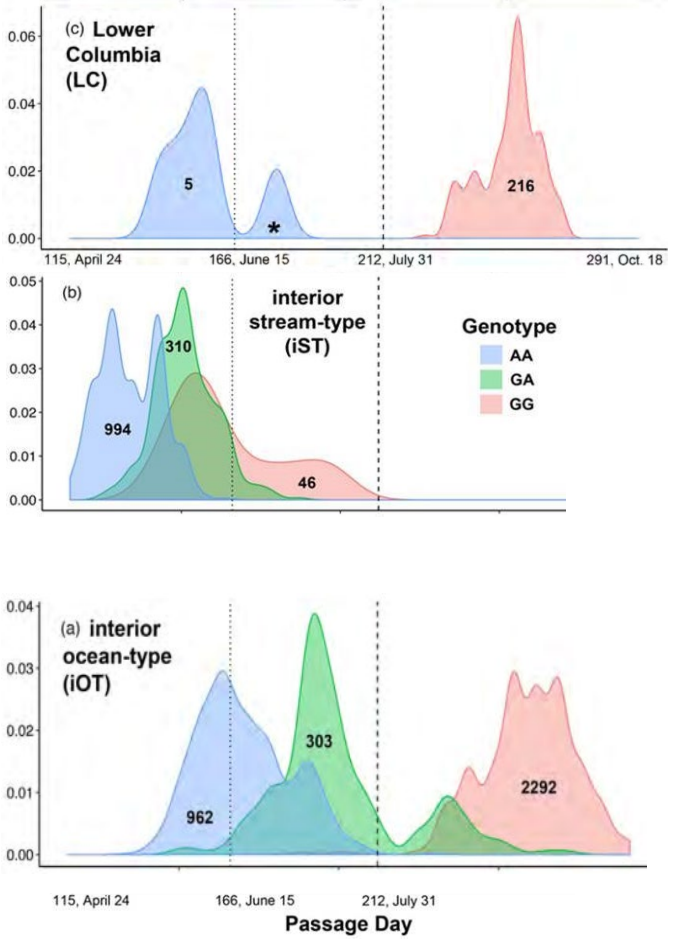


28 SNPs from GREB1L/ROCK1 region



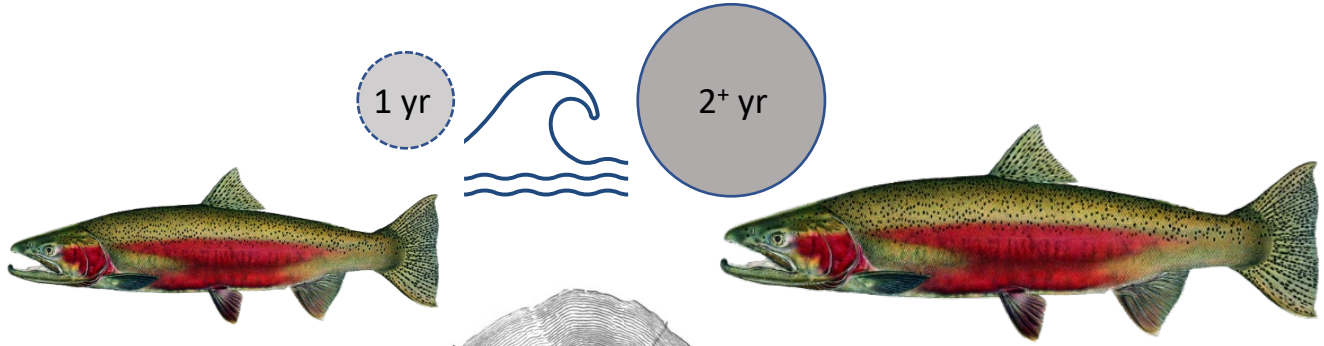
Genotypes explain 50-80% of variation in run-timing

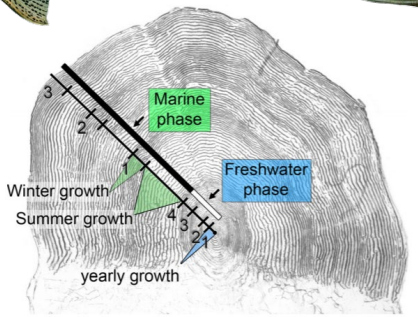
(n =5,149)



Willis et al. 2021; Evol. Appl.

Age at Maturity: 1-ocean vs. 2-ocean steelhead



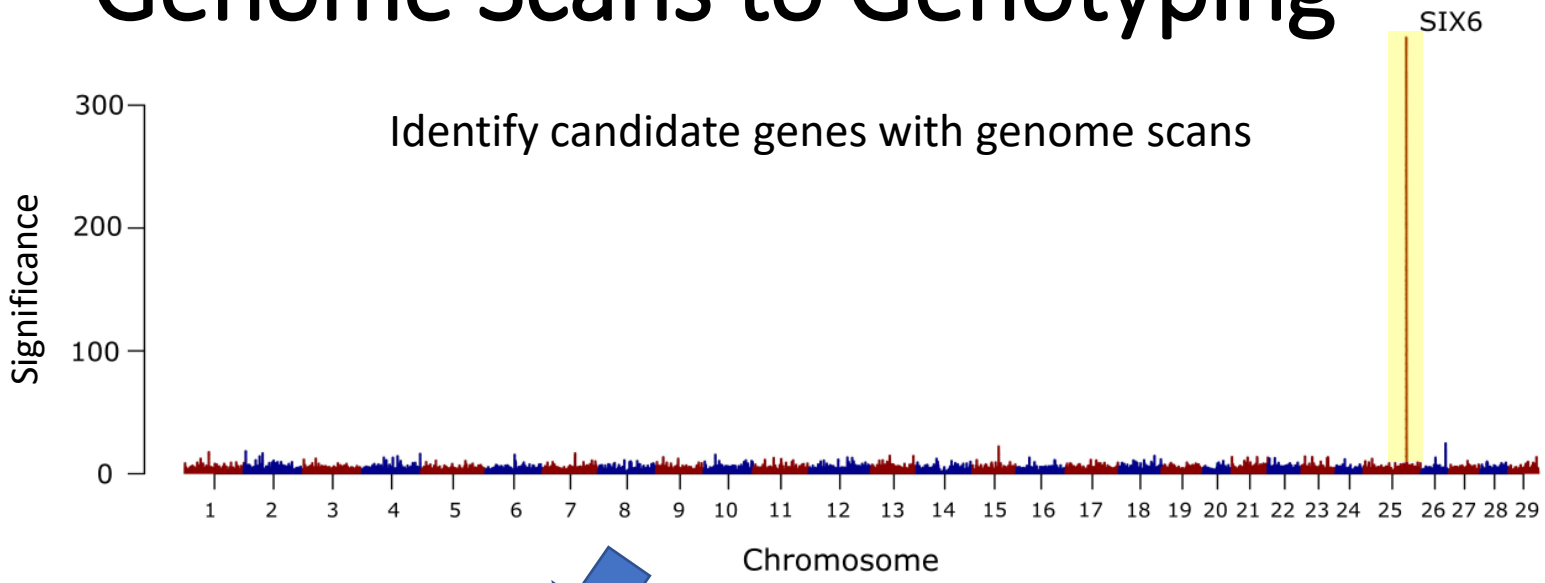


Scales for aging phenotypes

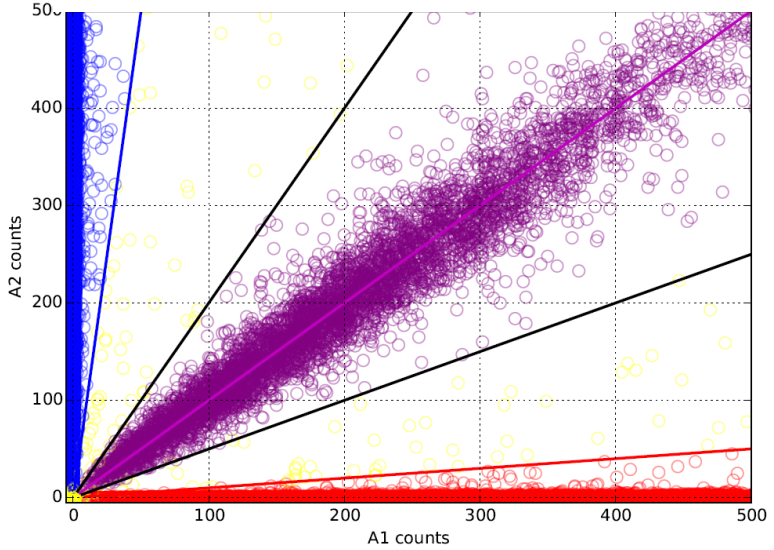
Waters et al. 2021, Mol. Ecol.

Willis et al. 2020, Evol. Appl.

Genome Scans to Genotyping

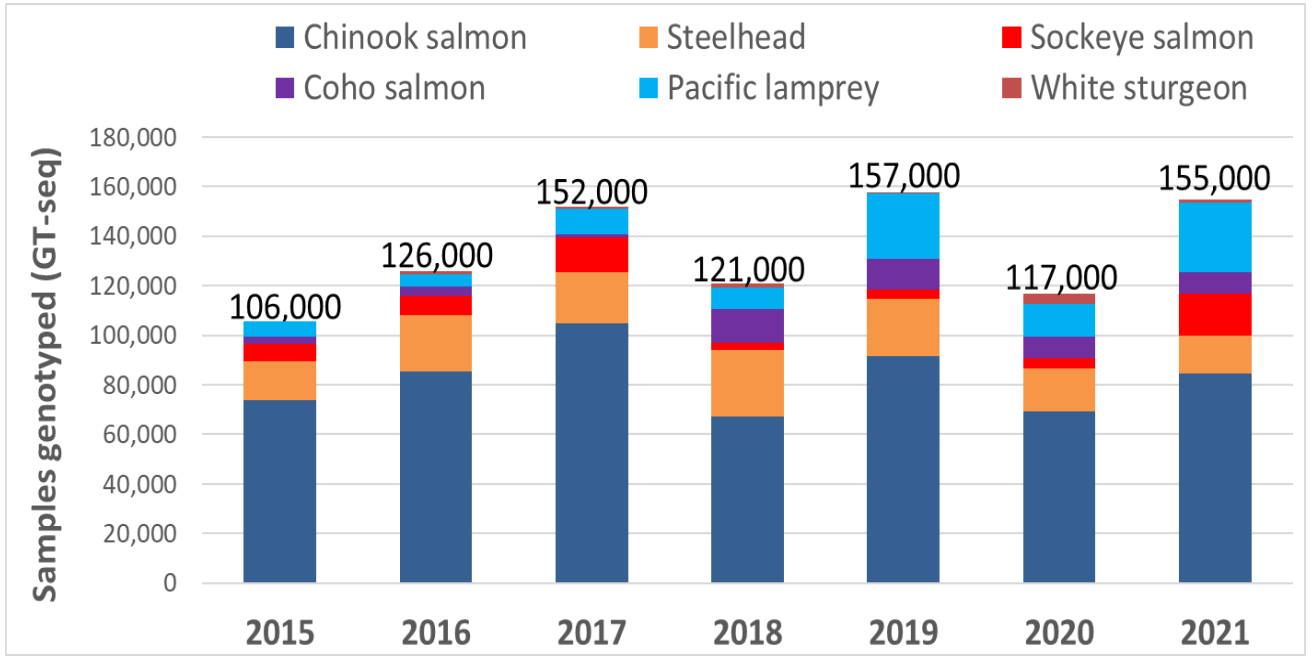


Develop Markers for Genotyping



GT-seq; Campbell & Narum 2015, Mol. Ecol. Res.

Enables monitoring of many individuals



Conservation & Recovery Goals

Maintain genetic diversity that allows salmonid populations to persist

Short-term: single events (e.g., flood or drought)

Long-term: climate change (frequent stochastic events)

IDFG Genetic Monitoring of Snake River Salmon and Steelhead stocks: 2010-031-00

Matthew Campbell (IDFG)
Fisheries Genetics Program Coordinator

Presentation to Fish and Wildlife Committee Members (NPCC)
Tuesday, October 4th, 2022

Primary Collaborators: Shawn Narum, Jon Hess
Columbia River Inter-Tribal Fish Commission

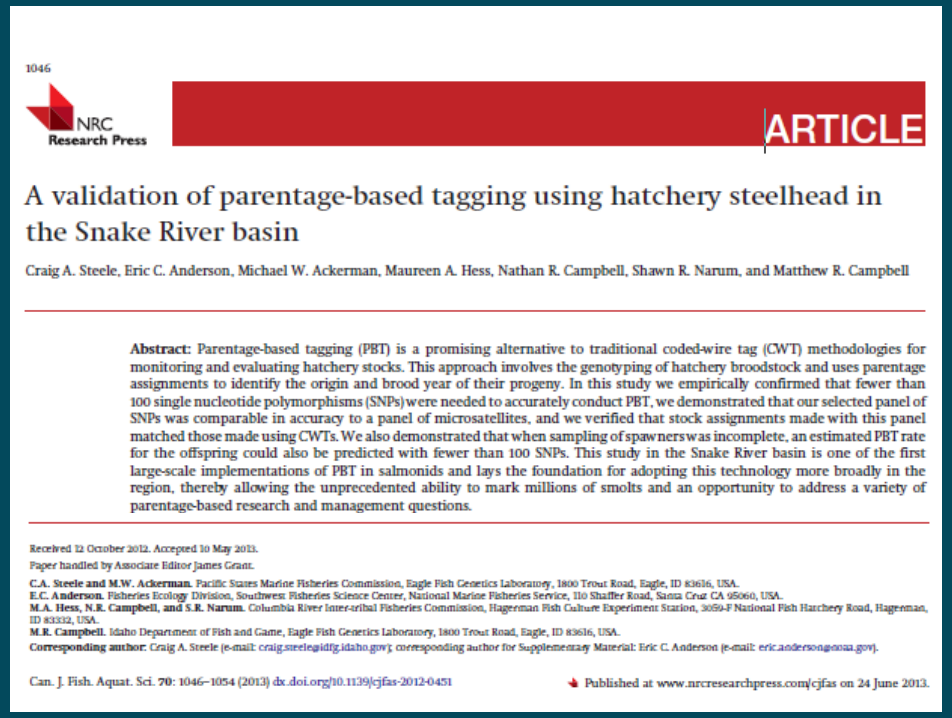
Co-collaborators:
Idaho Power Company
Lower Snake River Compensation Plan (USFWS)
Pacific States Marine Fisheries Commission
Nez Perce Tribe

Primary Staff:
John Hargrove, PhD
Audrey Harris, M.S.
Katharine Coykendall, PhD
Jesse McCane

Major achievements during proof-of-concept period:

Parentage Based Tagging-

- Accuracy- PBT is accurate and matched CWT assigments CWTs (Steele et al 2013)
- Integration- Same genetic marker panel for GSI and PBT
- Tag rates- High realized tag rates 2009 - Present (>95%)
- Utility- Powerful technology to address multiple management and research questions throughout the CRB



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NRC Research Press

ARTICLE

A validation of parentage-based tagging using hatchery steelhead in the Snake River basin

Craig A. Steele, Eric C. Anderson, Michael W. Ackerman, Maureen A. Hess, Nathan R. Campbell, Shawn R. Narum, and Matthew R. Campbell

Abstract: Parentage-based tagging (PBT) is a promising alternative to traditional coded-wire tag (CWT) methodologies for monitoring and evaluating hatchery stocks. This approach involves the genotyping of hatchery broodstock and uses parentage assignments to identify the origin and brood year of their progeny. In this study we empirically confirmed that fewer than 100 single nucleotide polymorphisms (SNPs) were needed to accurately conduct PBT, we demonstrated that our selected panel of SNPs was comparable in accuracy to a panel of microsatellites, and we verified that stock assignments made with this panel matched those made using CWTs. We also demonstrated that when sampling of spawners was incomplete, an estimated PBT rate for the offspring could also be predicted with fewer than 100 SNPs. This study in the Snake River basin is one of the first large-scale implementations of PBT in salmonids and lays the foundation for adopting this technology more broadly in the region, thereby allowing the unprecedented ability to mark millions of smolts and an opportunity to address a variety of parentage-based research and management questions.

Received 12 October 2012. Accepted 10 May 2013.
Paper handled by Associate Editor James Grant.

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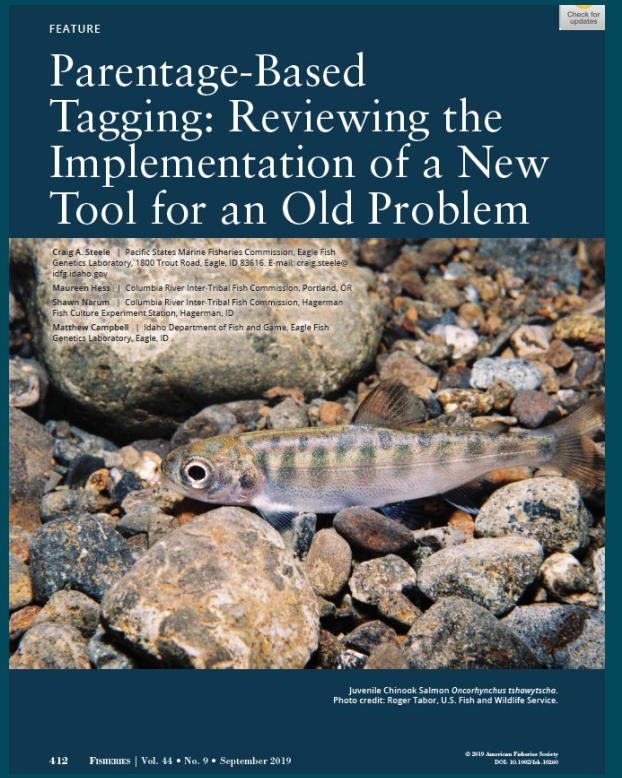
M.A. Hess, N.R. Campbell, and S.R. Narum. Columbia River Inter-tribal Fisheries Commission, Hagerman Fish Culture Experiment Station, 3059-F National Fish Hatchery Road, Hagerman, ID 83332, USA.
M.R. Campbell. Idaho Department of Fish and Game, Eagle Fish Genetics Laboratory, 1800 Trout Road, Eagle, ID 83616, USA.
Corresponding author: Craig A. Steele (e-mail: craig.steele@idfg.idaho.gov); corresponding author for Supplementary Material: Eric C. Anderson (e-mail: eric.anderson@noaa.gov).

Can. J. Fish. Aquat. Sci. 70: 1046–1054 (2013) dx.doi.org/10.1139/cjfas-2012-0451 Published at www.nrcresearchpress.com/cjfas on 24 June 2013.



FEATURE

Check for updates

Parentage-Based Tagging: Reviewing the Implementation of a New Tool for an Old Problem

Craig A. Steele | Pacific States Marine Fisheries Commission, Eagle Fish Genetics Laboratory, 1800 Trout Road, Eagle, ID 83616. E-mail: craig.steele@idfg.idaho.gov
Maureen Hess | Columbia River Inter-Tribal Fish Commission, Portland, OR
Shawn Narum | Columbia River Inter-Tribal Fish Commission, Hagerman Fish Culture Experiment Station, Hagerman, ID
Matthew Campbell | Idaho Department of Fish and Game, Eagle Fish Genetics Laboratory, Eagle, ID

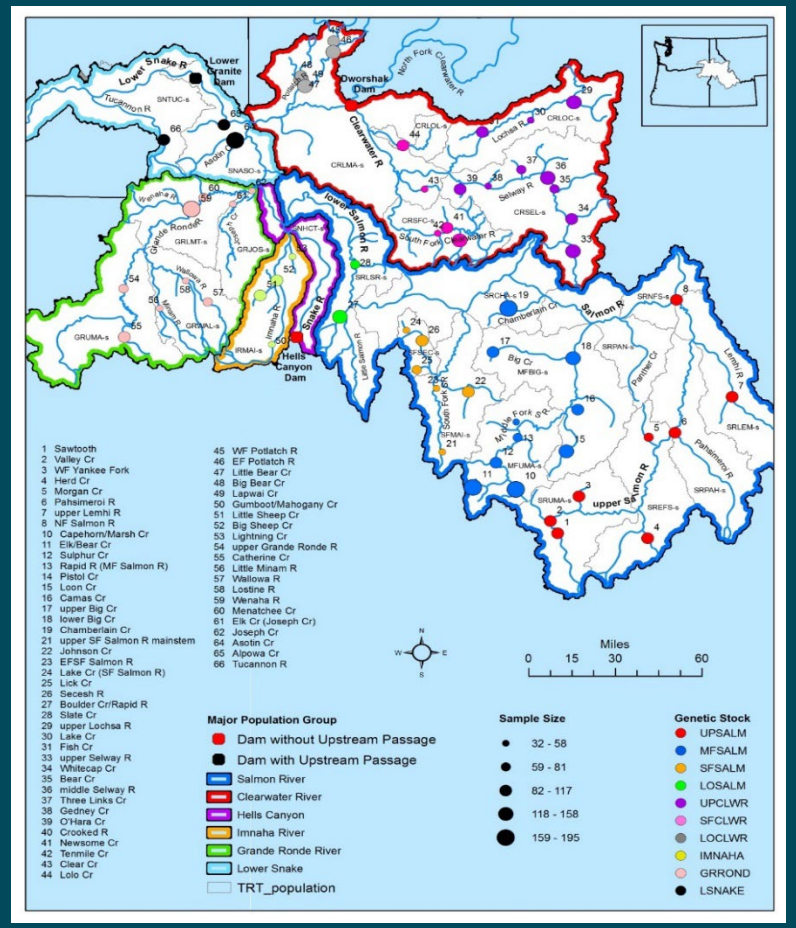
Juvenile Chinook Salmon *Oncorhynchus tshawytscha*. Photo credit: Roger Tabor, U.S. Fish and Wildlife Service.

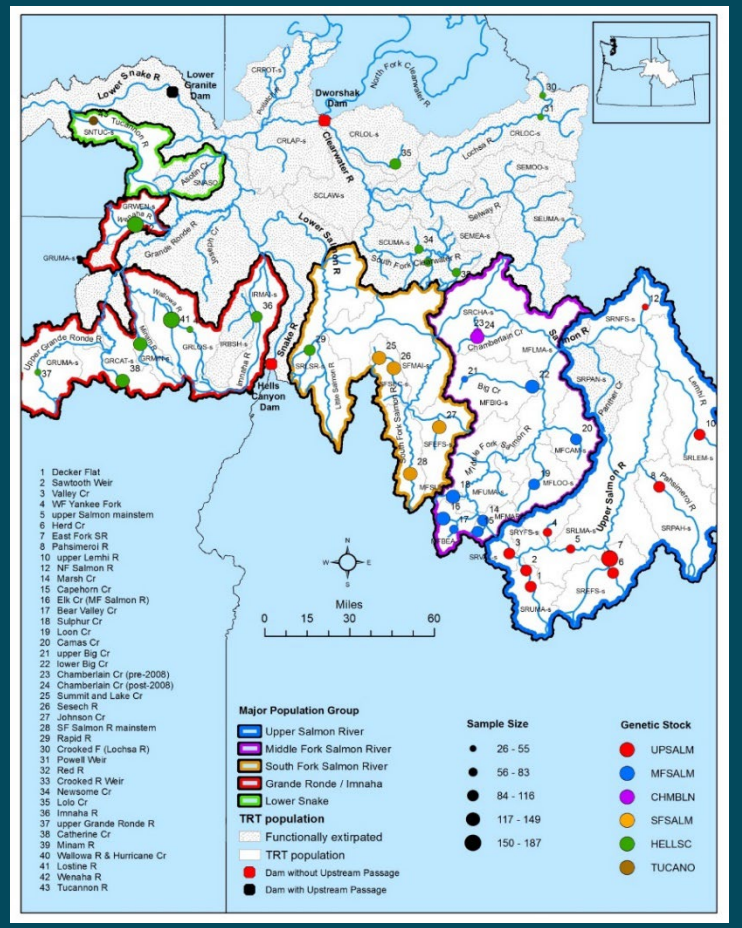
DOI: 10.1002/fsh.10260

Major achievements:

Genetic Stock Identification-

- Comprehensive GSI SNP genetic baselines for both species
  - Chinook Salmon: Sample collections represent 31 TRT pops, 6 Genetic Stocks spanning 5 MPGs
  - Steelhead: Sample collections represent 23 TRT pops, 10 Genetic Stocks spanning 6 MPGs
- Baselines incorporated into Columbia River genetic baselines (CRITFC)

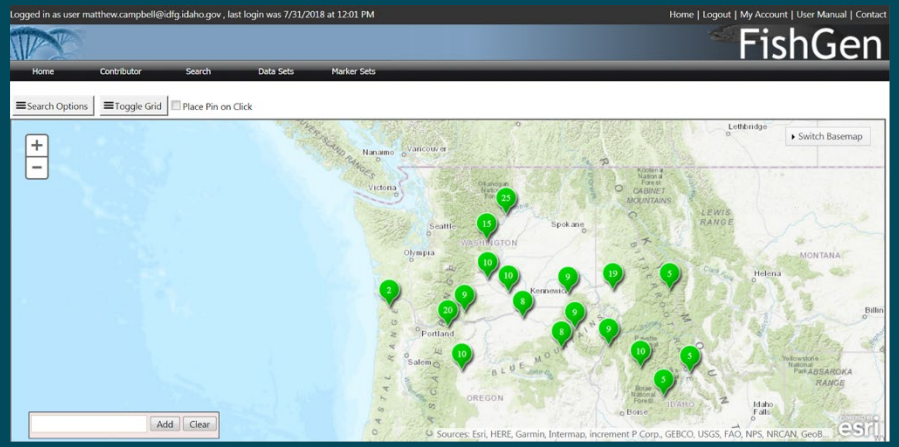




Major achievements:

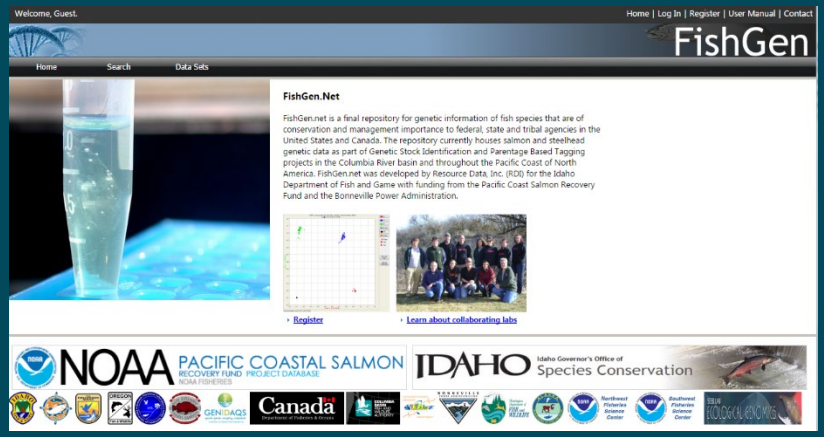
Both Projects-

- FishGen Database
- Additional funding from PSMFC



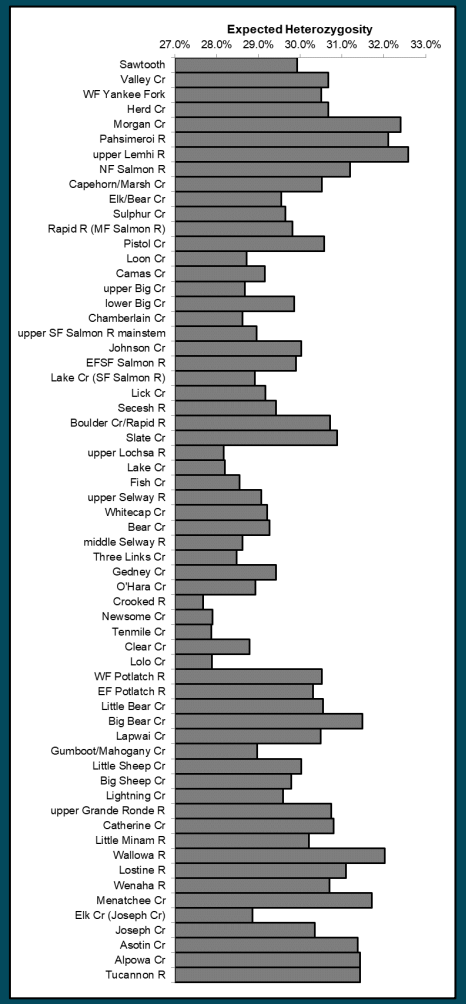
All PBT/GSI baselines available on FishGen

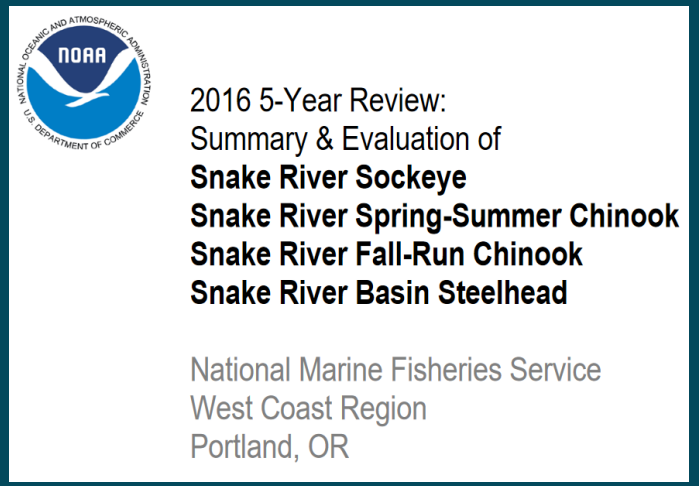
- ~500,000 Chinook Salmon
- ~150,000 Steelhead
- Standardized genetic marker panels
- Publicly available

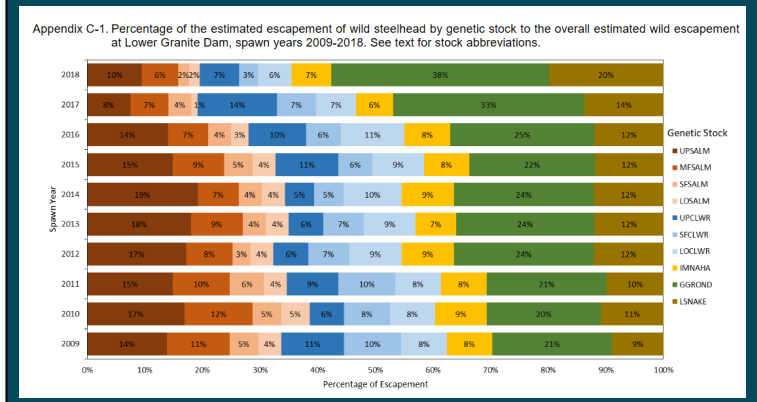


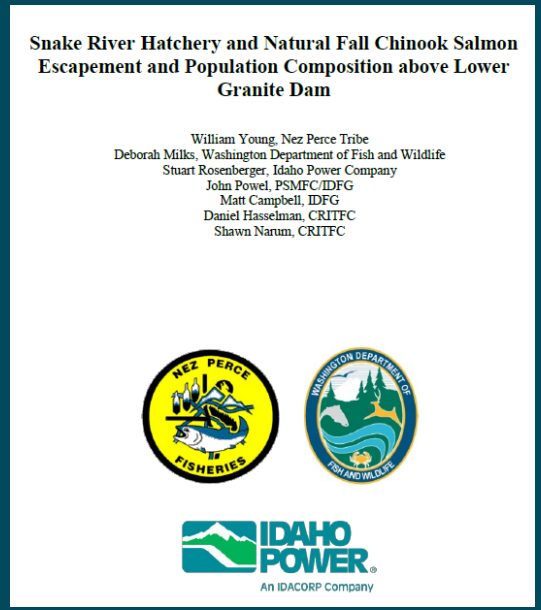
Transition to long-term status and trend monitoring programs

Following completion of proof-of-concept phase of these projects, managers throughout the Columbia River Basin incorporated GSI and PBT for long-term status and trend monitoring of steelhead and Chinook Salmon stocks





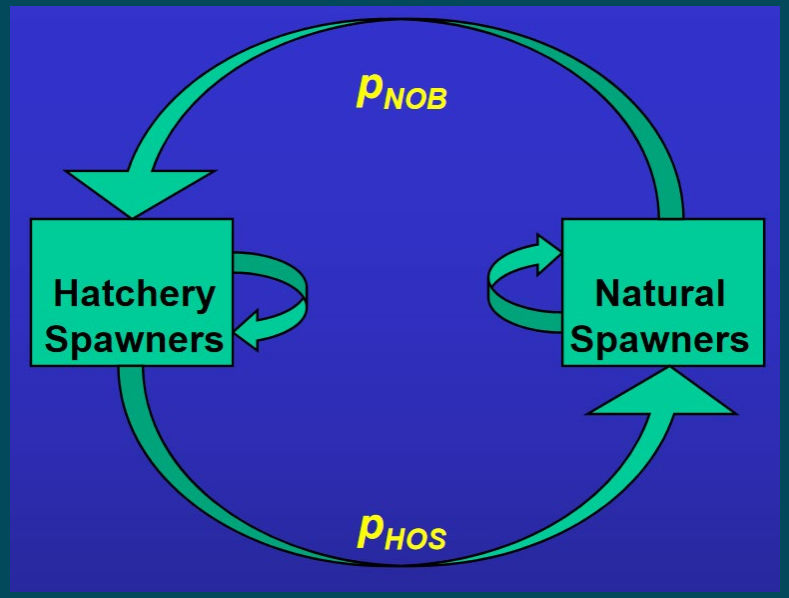




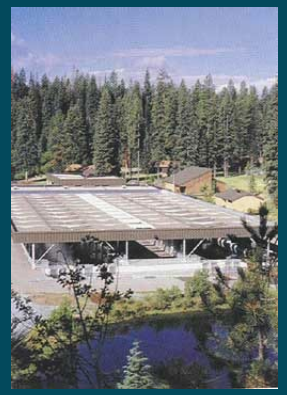
Some brief examples:

Long-term status and trend monitoring programs

- ✓ Monitoring effectiveness of integrated hatchery programs
  - Estimate PNI
  - Adult-to-adult productivity



Calculate and report annual estimates of Proportion of Natural Influence:
PNI ≈ pNOB / (pNOB + pHOS)



McCall Fish Hatchery

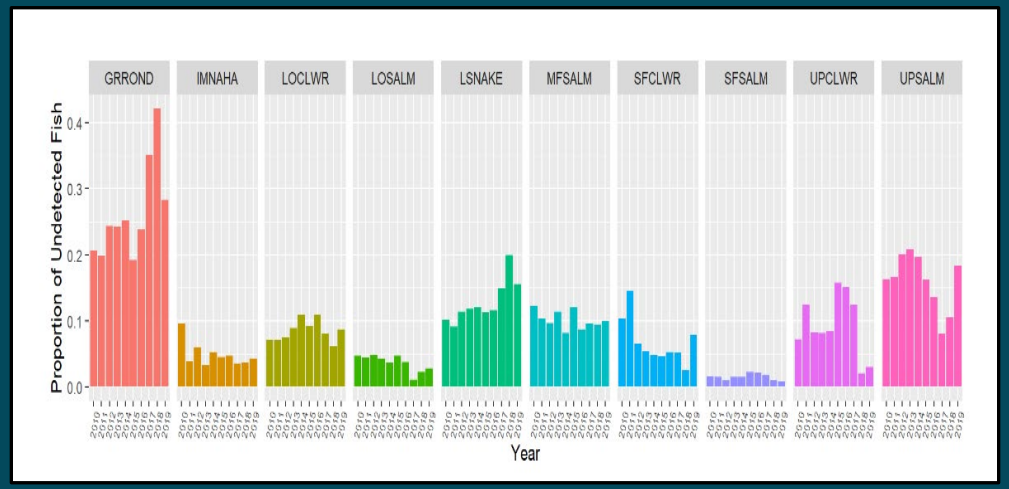
Pahsimeroi Fish Hatchery

Sawtooth Fish Hatchery

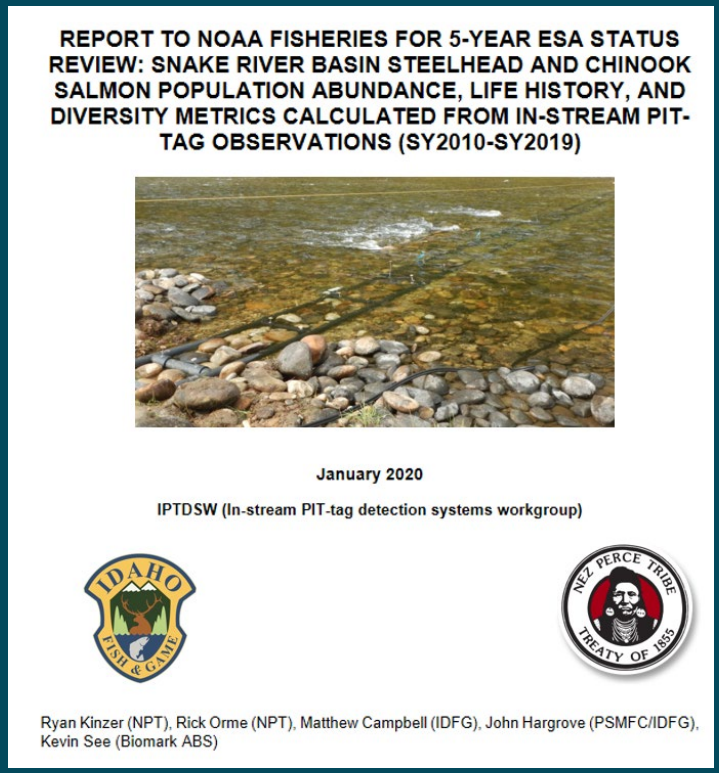
Lyons Ferry Fish Hatchery

Long-term status and trend monitoring programs

- ✓ Summarize life-history and genetic diversity of steelhead and spring/summer Chinook Salmon that are detected at instream pit tag detection systems in the Snake River basin
  - Separate wild and hatchery fish
  - Provide genetic sex and estimates of genetic diversity and structure
  - Provide GSI assignments of undetected fish



Proportions of undetected steelhead by genetic stock by year for spawn years 2010–2019



REPORT TO NOAA FISHERIES FOR 5-YEAR ESA STATUS REVIEW: SNAKE RIVER BASIN STEELHEAD AND CHINOOK SALMON POPULATION ABUNDANCE, LIFE HISTORY, AND DIVERSITY METRICS CALCULATED FROM IN-STREAM PIT-TAG OBSERVATIONS (SY2010-SY2019)

January 2020

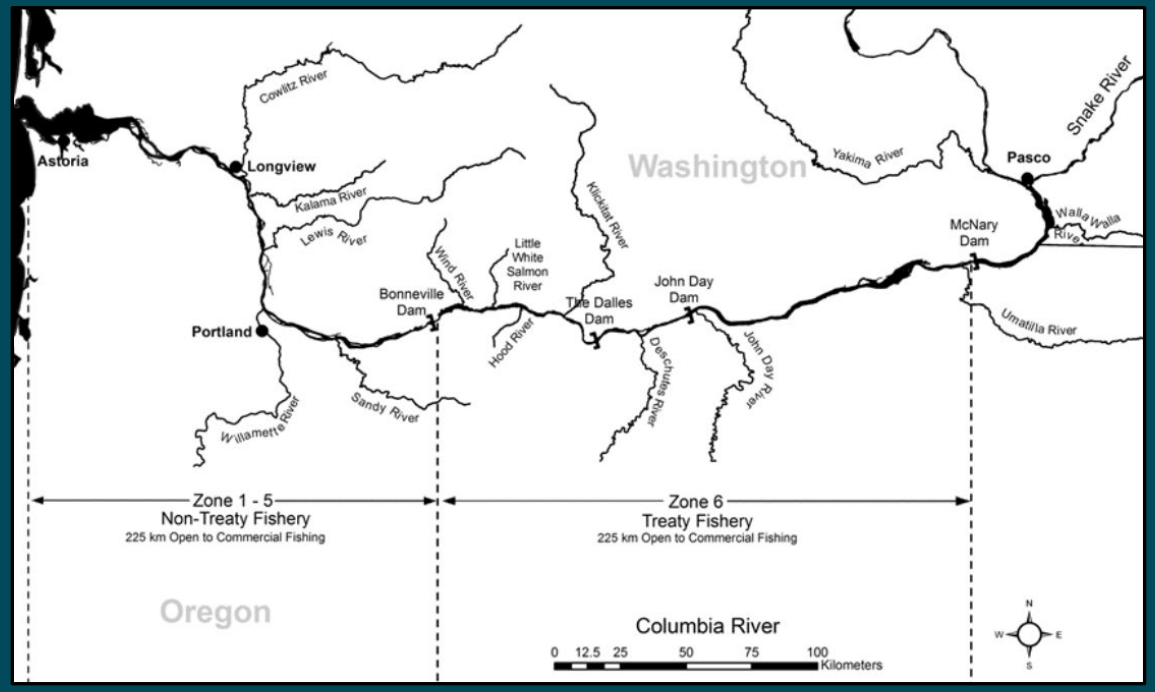
IPTDSW (In-stream PIT-tag detection systems workgroup)

Ryan Kinzer (NPT), Rick Orme (NPT), Matthew Campbell (IDFG), John Hargrove (PSMFC/IDFG), Kevin See (Biomark ABS)

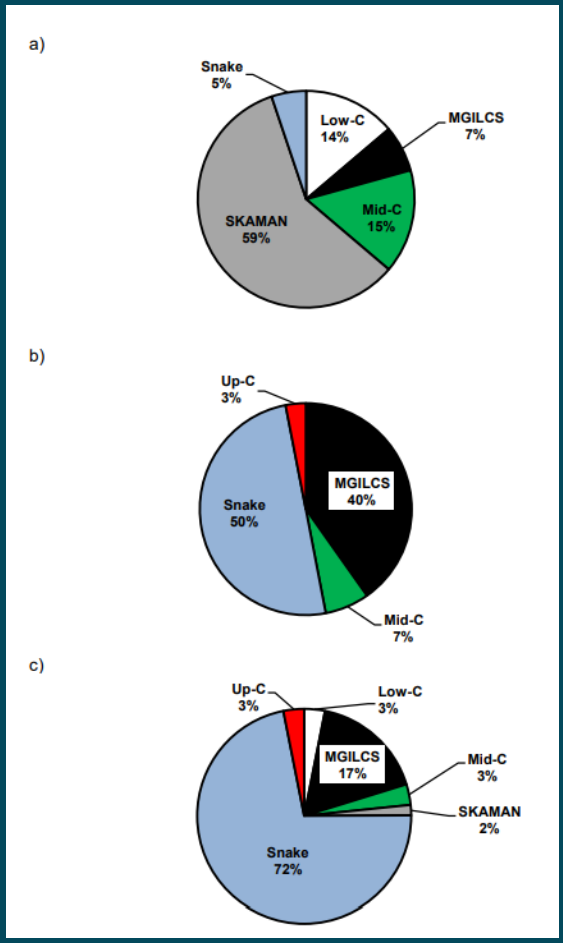
Long-term status and trend monitoring programs

Some examples of projects that are generating status and trend monitoring data:

- ✓ Estimate the wild and hatchery stock composition of adult steelhead harvested in mainstem fisheries extending from the Lower Columbia River upstream to the Snake Basins of Idaho, Oregon and Washington.



Multi-agency effort to estimate stock composition of sport and tribal harvested steelhead in the Columbia River corridor



Stock composition in Zone 6 harvest

Example: VSP Monitoring in the Snake River Basin

VSP stands for viable salmonid population. NOAA uses four key parameters to evaluate a population's viability

- Abundance
- Population growth rate
- Spatial Structure
- Diversity

These parameters can be estimated annually for the entire Snake River basin using a comprehensive sampling and genetic program at Lower Granite Dam

VSP Monitoring @LGR Collaborators

Bonneville Power Administration (BPA); projects:

- ✓ 1990-055-00 Idaho Steelhead Monitoring and Evaluation Studies
- ✓ 1991-073-00 Idaho Natural Production Monitoring and Evaluation Program
- ✓ 2010-026-00 Chinook and Steelhead Genotyping for Genetic Stock Identification (GSI) at Lower Granite Dam
- ✓ 2010-031-00 Snake River Chinook and Steelhead Parental Based Tagging (PBT)

- Idaho Office of Species Conservation (IOSC)
- Idaho Power Company (IPC)
- Northwest Power and Conservation Council (NPCC)
- Pacific States Marine Fisheries Commission (PSMFC)
- Quantitative Consultants, Inc. (QCI)
- U. S. Fish and Wildlife Service, Lower Snake River Compensation Program (LSRCP)
- National Marine Fisheries Service (NMFS)

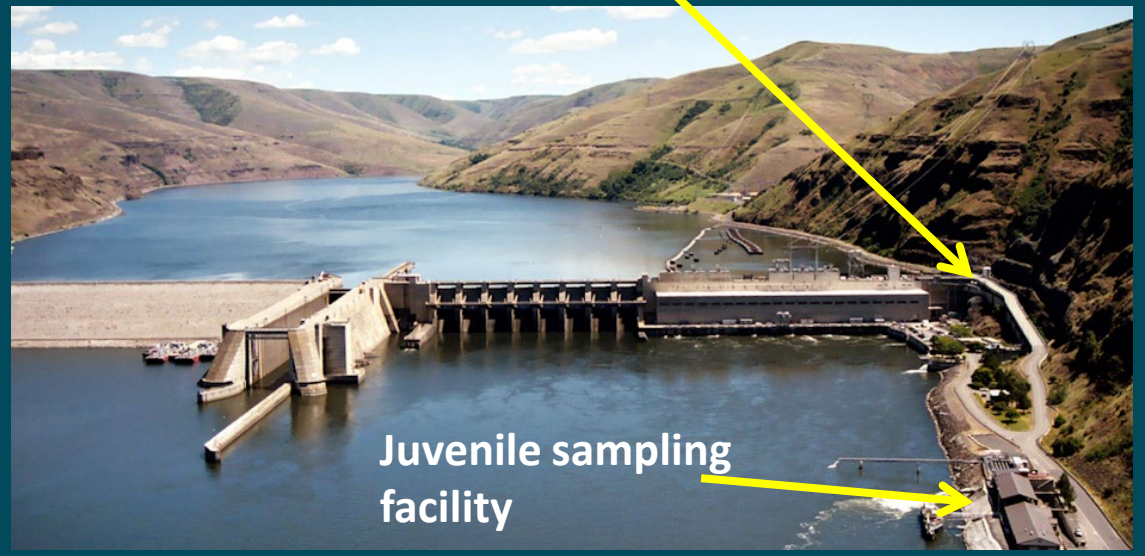
Lower Granite Dam

- Facilities and programs in place to representatively sample fish during adult and juvenile migrations
  - **3,500 – 4,500 adults sampled annually**
  - **1,500 – 2,500 juveniles sampled annually**

Adult Trapping Facility

Counting Window

Adult Fish Ladder

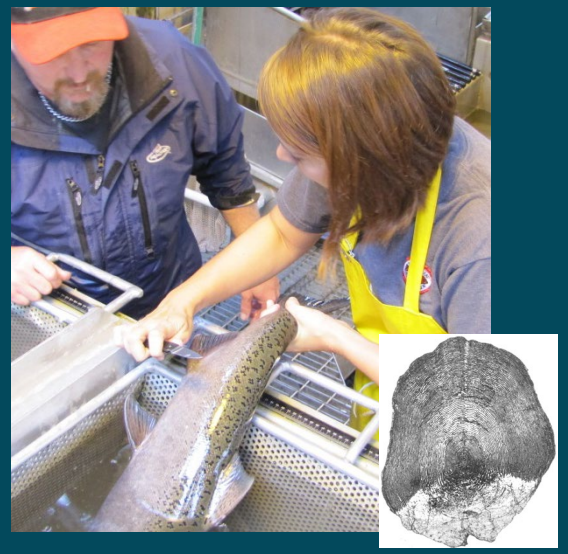


LGR Bio-sampling

PIT Tag

Tissue (Genetics and Sex)

Scale (Age)



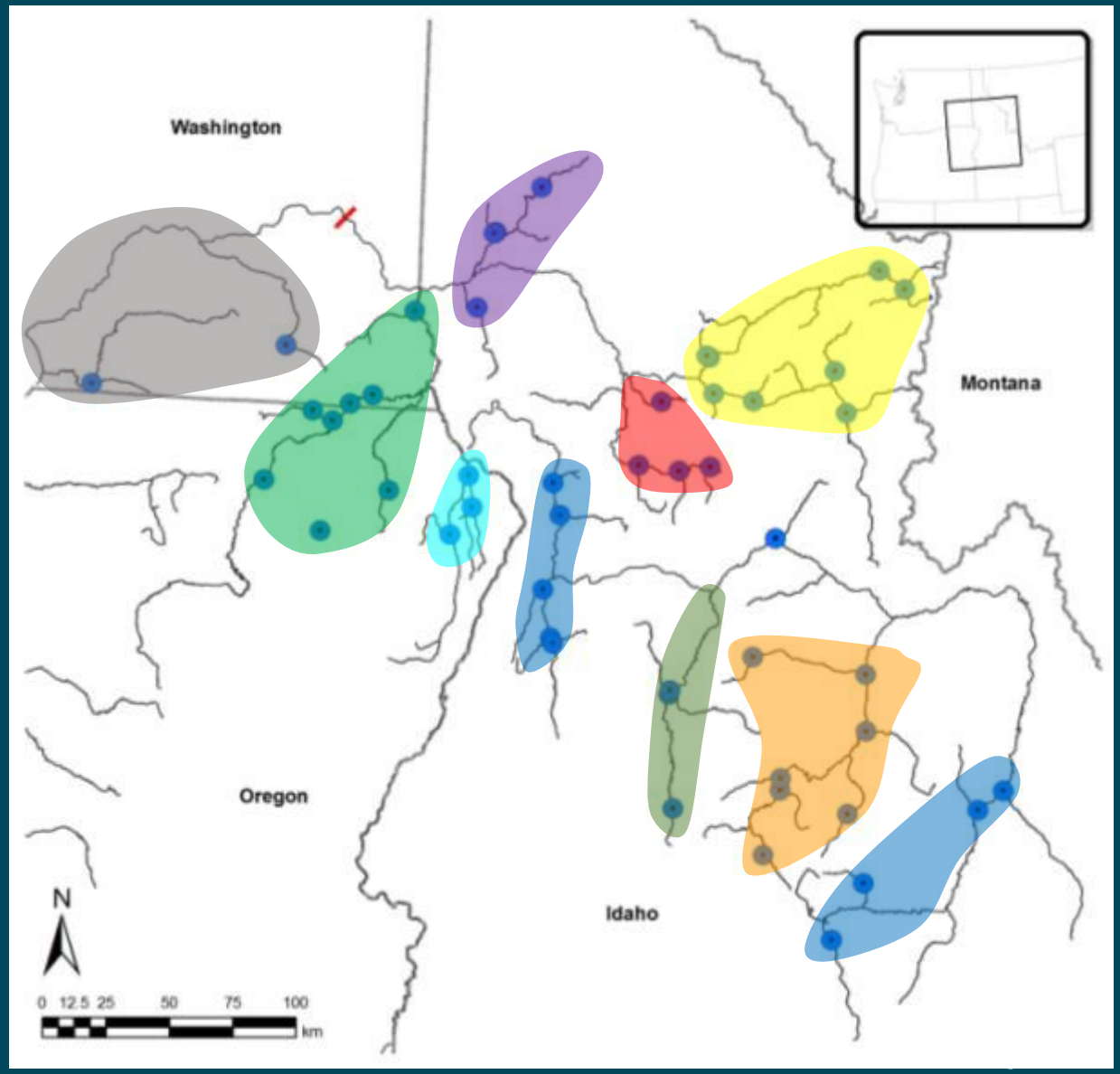
Length

*Trapping date also recorded

Wild Abundance by Genetic Stock

What genetic stock am I from?

Our goal with this sampling is to partition the returning wild run over LGR into their genetic stocks

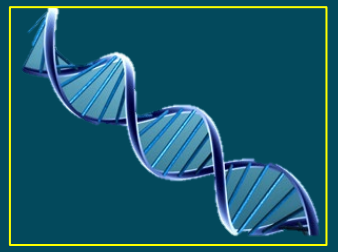


Wild versus Hatchery Determination

Am I hatchery or wild?

LGR Trap
Phenotypic wild

Hatchery PBT
Match



NO

YES

WILD

AD-intact hatchery

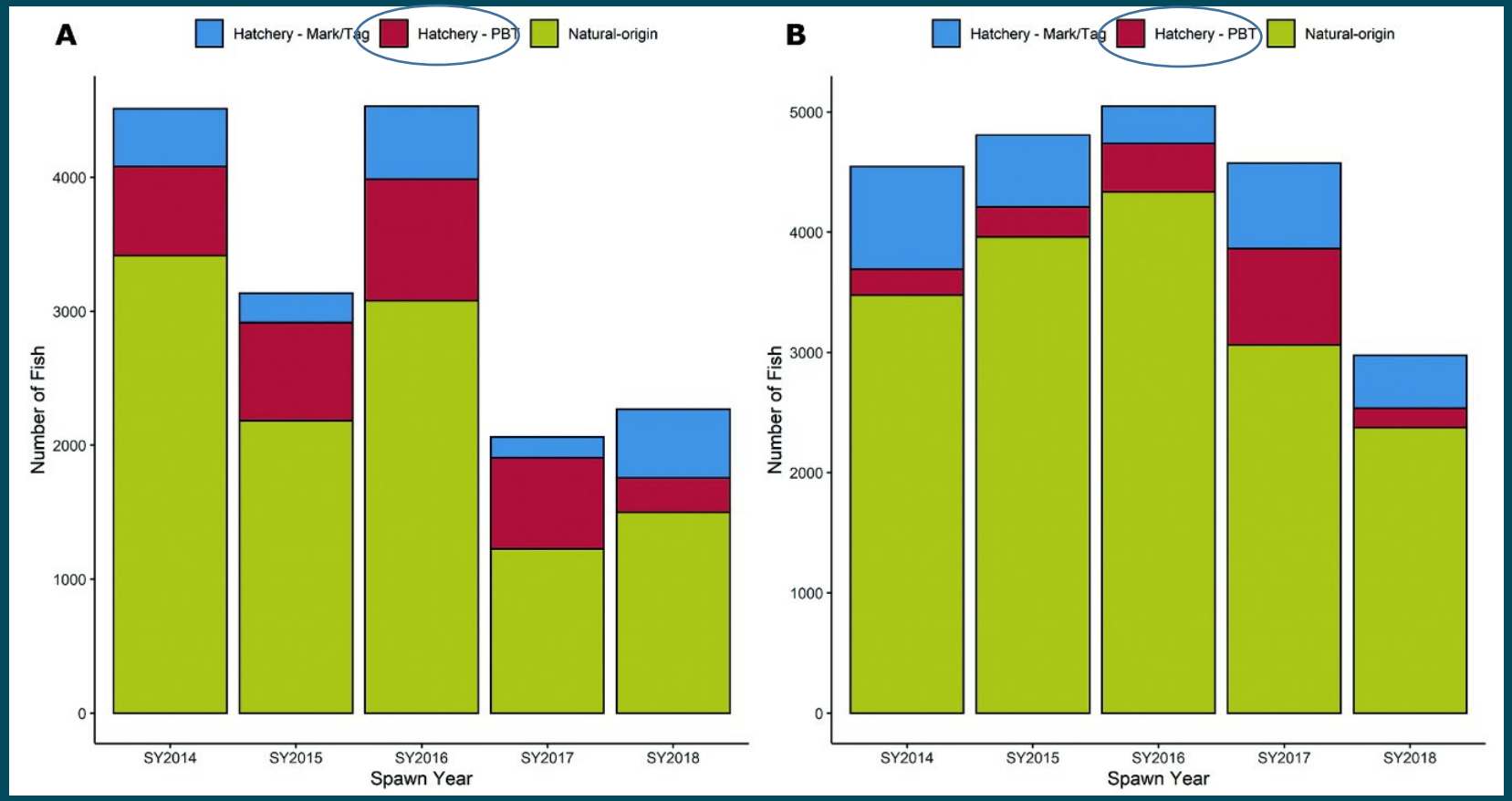
Some hatchery fish are unclipped/marked:

- Intentionally released
- Miss-clipped
- CWT/PIT shed
- CWT/PIT undetected

NOAA FISHERIES
National Oceanic and Atmospheric Administration

NOAA Requires accurate estimates of wild abundance!!!!!

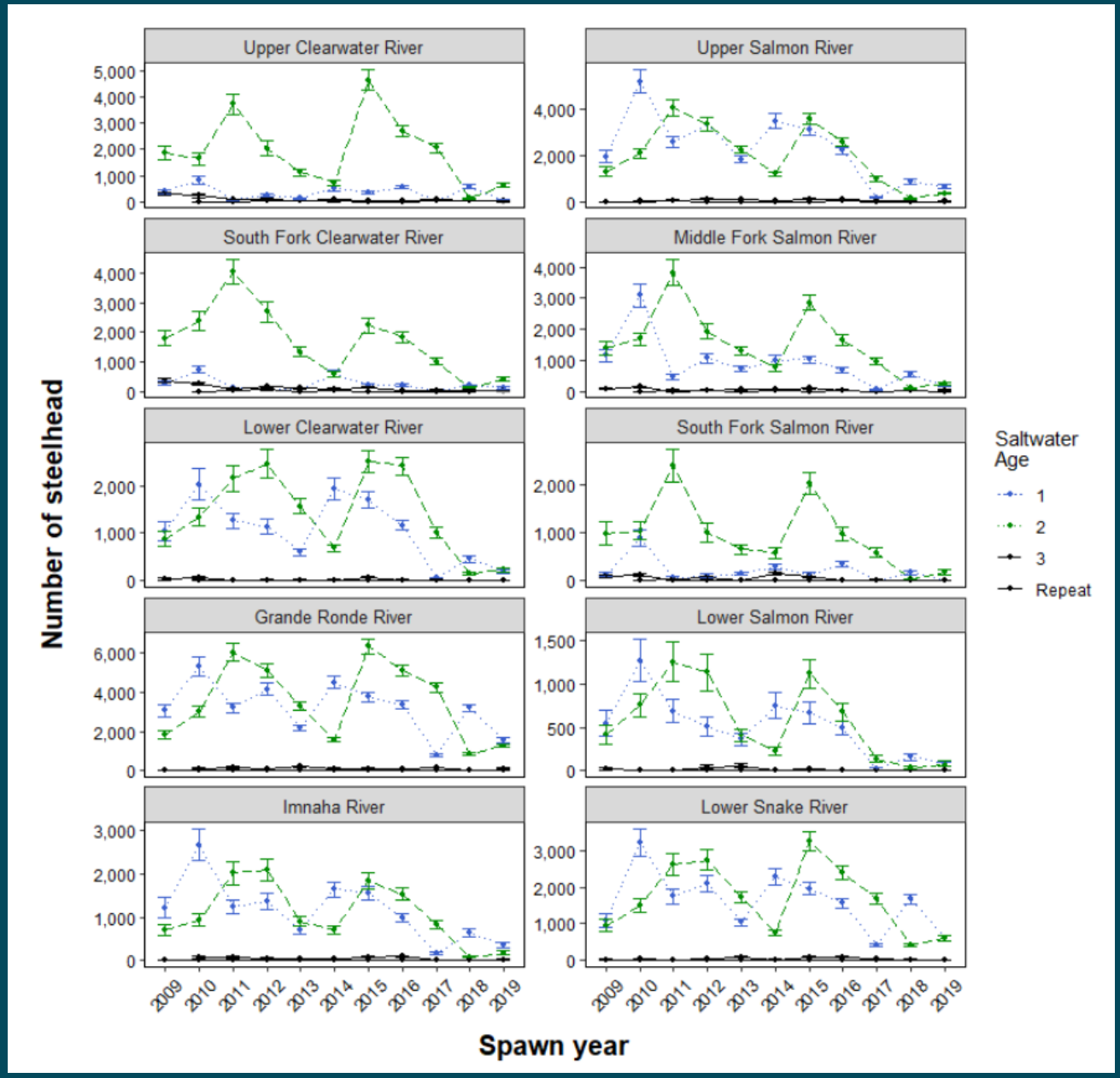
Wild versus Hatchery Determination



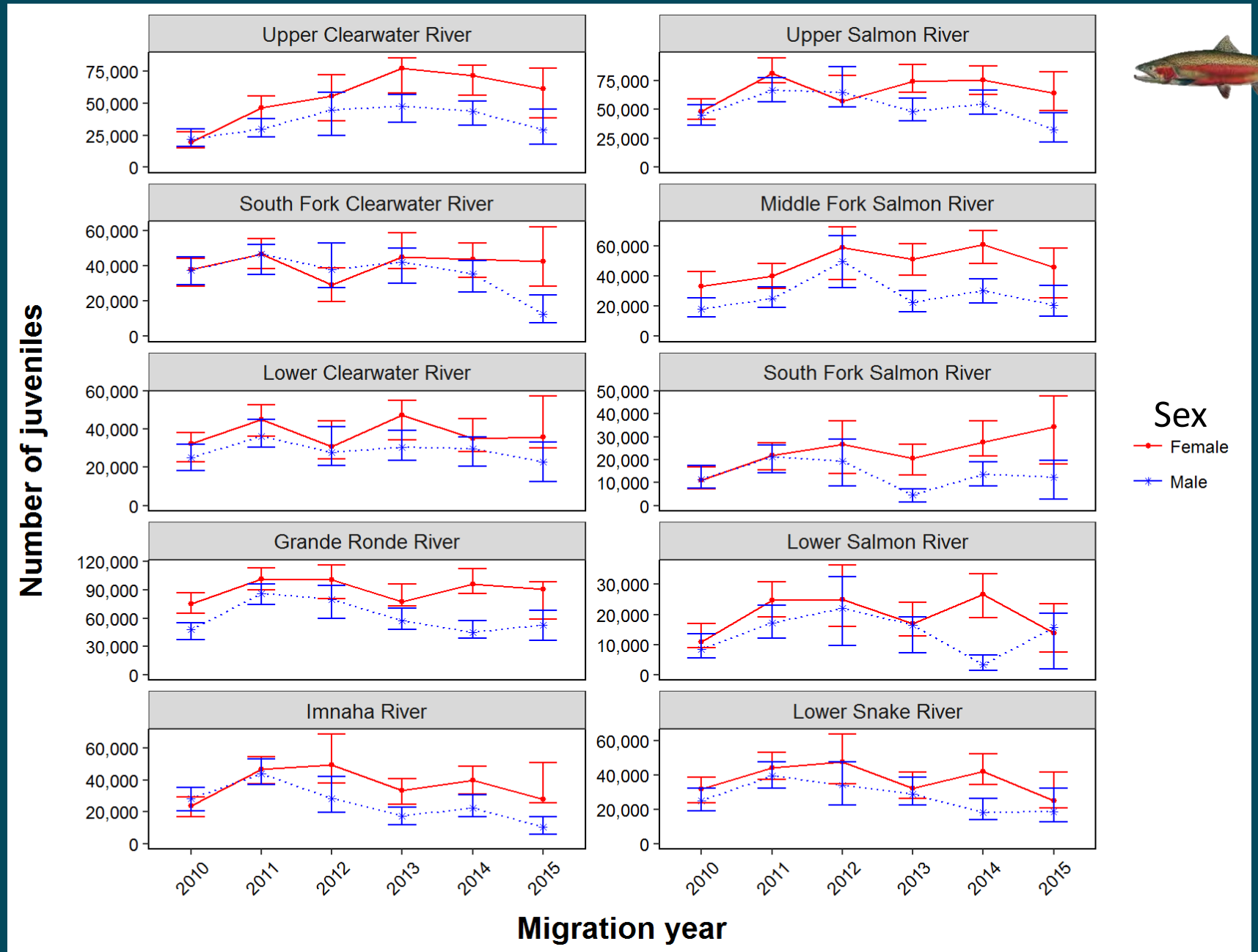
Example (SY2017): PBT makes a difference!!!!!!

Species	Without PBT	With PBT	Difference	%
Steelhead	19,668	15,576	4,092	20.4%
Chinook	9,037	5,793	3,244	35.9%

Wild Escapement – Genetic Stock and saltwater age



Wild juvenile emigration – Genetic Stock by Sex



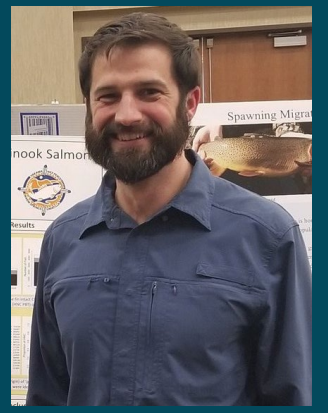
Summary:

1. Major accomplishments achieved for all original objectives

2. Demonstration of comprehensive utility of these genetic technologies for addressing conservation and management issues of importance to the Council and state, tribal and federal fisheries managers

Reasons to be excited about the future?

- # Improvements in genetic markers and genetic baselines
  - John Hargrove continued work to improve and summarize GSI baseline for steelhead (manuscript in prep.)
  - Currently working on improvements to Chinook Salmon GSI Baseline



Panel	GRROND	IMNAHA	LOWCLWR	LOWSALM	LSNAKE	MFSALM	SFCLWR	SFSALM	UPCLWR	UPSALM
v3.1 - 176 SNPs	0.67	0.68	0.66	0.52	0.41	0.90	0.89	0.91	0.93	0.74
v4.0 - 176 SNPs	0.66	0.58	0.58	0.56	0.41	0.87	0.88	0.86	0.91	0.72
v4.0 - 334 SNPs	0.80	0.74	0.71	0.62	0.49	0.92	0.90	0.99	0.95	0.86
v4.0 - 334 SNP/MH	0.85	0.77	0.73	0.64	0.56	0.93	0.91	0.99	0.96	0.88
Improvement	**0.19**	**0.09**	**0.07**	**0.12**	**0.15**	**0.03**	**0.02**	**0.08**	**0.03**	**0.13**

Self-assignment rates (proportion correct to genetic stock)

Grandparentage Testing

Thomas Delomas
Quantitative Geneticist
Kingston, RI
US Department of Agriculture (USDA) Agricultural Research Service (ARS)

North American Journal of Fisheries Management

ARTICLE

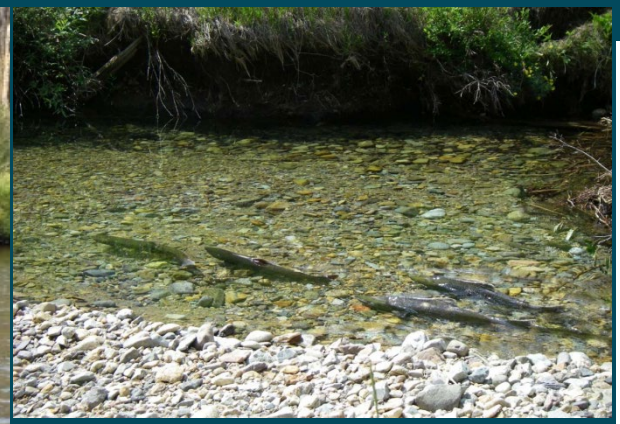
Grandparent inference from genetic data: The potential for parentage-based tagging programs to identify offspring of hatchery strays

Thomas A. Delomas, Matthew Campbell

First published: 27 October 2021 | https://doi-org.libproxy.boisestate.edu/10.1002/nafm.10714

• Benefits of PBT technology

➢ PBT also can be used to identify the origin of straying hatchery fish



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DOI: 10.1080/00028487.2016.1146163

ARTICLE

Maximum Likelihood Estimation of the Proportion of Hatchery-Origin Fish on Spawning Grounds Using Coded Wire Tagging and Parentage-Based Tagging

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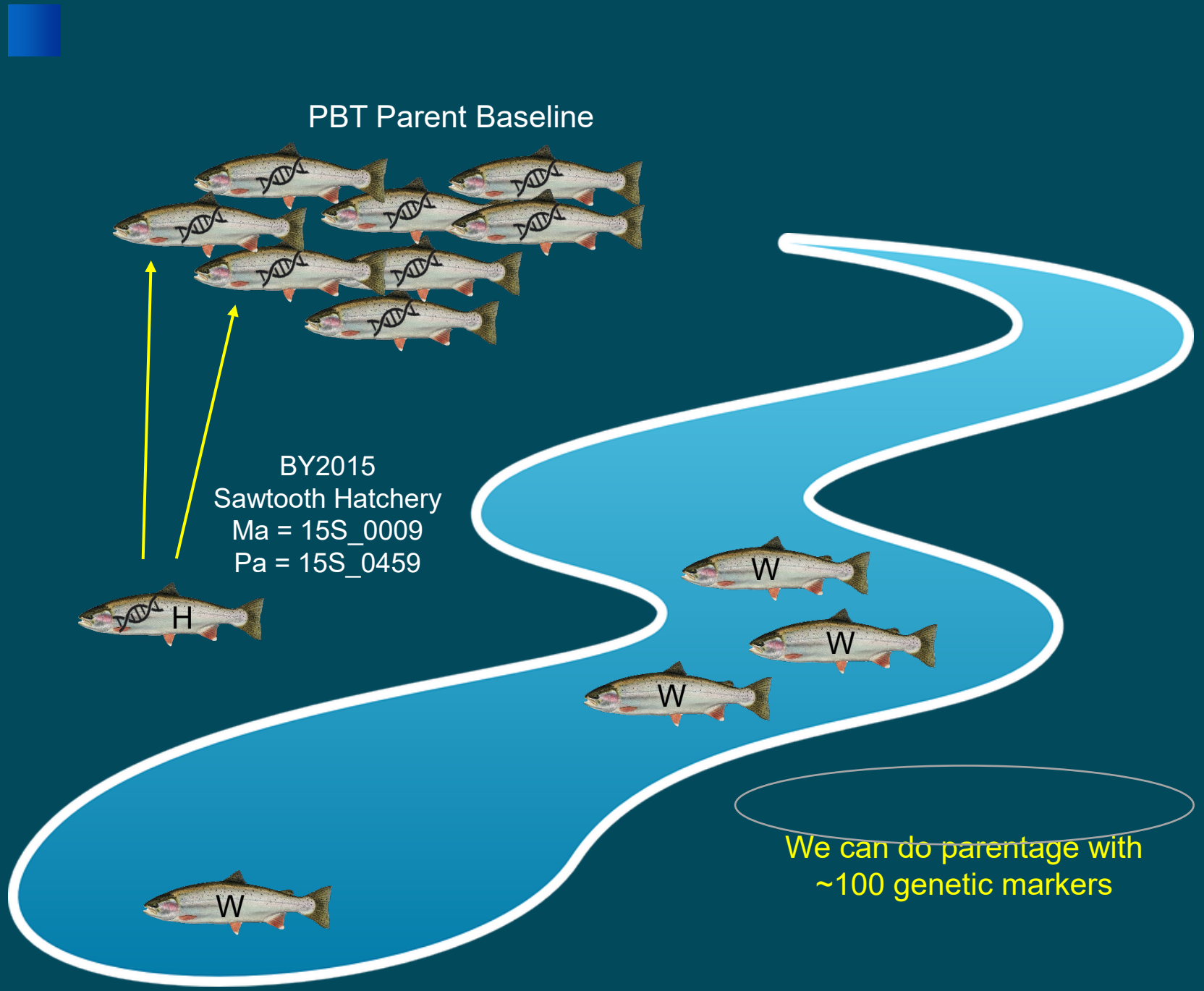
Bonneville Power Administration, 905 Northeast 11th Avenue, Portland, Oregon 97232, USA

Brian L. Maschhoff
Salmonetics, 7813 1st Avenue Northwest, Seattle, Washington 98117, USA

Hinrichsen et al (2016)-”*In the South Fork Salmon River application, there were 340% more PBT recoveries than CWT recoveries, leading to greater precision in release-specific values of p from maximum likelihood estimation.*”


PBT Parent Baseline
BY2015
Sawtooth Hatchery
Ma = 15S_0009
Pa = 15S_0459
H
W
W
W
W
We can do parentage with
~100 genetic markers

OmySALM19C_0003
710 mm

OmySAWT15S_0009
680 mm

OmySAWT15S_0459
680 mm

OmySAWT11S_0397
590 mm

OmySAT11S_0193
640 mm

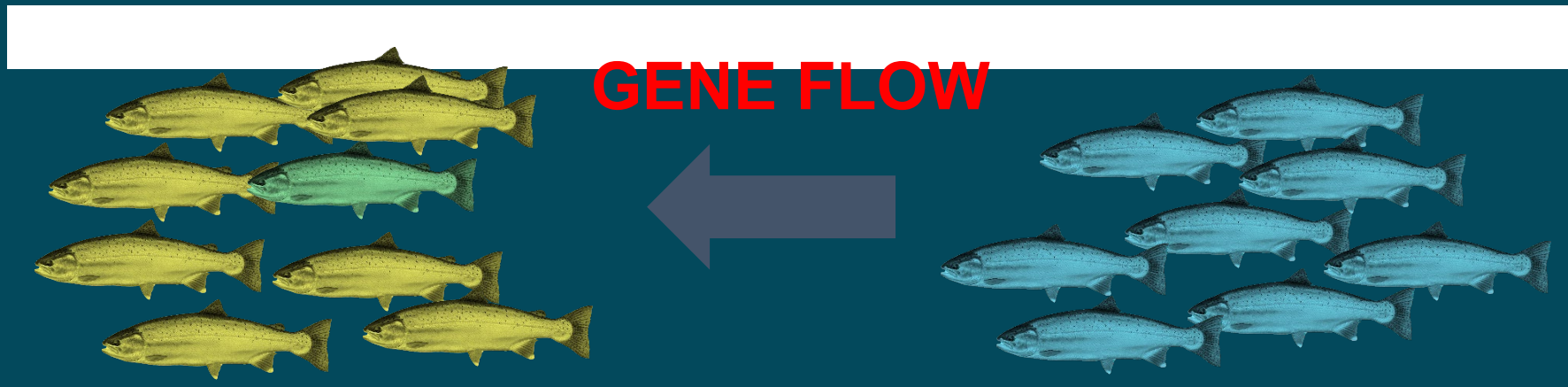
OmySAWT11S_0229
560 mm

OmySAWT11S_0025
660 mm

- **NOAA wants this information**

➢ Status assessments for ESA-listed salmon populations in the Snake River and Columbia River basins, require reliable estimates of the proportion of hatchery-origin spawners on the spawning grounds, or pHOS (McClure et al. 2003)

➢ However, pHOS is actually just a surrogate for what geneticists and managers would really like to monitor:



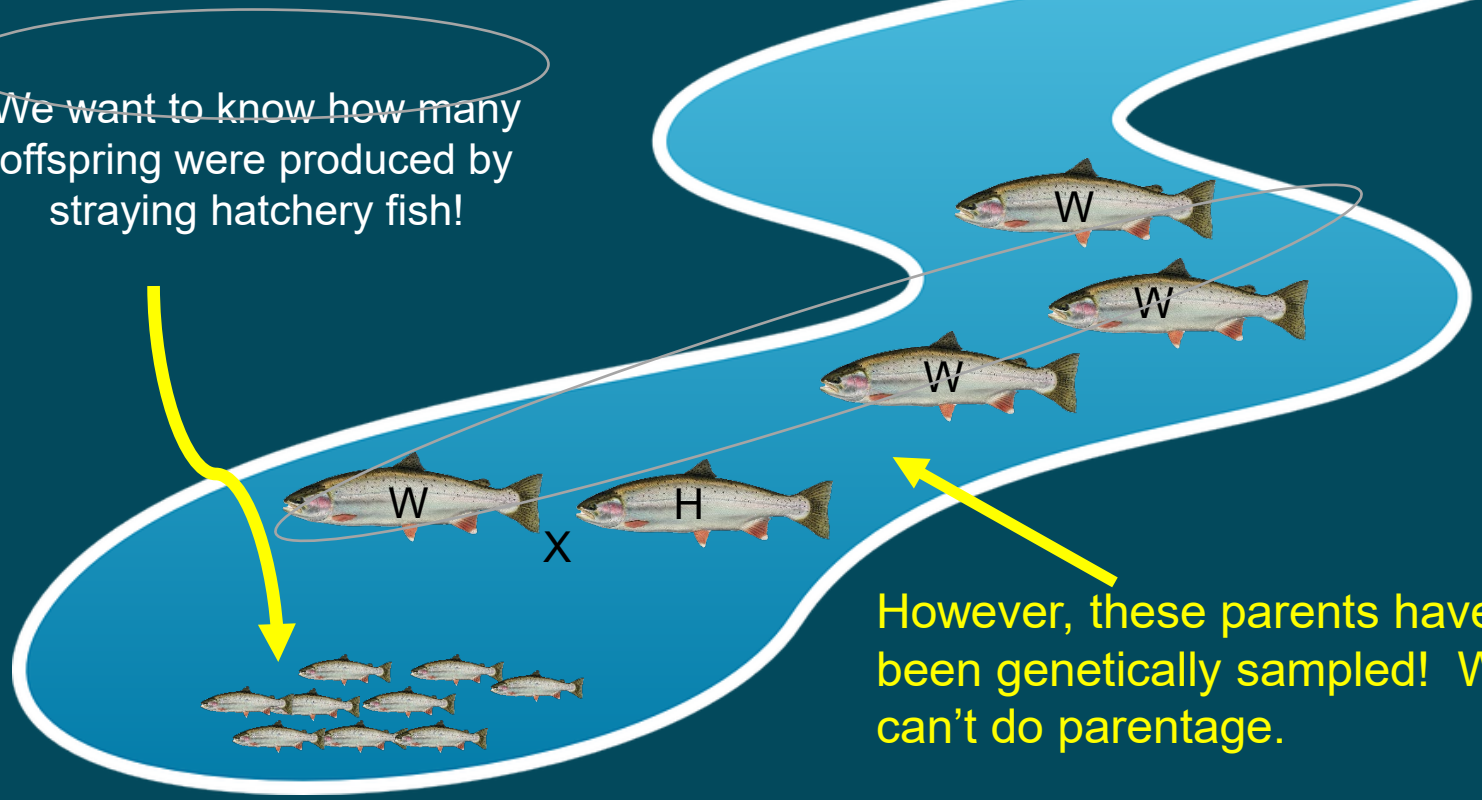
➢Gene flow only occurs if hatchery fish successfully mate with wild fish and produce offspring!

PBT Parent Baseline

We want to know how many offspring were produced by straying hatchery fish!

PBT Parent Baseline

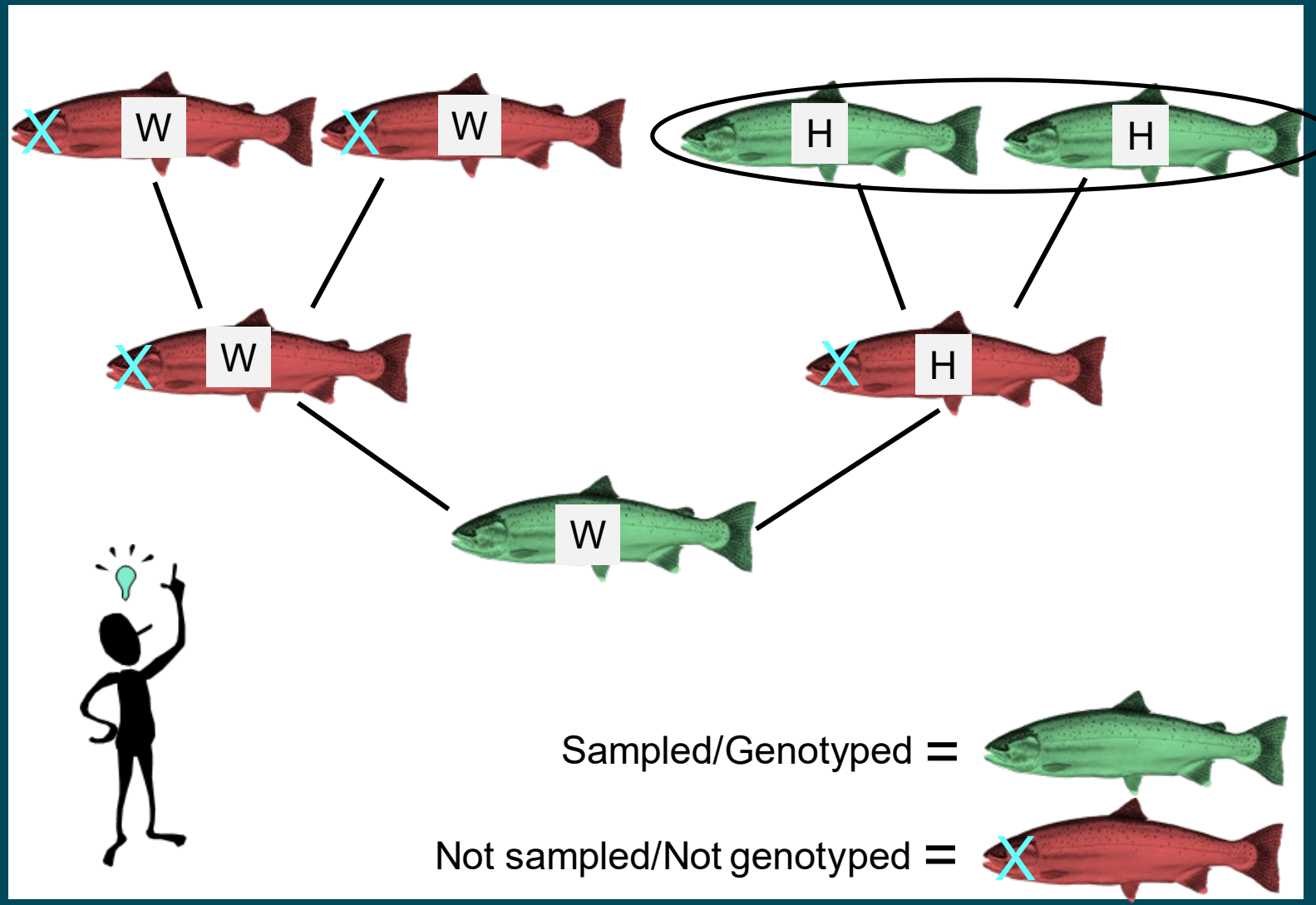
We want to know how many offspring were produced by straying hatchery fish!



However, these parents haven't been genetically sampled! We can't do parentage.

Genetic Sample
Date:
Species:
Sex: M F U
Field Number:
Location:
Collector Info:
Fork Length: (mm)
Comments:
OmySALM19C_0003
710 mm
OmySAWT15S_0009
680 mm
OmySAWT15S_0459
680 mm
590 mm
OmySAT11S_0193
640 mm
OmySAWT11S_0229
560 mm
660 mm

- **What are we testing?**
  - **With sufficient genetic markers we can extend PBT to identify grandparent-grandchild relationships**

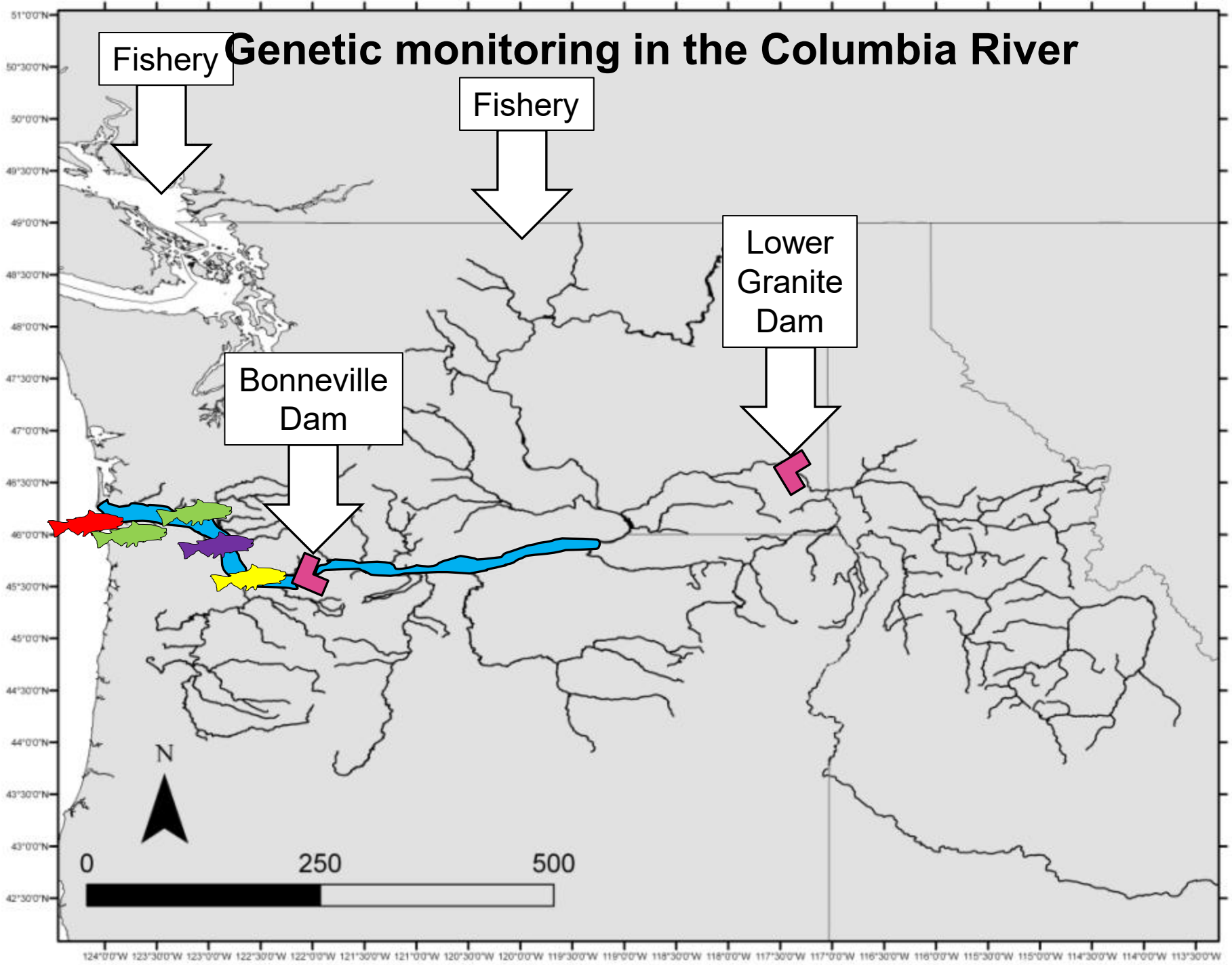


Current working on 2 POF studies

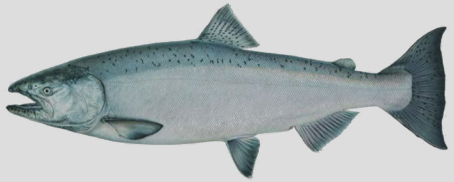
- We will be testing wild steelhead adults captured at Lower Granite Dam (samples in hand, largescale POC)
- But the technology can be applied at any life-stage
- Both juvenile and adult sampling is already conducted on many streams throughout the Snake River Basin

Jon’s up next!!!

Genetic monitoring in the Columbia River



Chinook salmon



Steelhead

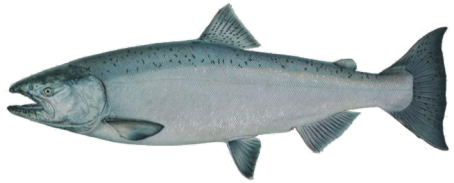
Sockeye salmon

Coho salmon

COUNTING FISHES FOR MANAGEMENT

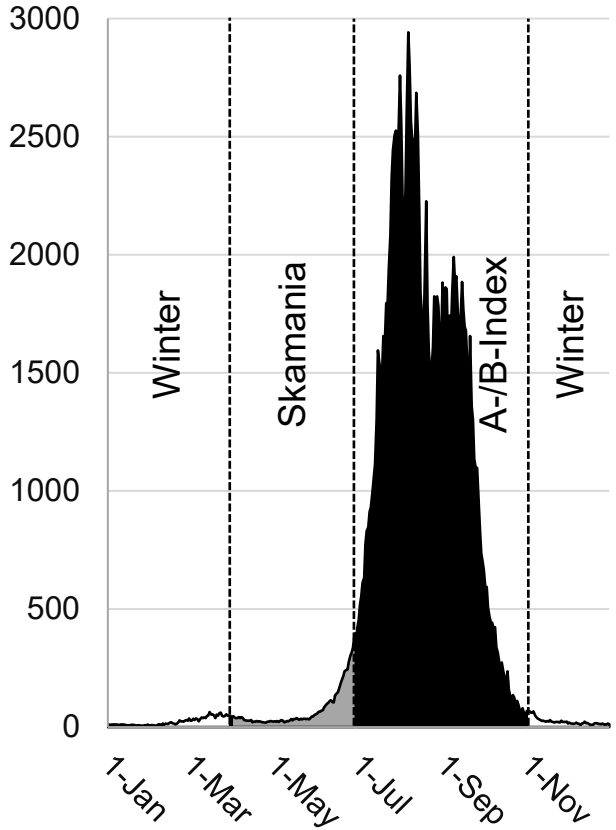
Steelhead

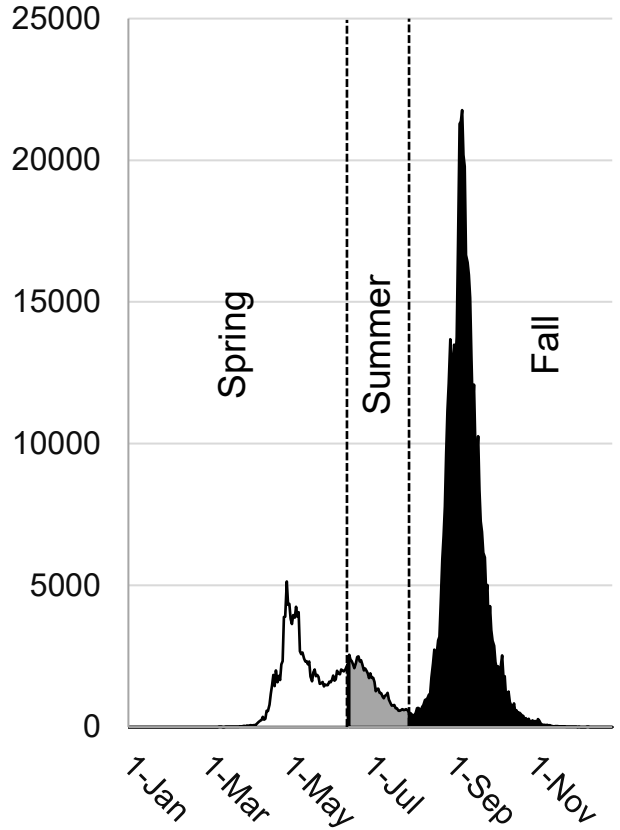
Chinook

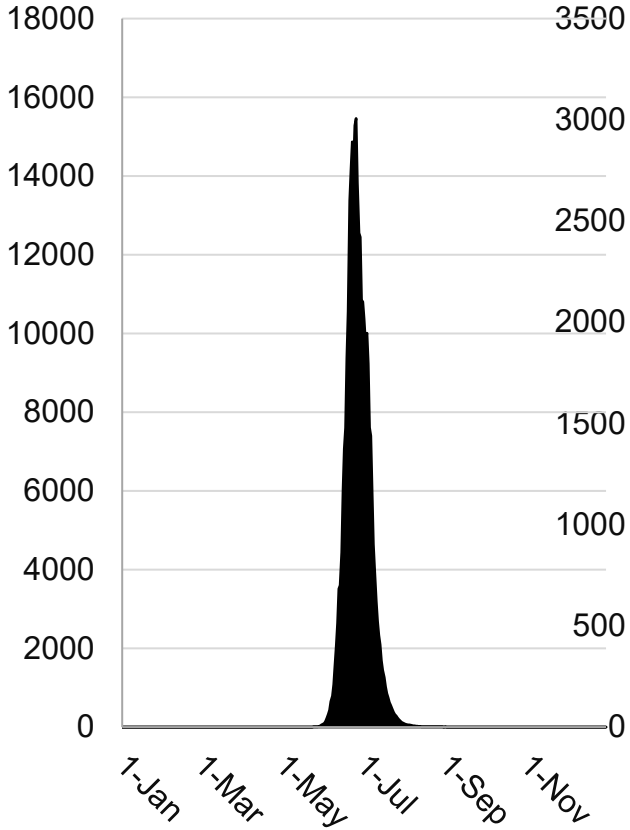


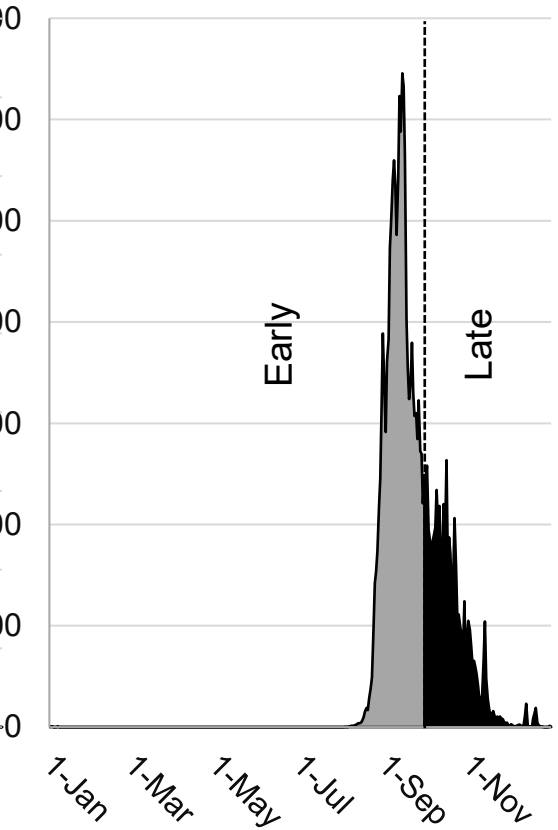
Sockeye

Coho

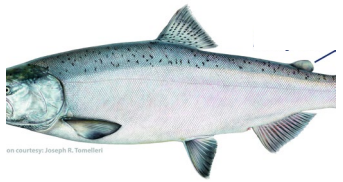






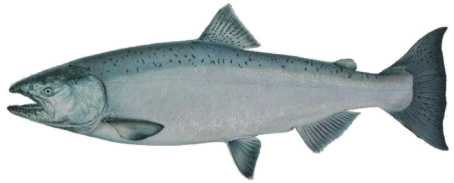


COUNTING FISHES FOR MANAGEMENT



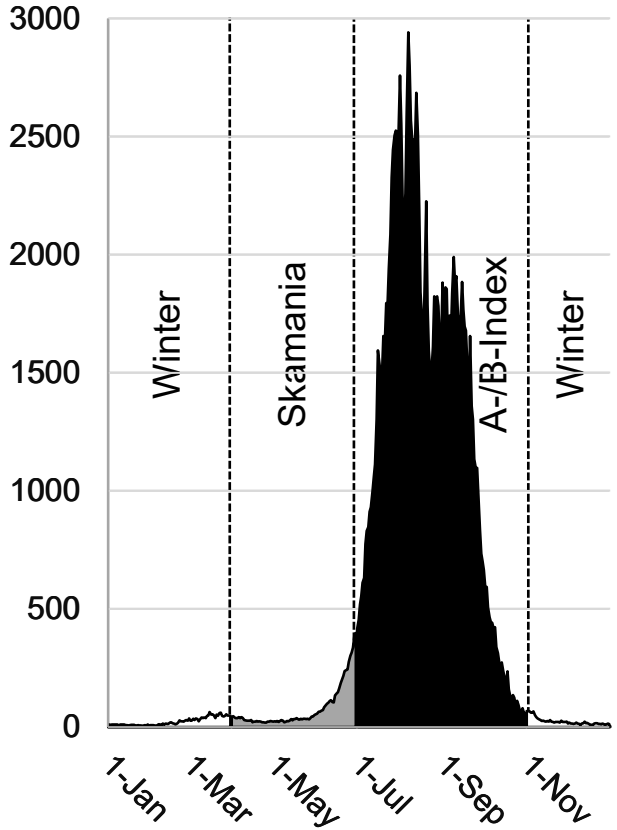
Steelhead

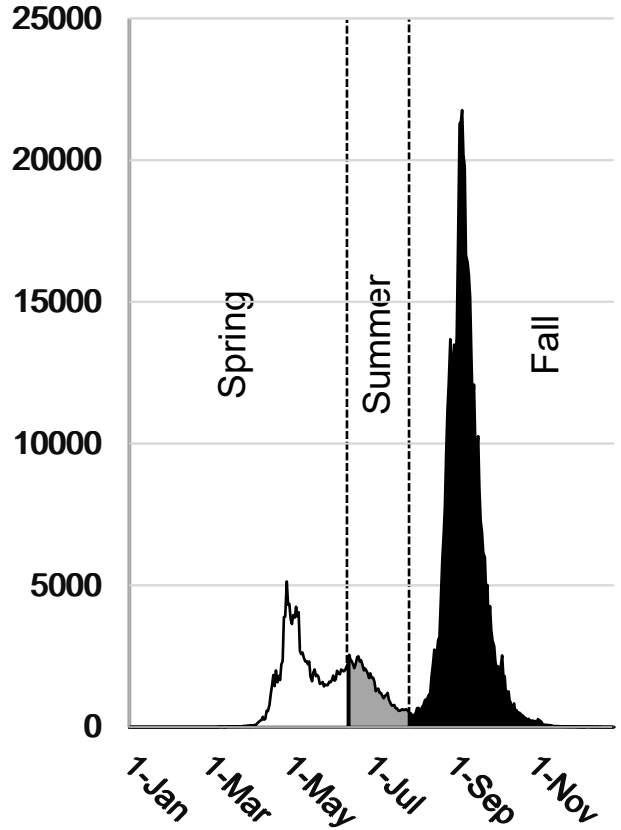
Chinook ★

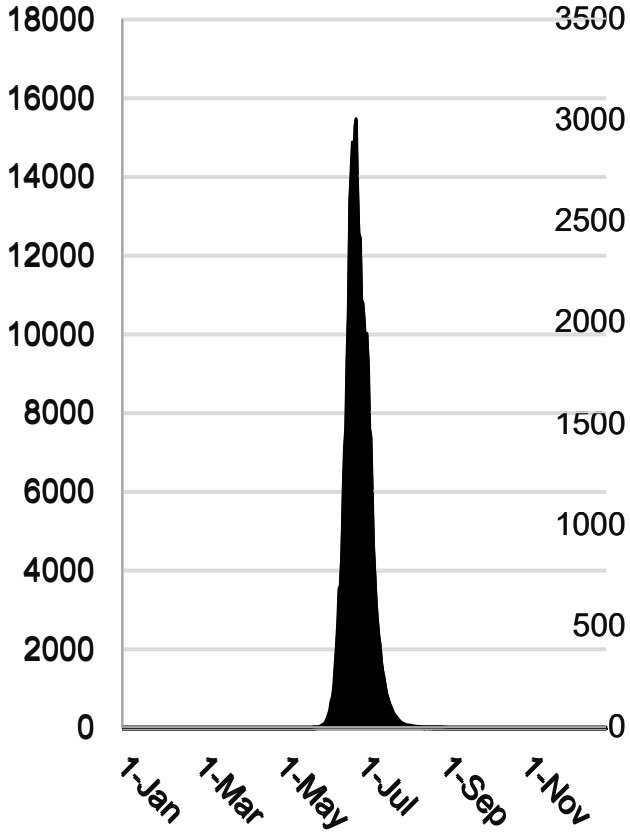


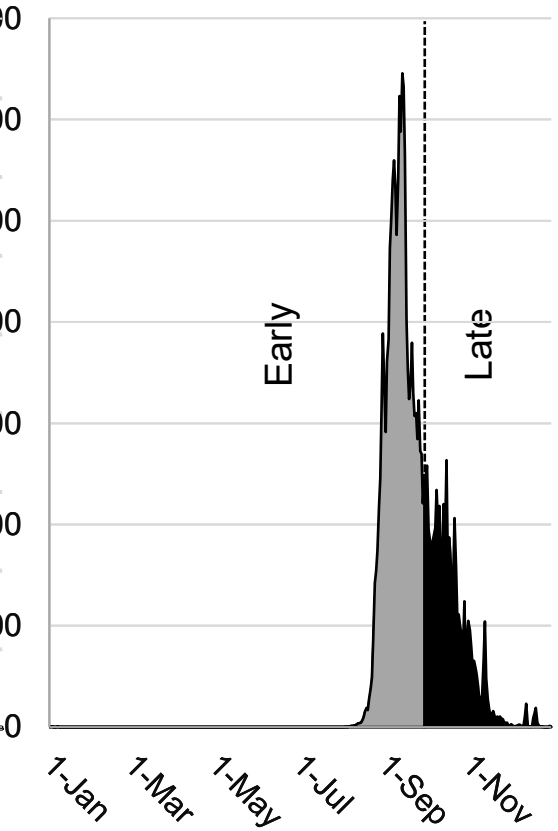
Sockeye ★

Coho ★





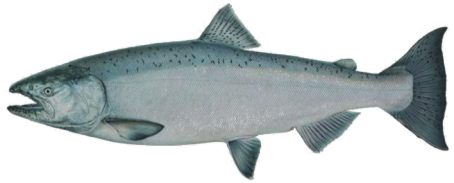




COUNTING FISHES FOR MANAGEMENT

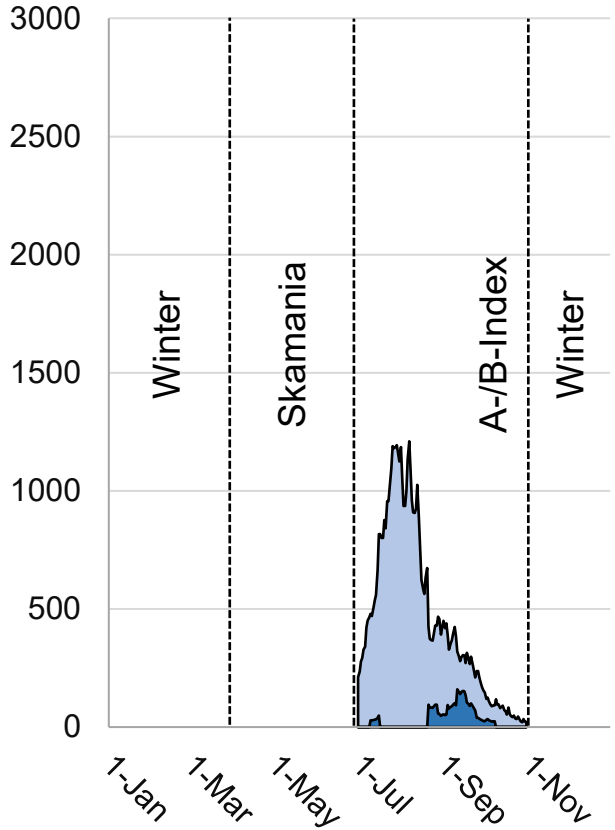
A-/B-Index Steelhead

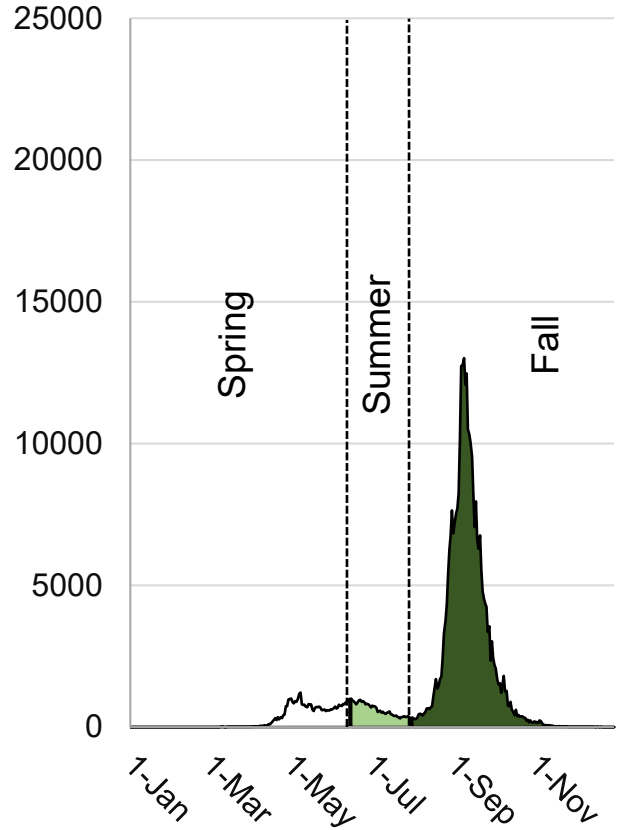
Chinook

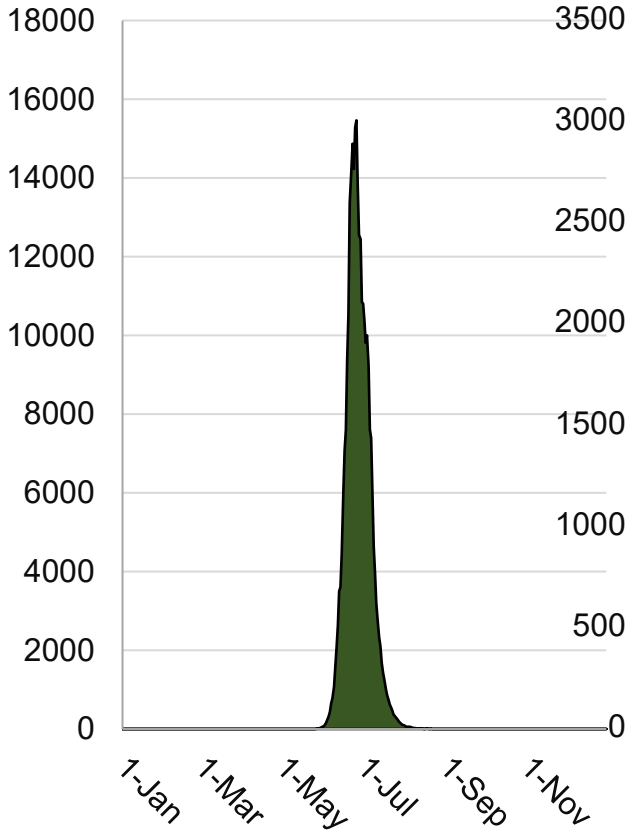


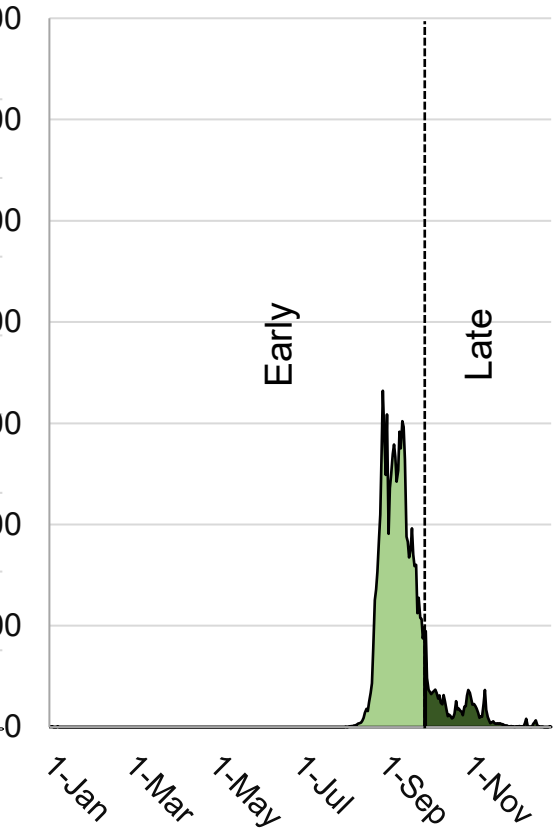
Sockeye

Coho







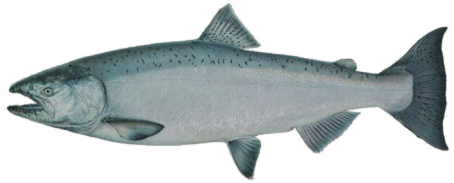


COUNTING FISHES FOR MANAGEMENT

PBT

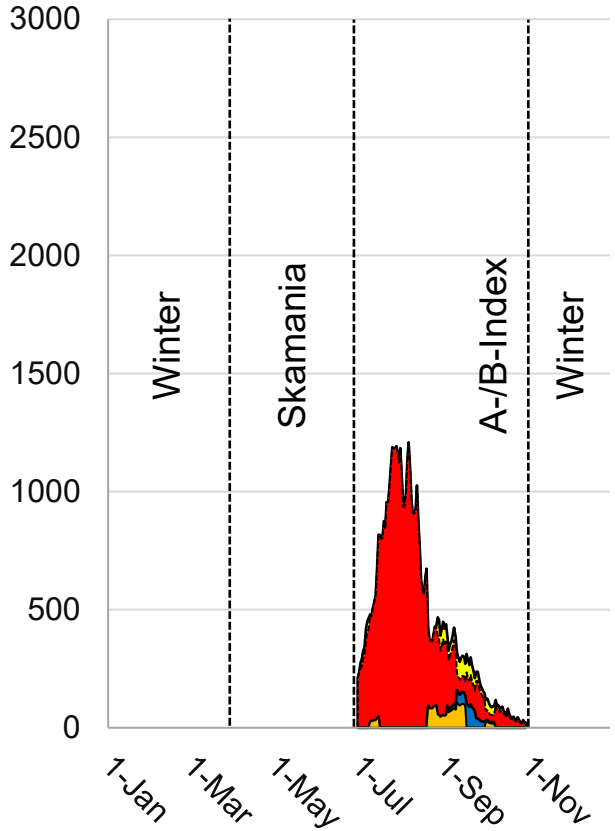
A-/B-Index Steelhead

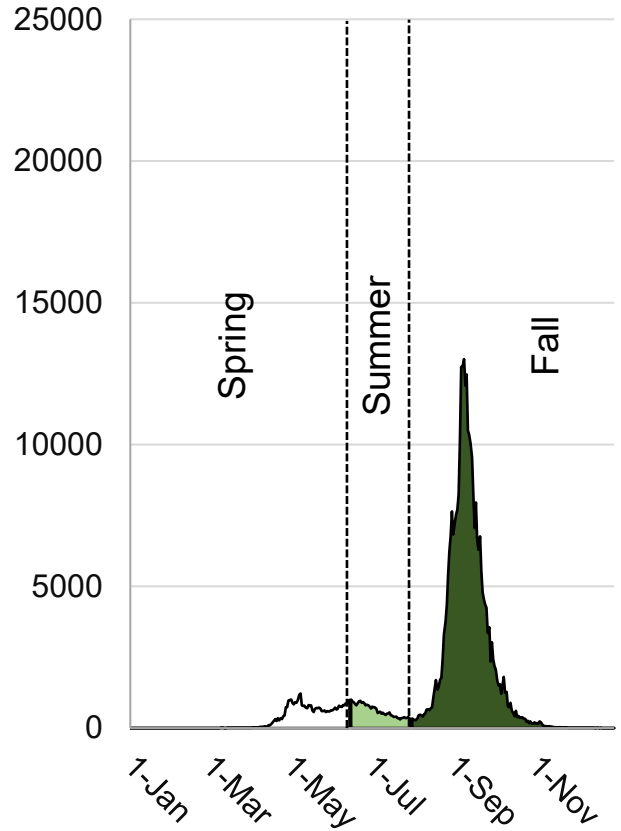
Chinook

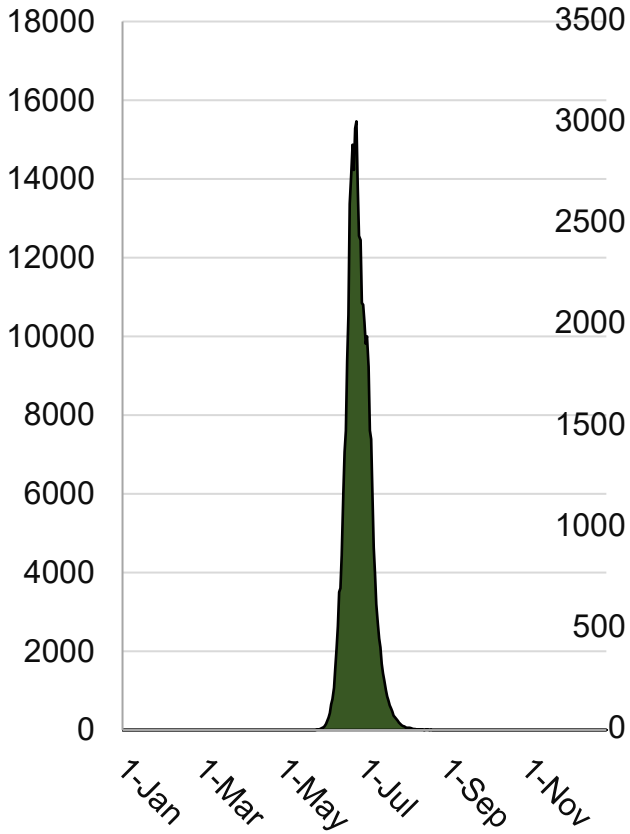


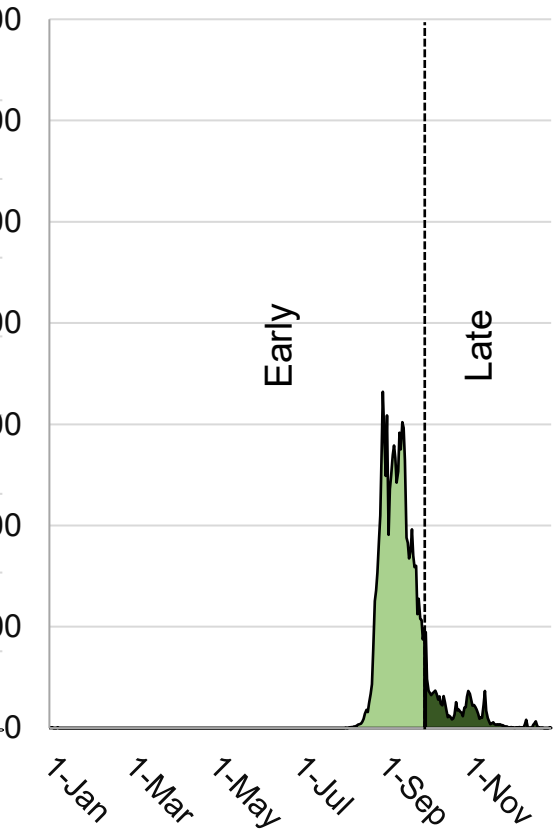
Sockeye

Coho

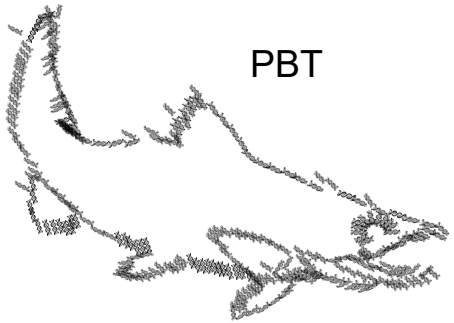




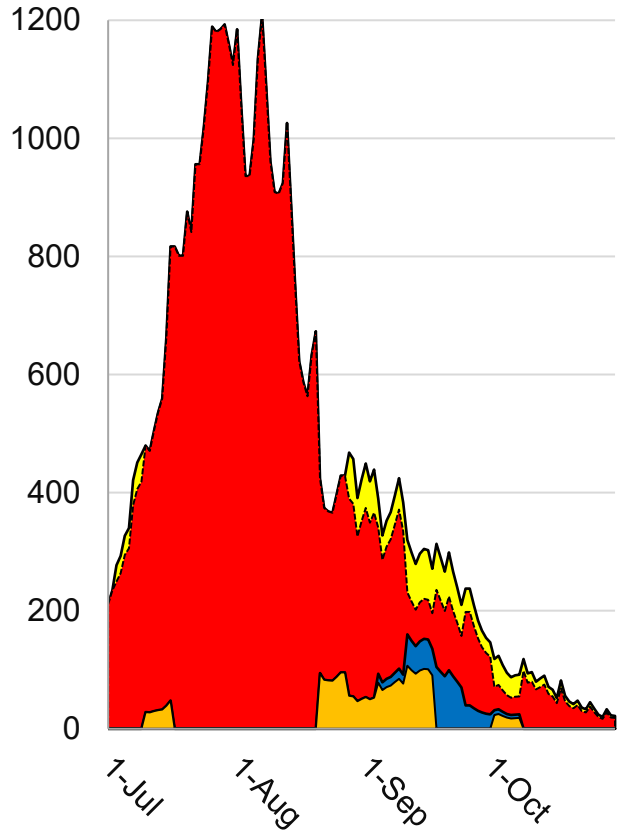




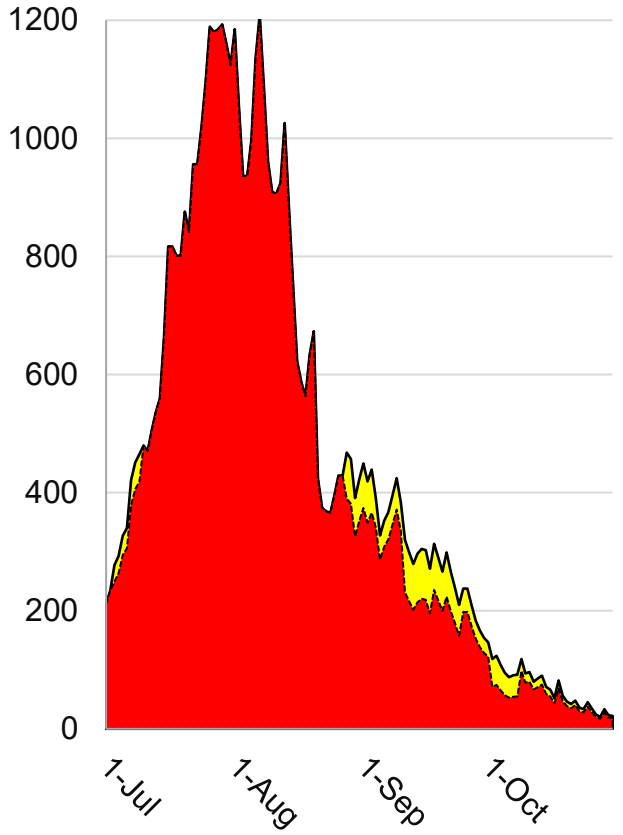
COUNTING FISHES FOR MANAGEMENT



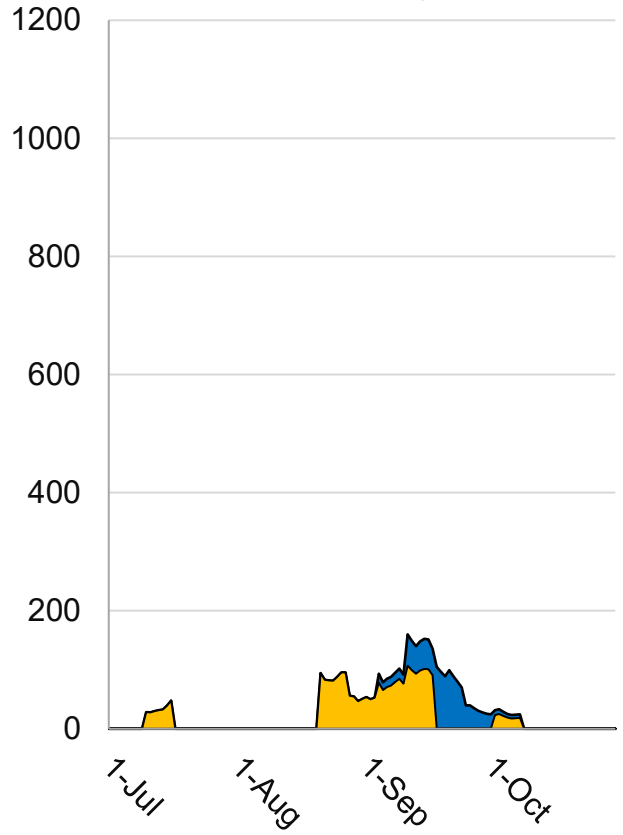
A-/B-Index Steelhead



A-Index Steelhead



B-Index Steelhead



COUNTING FISHES FOR MANAGEMENT

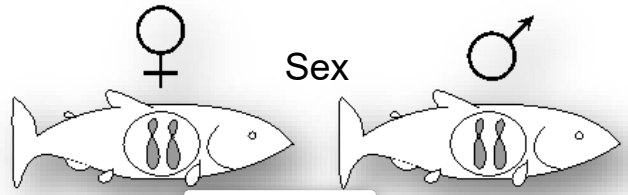
PBT

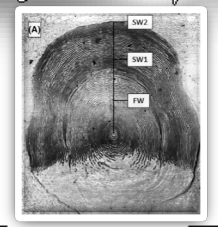
A-/B-Index Steelhead

A-Index Steelhead

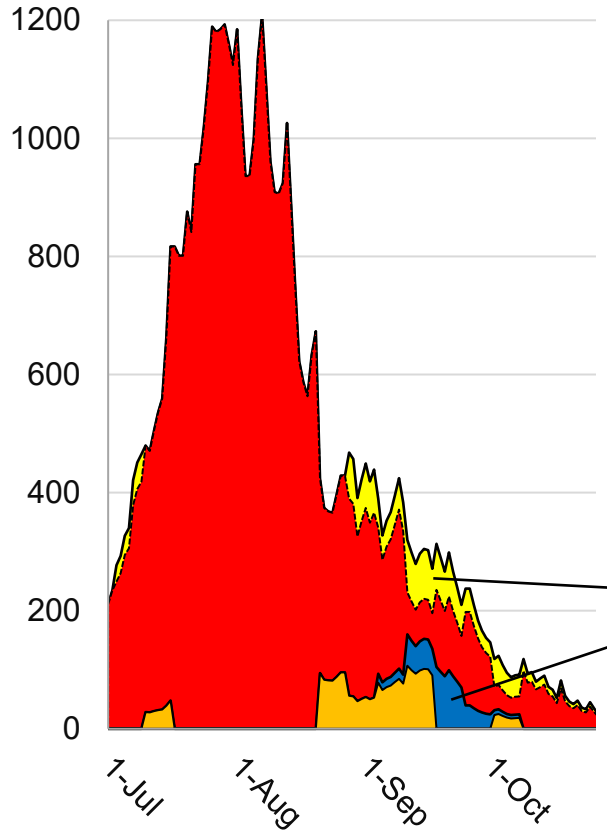
B-Index Steelhead

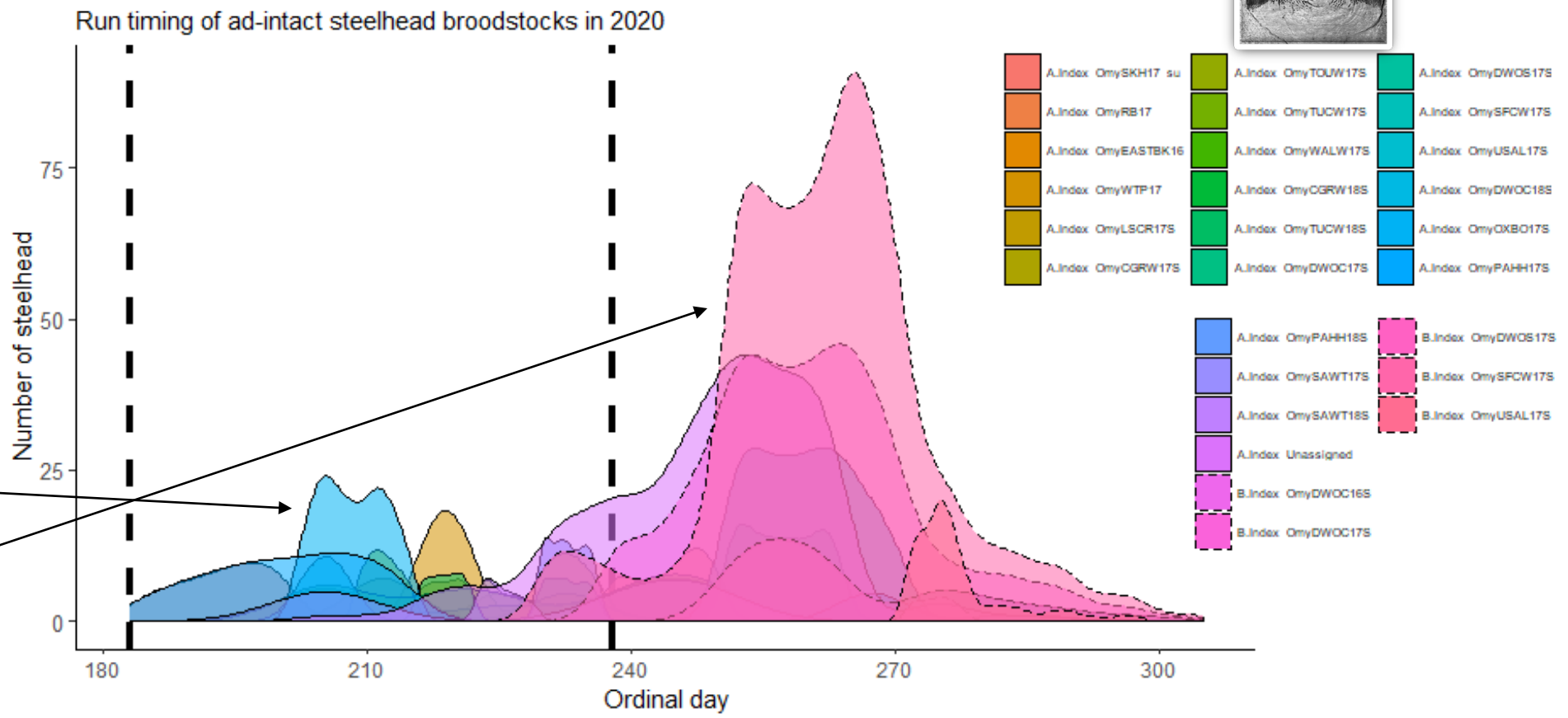
Sex





Ocean age





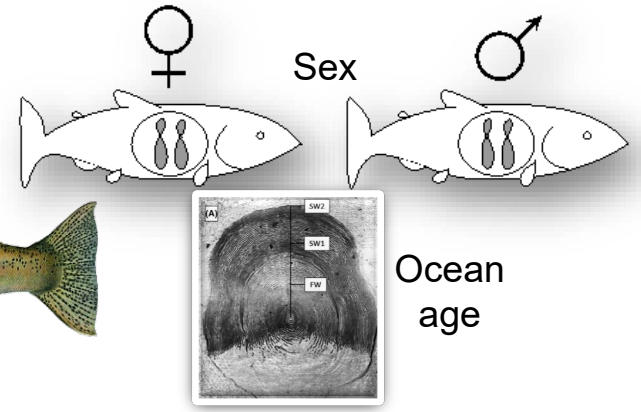
COUNTING FISHES FOR MANAGEMENT

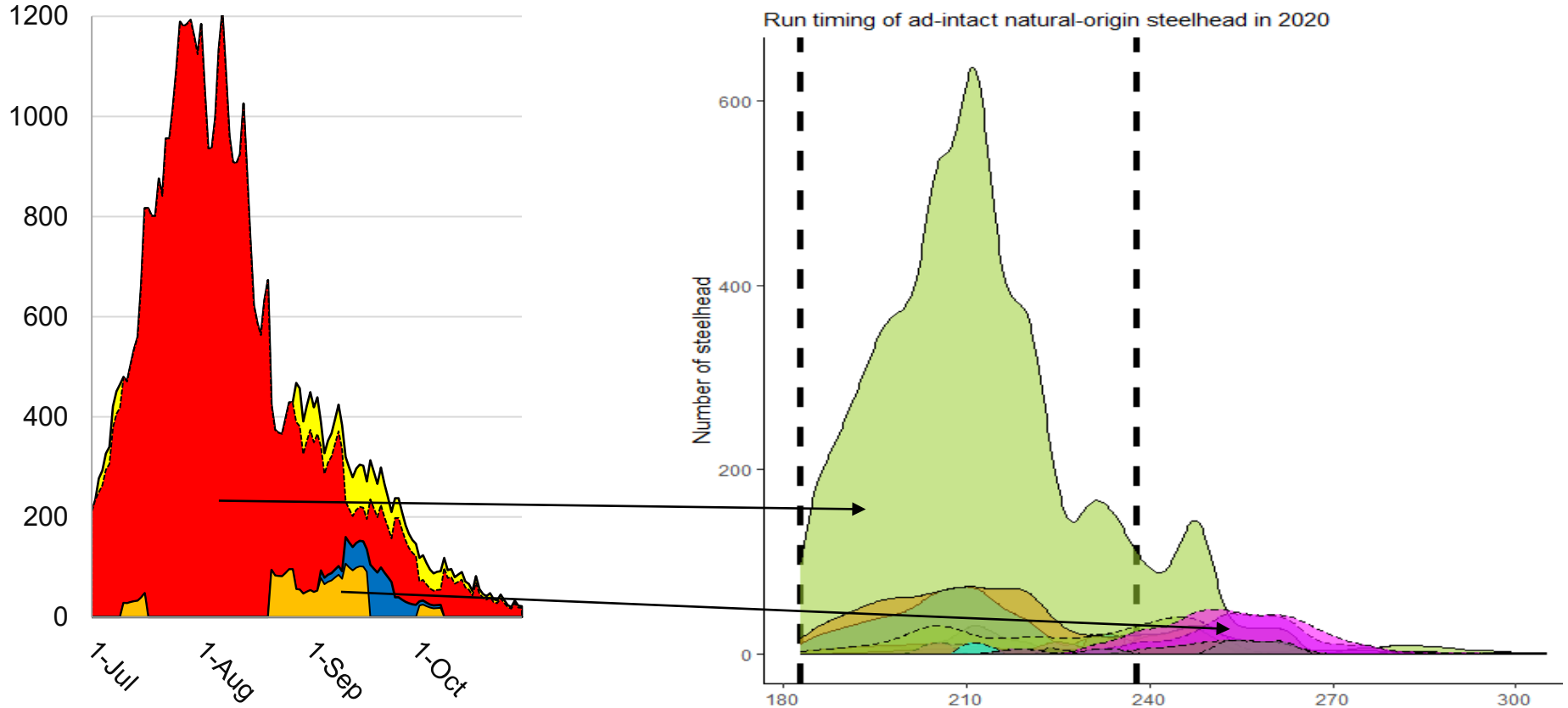
GSI

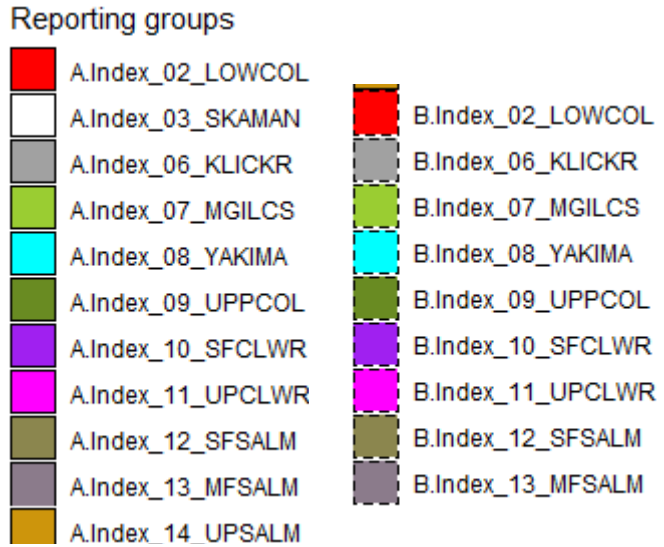
A-/B-Index Steelhead

A-Index Steelhead

B-Index Steelhead





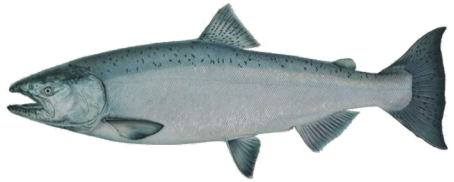


GENETIC STOCK ID BASELINES

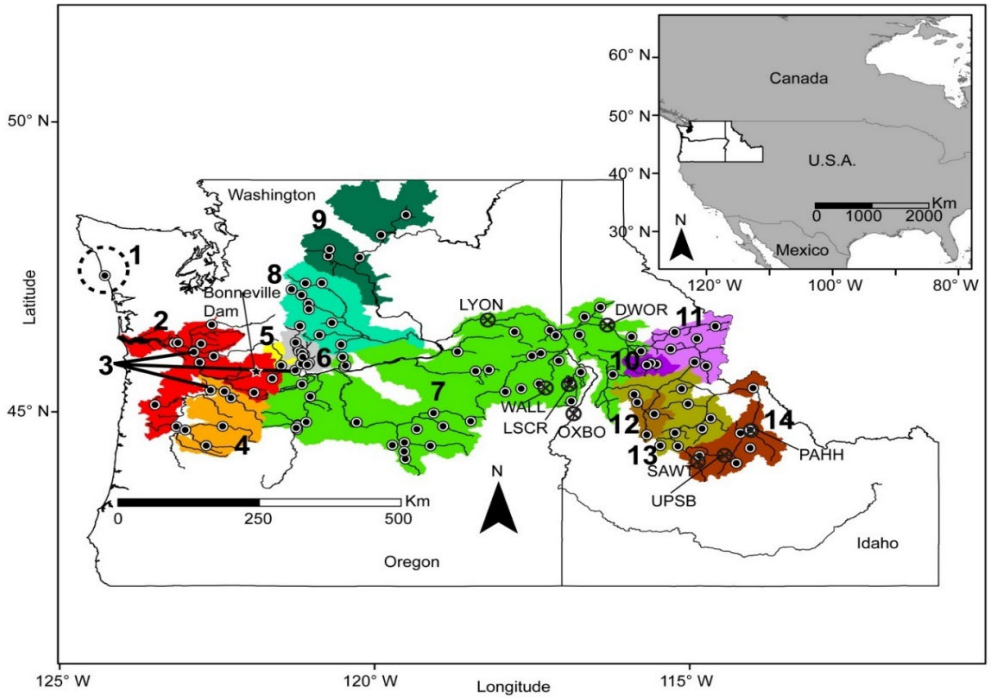
Utility to assign <u>natural origin</u> fish

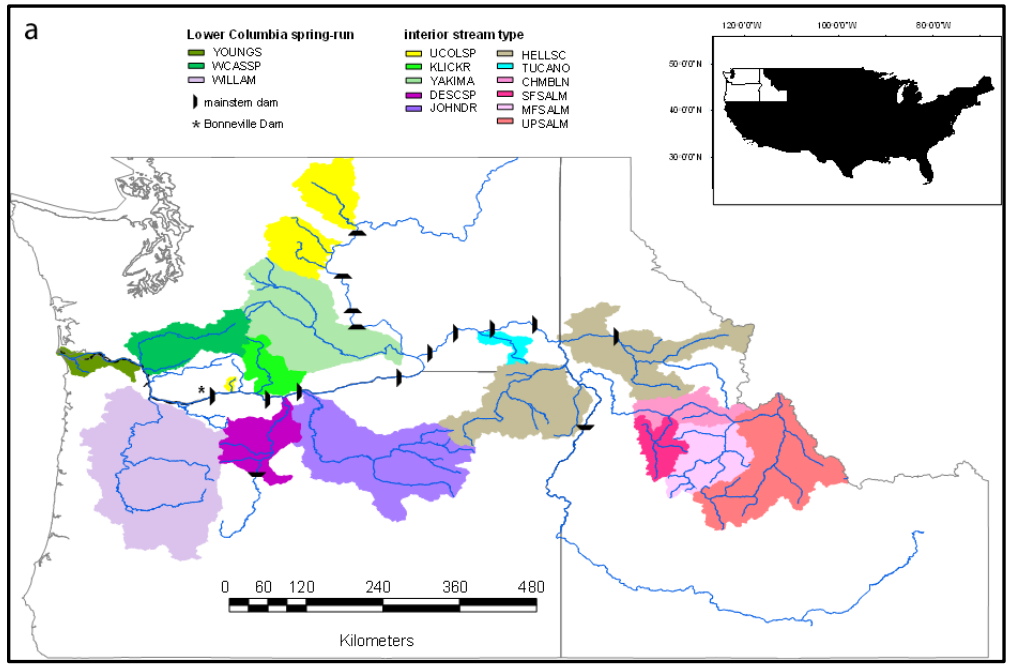
Genetic Stock Identification (GSI)

Steelhead



Chinook salmon



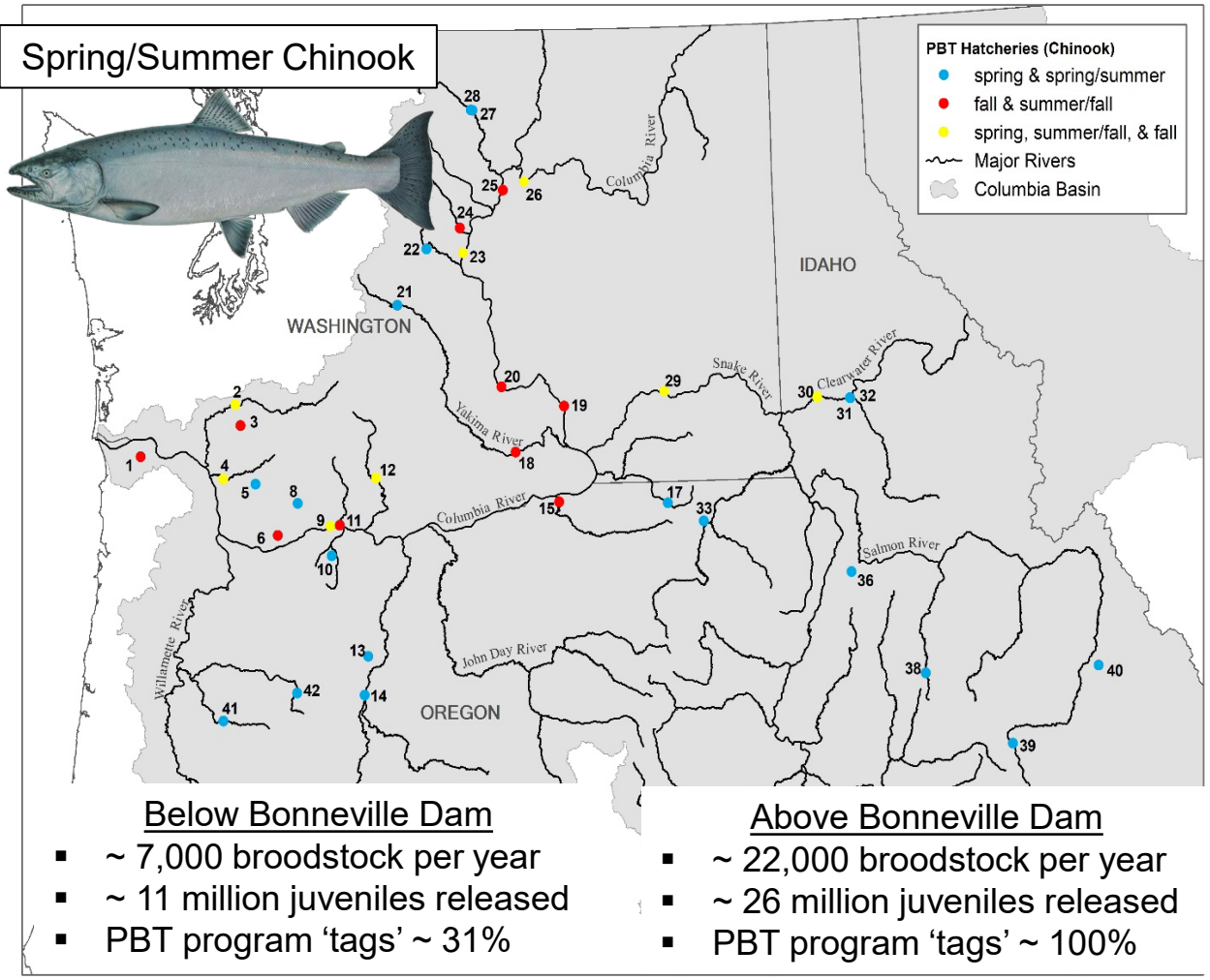


<u>Primary sockeye stocks</u>
-Wenatchee R.
-Okanogan R.
-Snake R.
-several kokanee stocks

Hess et al. 2022; BPA Report

Parentage Based Tagging (PBT)
- Complete baselines above Bonneville since 2013

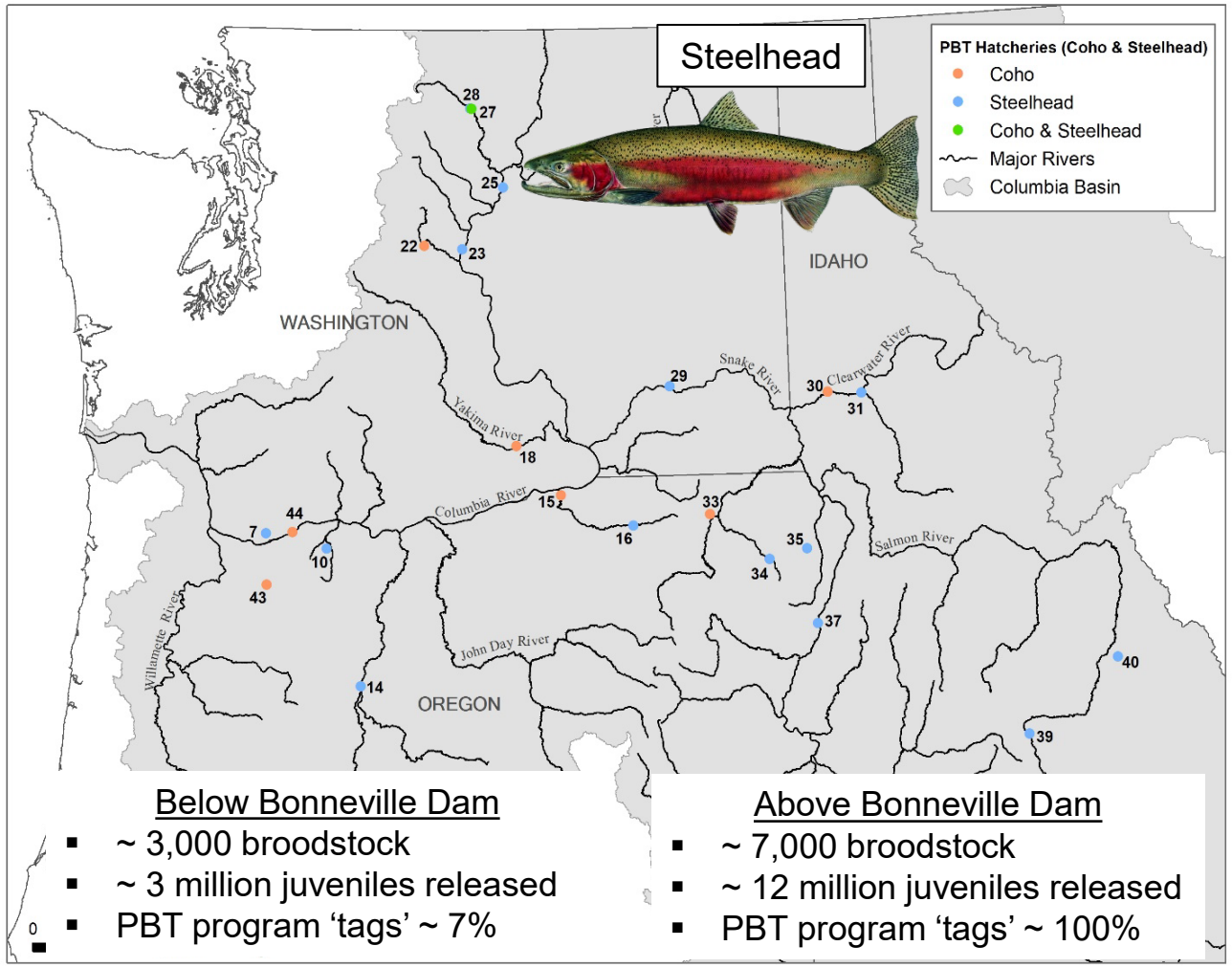
Chinook spawning hatcheries



Below Bonneville Dam
- ~ 7,000 broodstock per year
- ~ 11 million juveniles released
- PBT program 'tags' ~ 31%

Above Bonneville Dam
- ~ 22,000 broodstock per year
- ~ 26 million juveniles released
- PBT program 'tags' ~ 100%

Steelhead & Coho spawning hatcheries

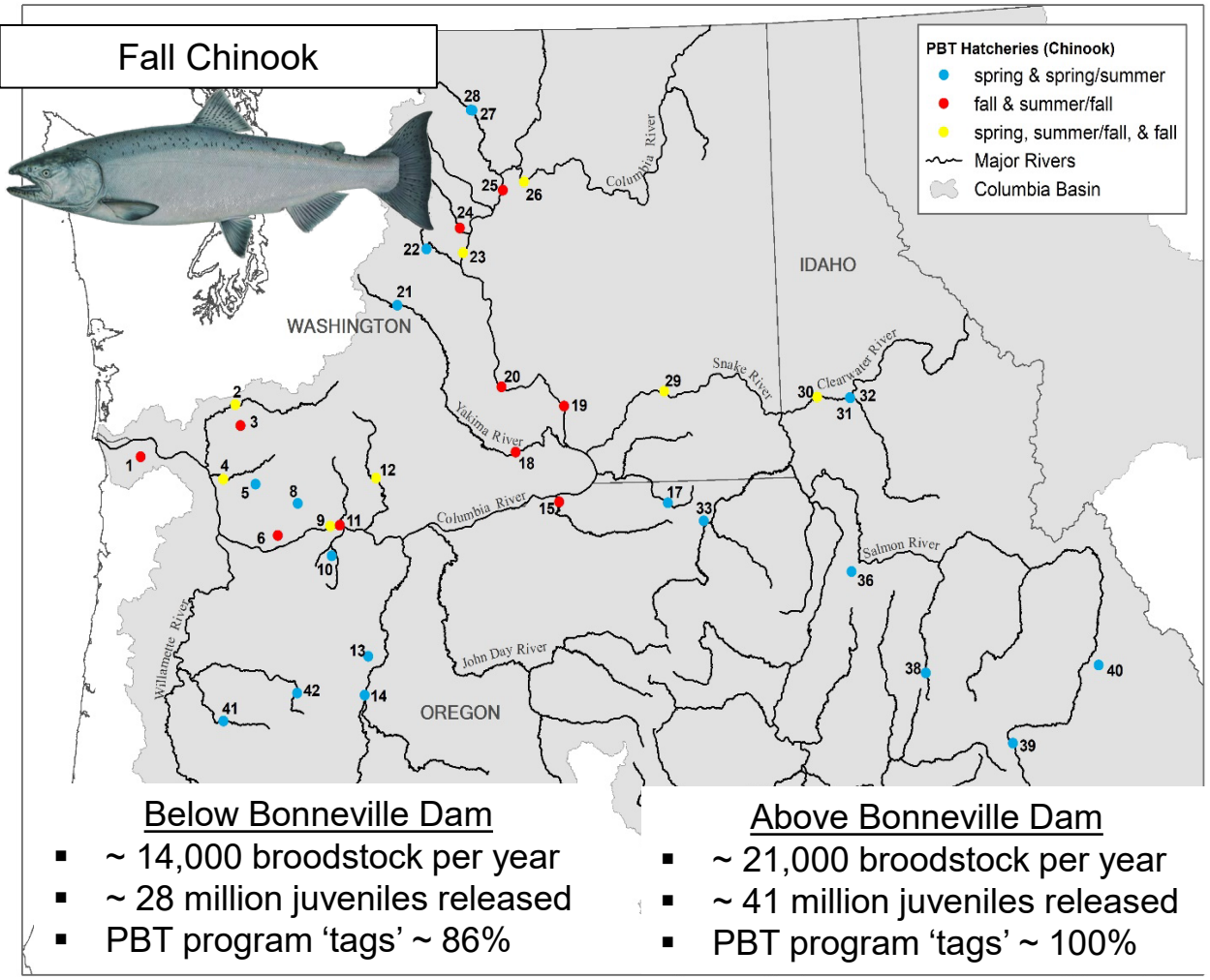


Below Bonneville Dam
- ~ 3,000 broodstock
- ~ 3 million juveniles released
- PBT program 'tags' ~ 7%

Above Bonneville Dam
- ~ 7,000 broodstock
- ~ 12 million juveniles released
- PBT program 'tags' ~ 100%

Parentage Based Tagging (PBT)
- Complete baselines above Bonneville since 2013

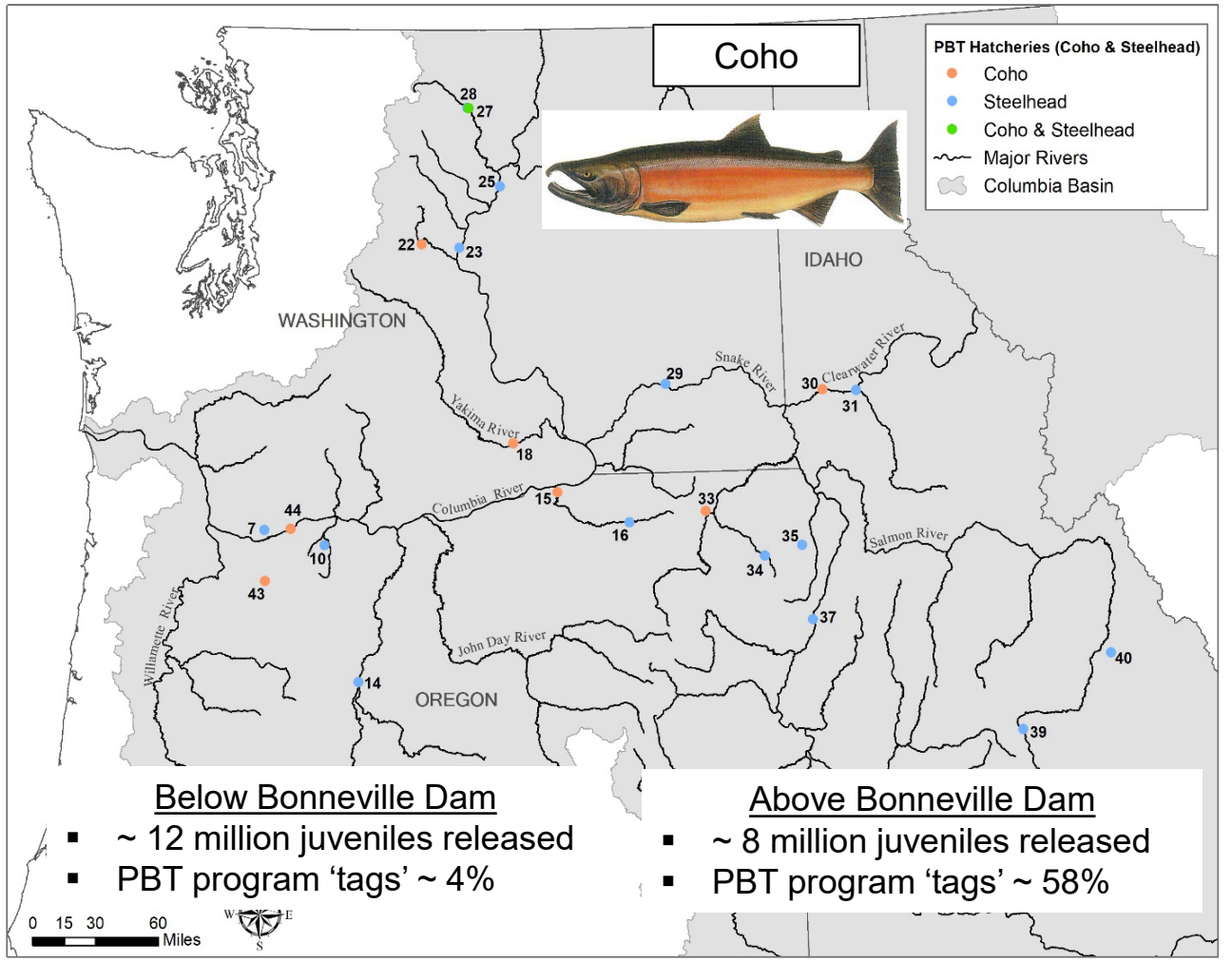
Chinook spawning hatcheries



Below Bonneville Dam
- ~ 14,000 broodstock per year
- ~ 28 million juveniles released
- PBT program 'tags' ~ 86%

Above Bonneville Dam
- ~ 21,000 broodstock per year
- ~ 41 million juveniles released
- PBT program 'tags' ~ 100%

Steelhead & Coho spawning hatcheries



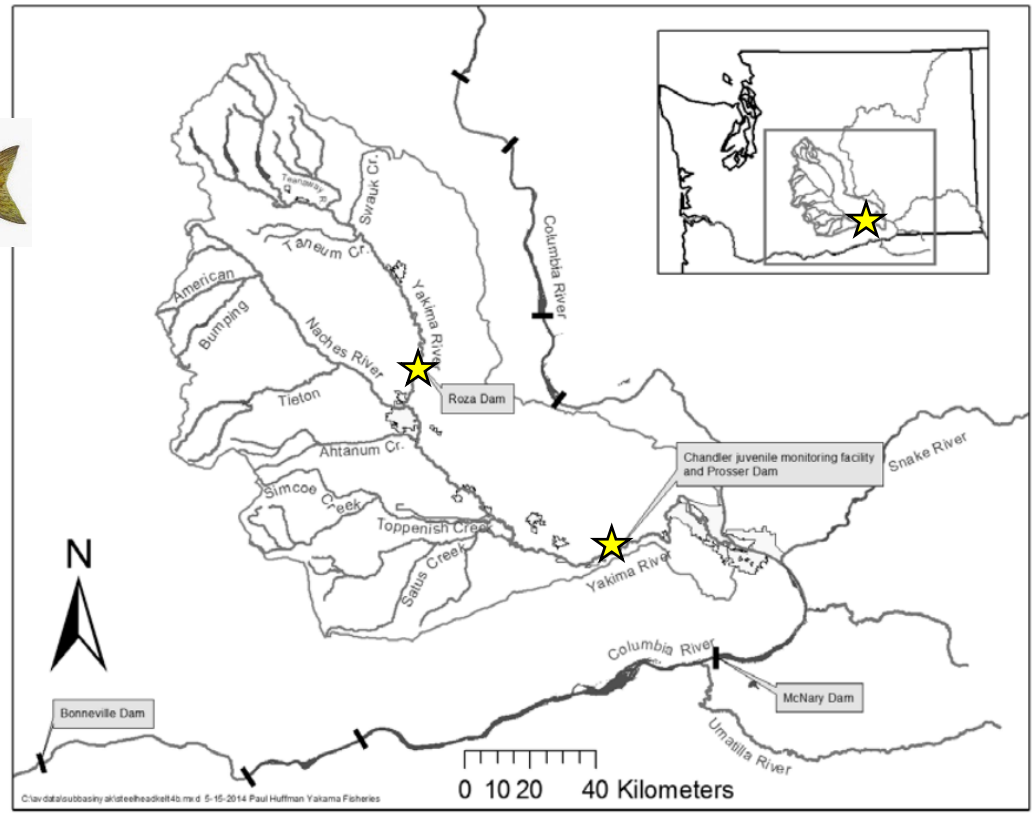
Below Bonneville Dam
- ~ 12 million juveniles released
- PBT program 'tags' ~ 4%

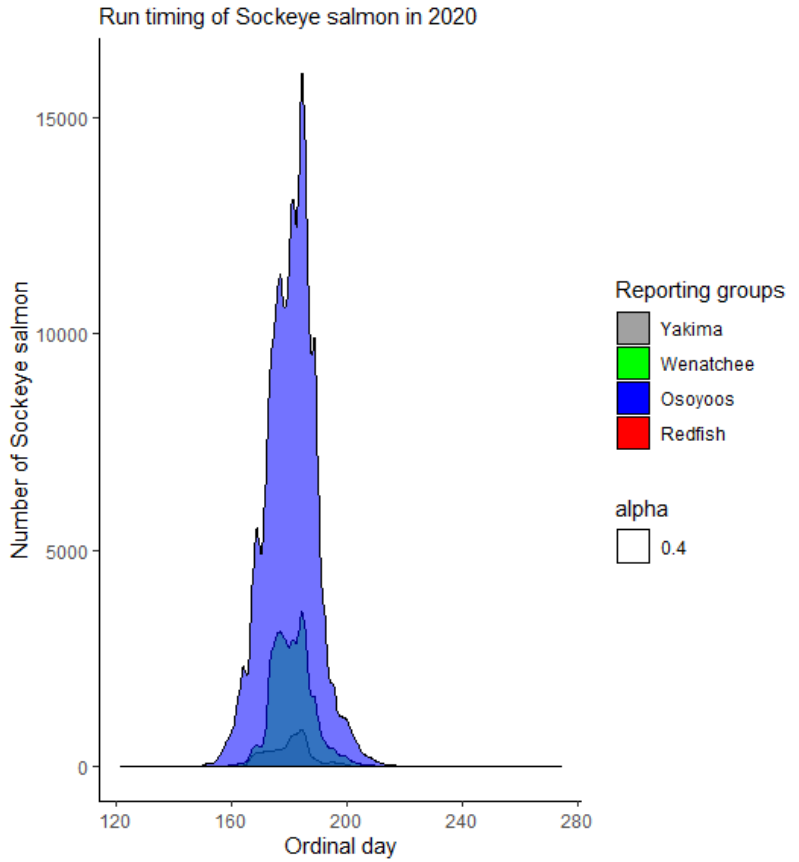
Above Bonneville Dam
- ~ 8 million juveniles released
- PBT program 'tags' ~ 58%

Parentage Based Tagging (PBT)
- Complete baselines above Bonneville since 2013

Sockeye reintroduction

Sockeye

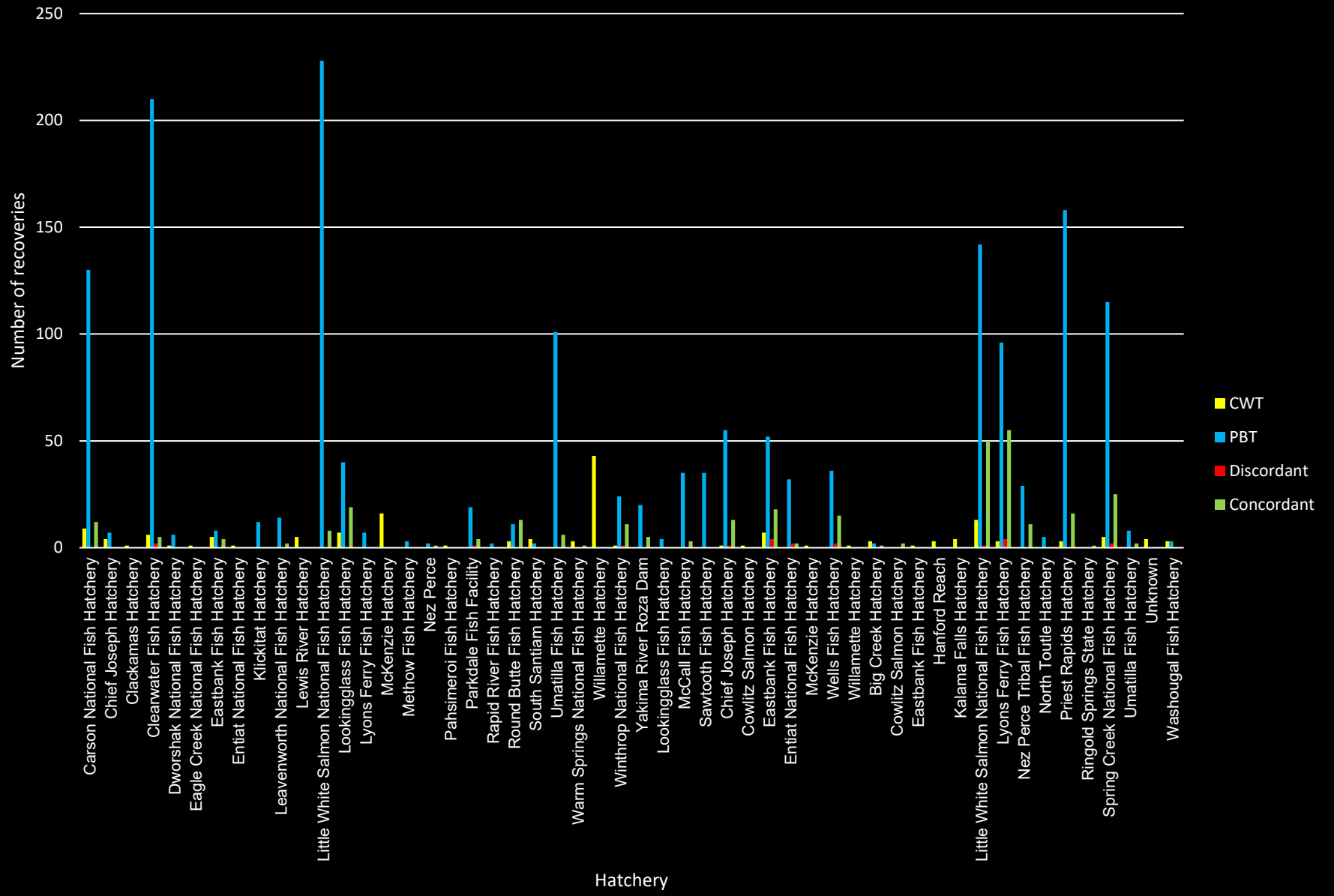


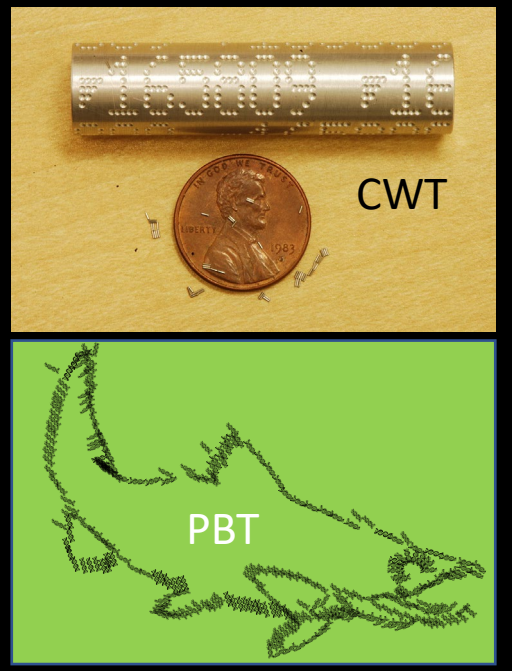


Above Bonneville Dam

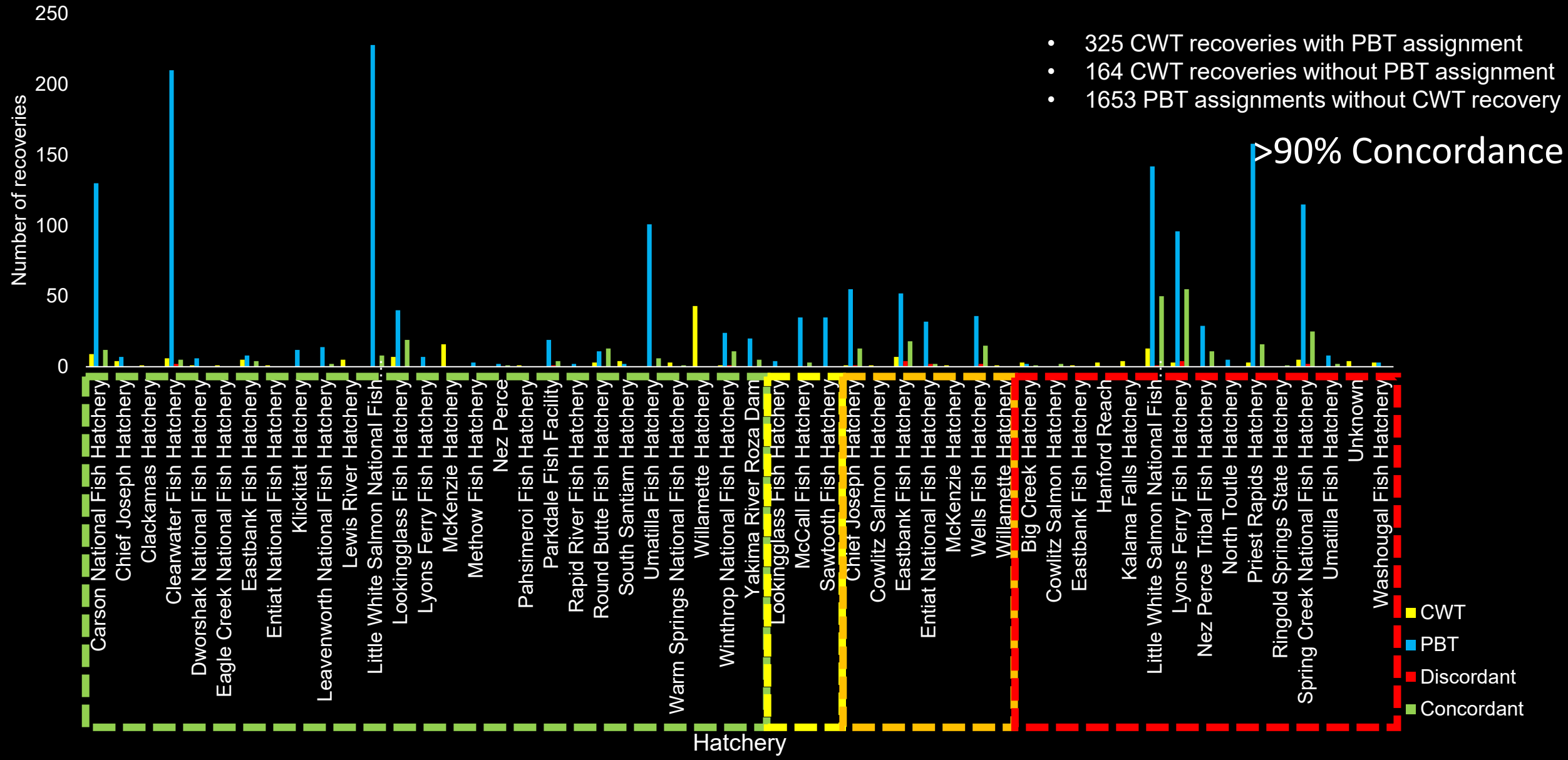
- ~ 10,000 adult transplants per year
- PBT program 'tags' ~ 50%

Coded Wire Tag and Parentage-Based Tag Comparisons of recoveries in the chinook fisheries of 2018





Coded Wire Tag and Parentage-Based Tag Comparisons of recoveries in the chinook fisheries of 2018

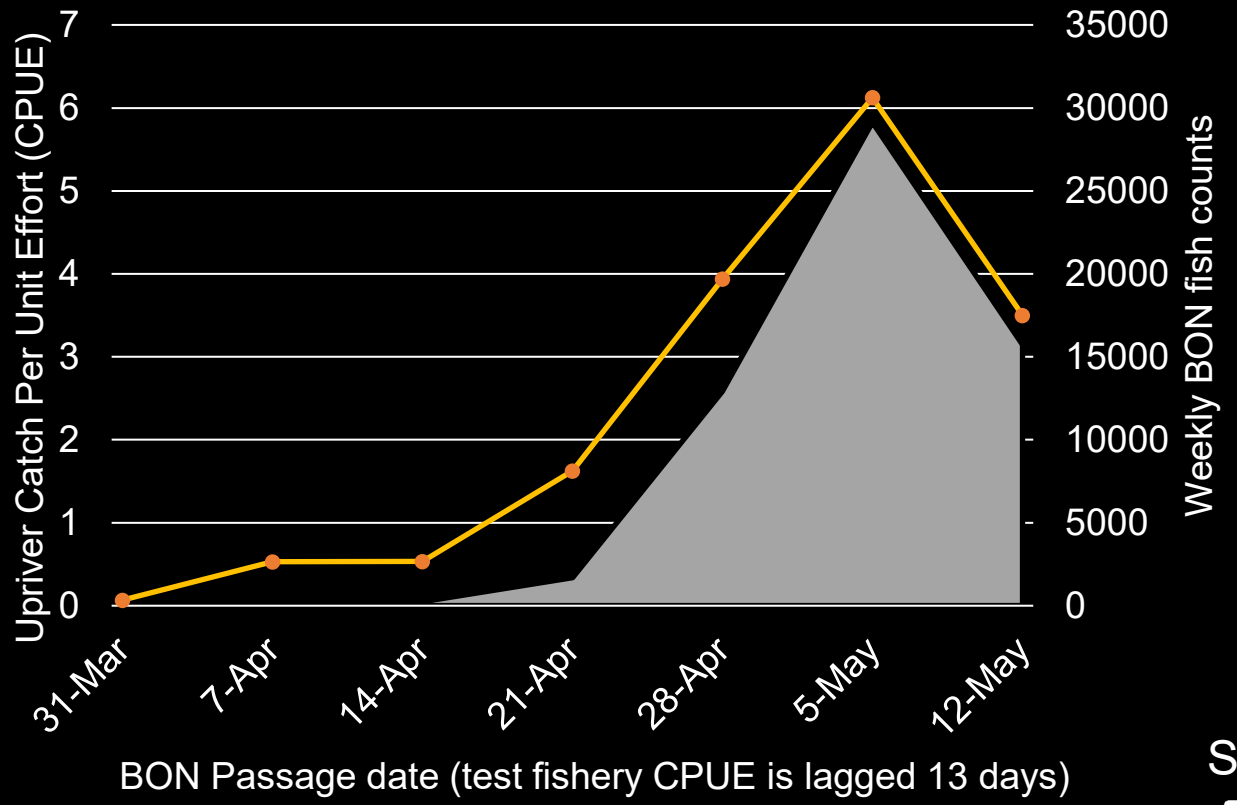


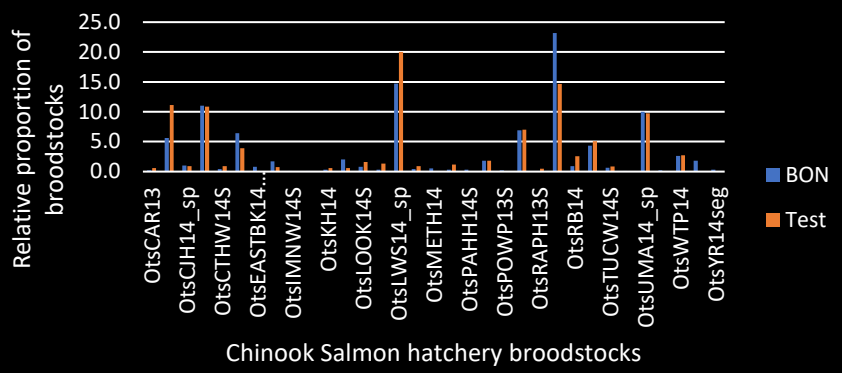
- 325 CWT recoveries with PBT assignment
- 164 CWT recoveries without PBT assignment
- 1653 PBT assignments without CWT recovery

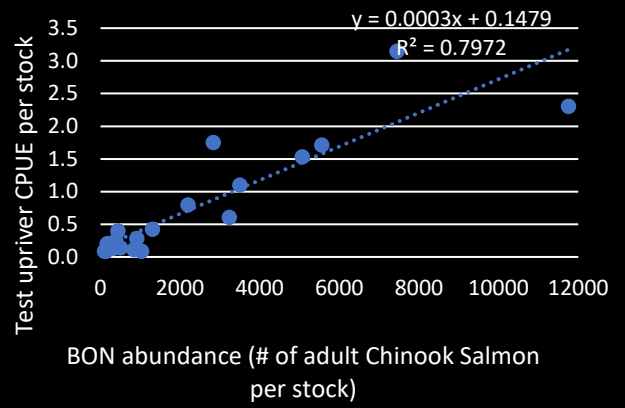
>90% Concordance

GENETIC APPLICATIONS IN FISHERIES MANAGEMENT

Spring Chinook Test Fishery



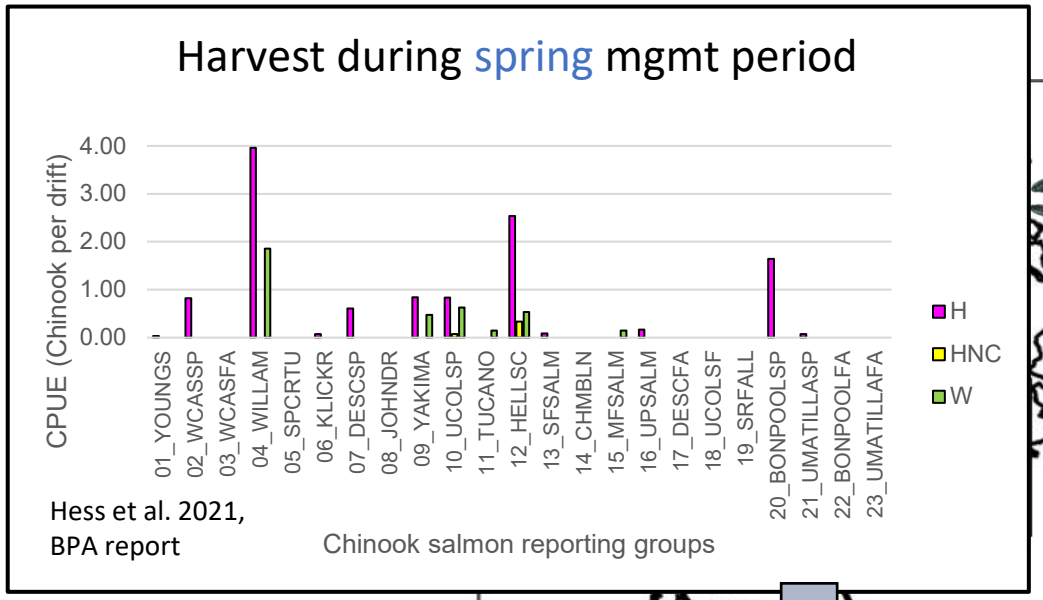


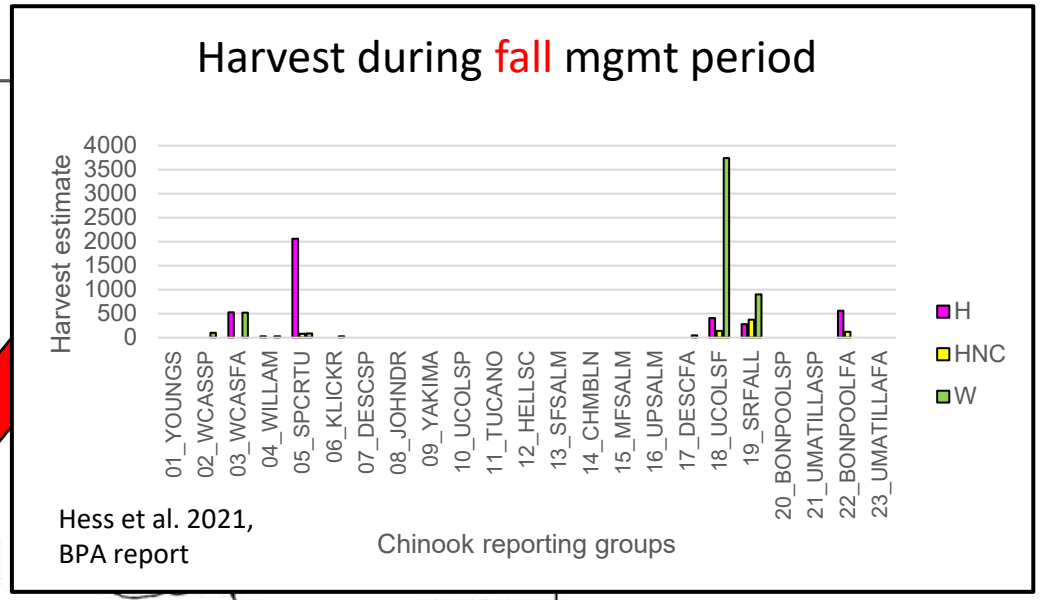


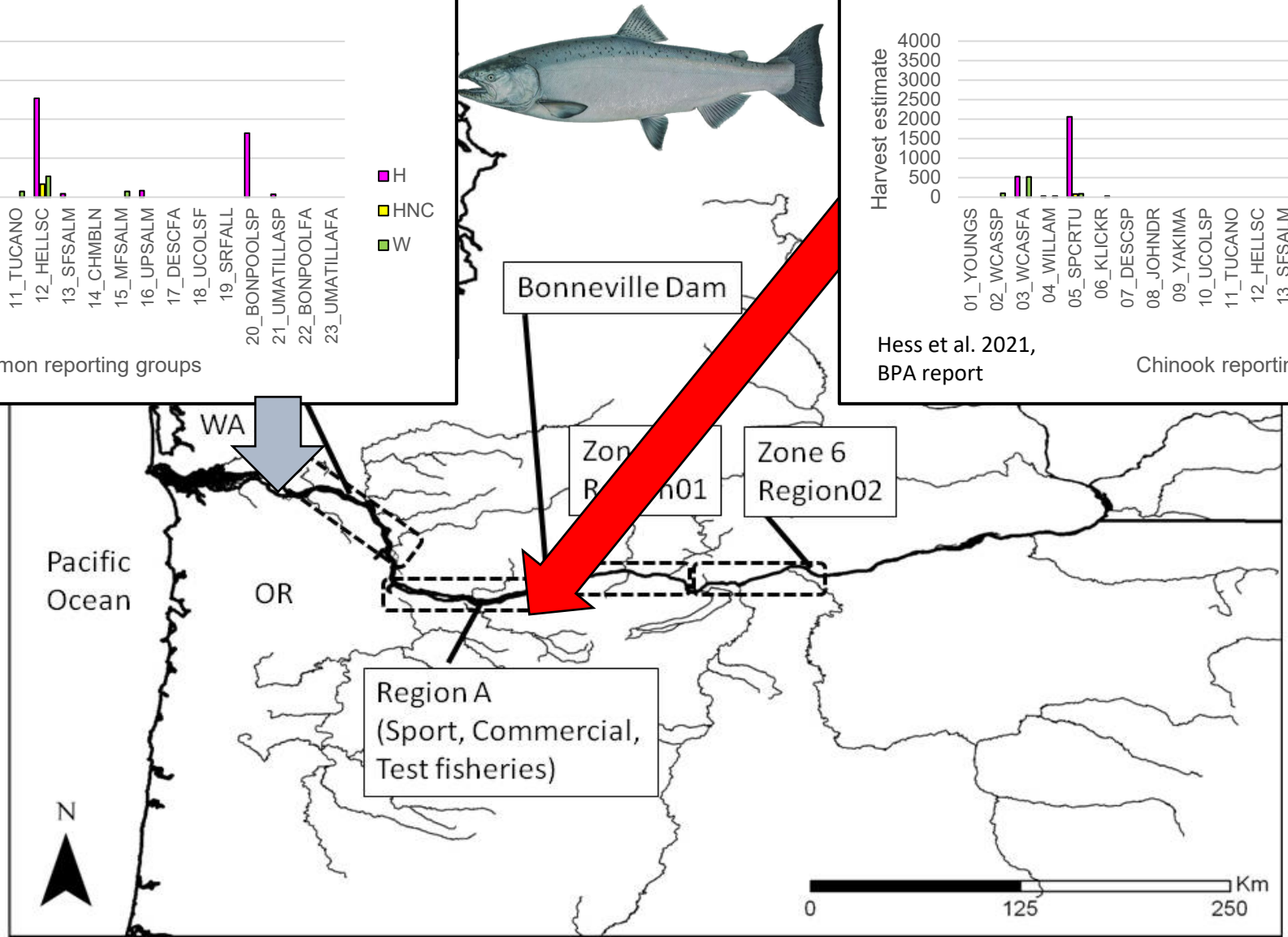
Spring Chinook Test Fishery

STOCK ID OF MAINSTEM HARVEST
Stock specific harvest annually since 2009

Chinook salmon





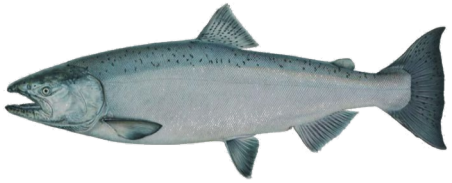


- Hatchery clipped
- Hatchery unclipped
- W; Natural origin

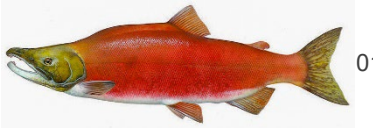
In-season analyses of stocks (since 2017)

Results provided at two-week intervals throughout run

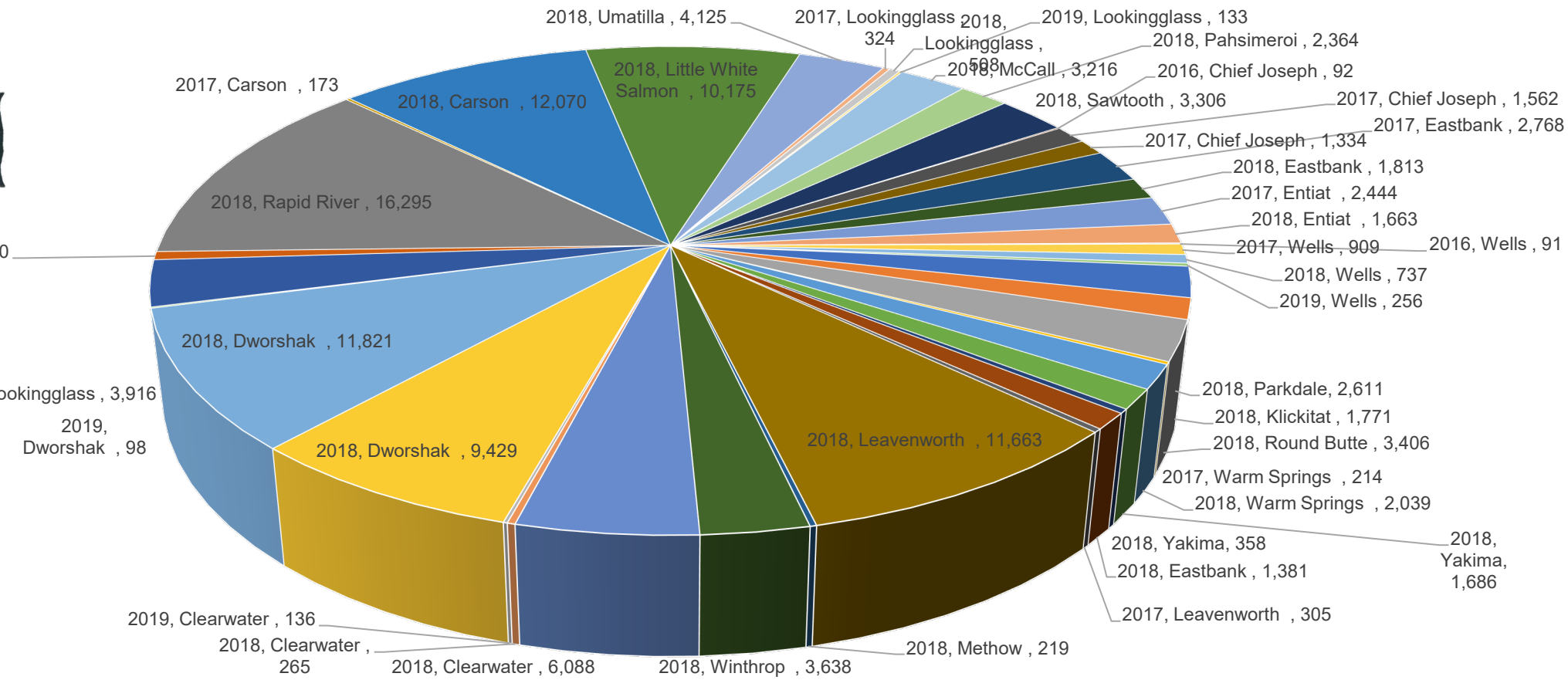
Spring Chinook



Sockeye



Steelhead



Hatchery clipped adult-sized Chinook salmon passing Bonneville Dam through June 15, 2022.