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October 6, 2026

MEMORANDUM

TO: **Council Members**

FROM: **Windy Schoby, Fish and Wildlife Policy Analyst - Idaho**

SUBJECT: **Update on Genetic Tools - Parentage Based Tagging (PBT), Genetic Stock Identification (GSI), and the broader genetic monitoring network supported by the Fish and Wildlife Program**

BACKGROUND:

Presenters:

Matt Campbell, Fisheries Genetics Program Coordinator, Idaho Department of Fish and Game

Dr. Shawn Narum, Chief Scientist, Columbia River Inter-Tribal Fish Commission

Dr. Jon Hess, Senior Fishery Geneticist, Columbia River Inter-Tribal Fish Commission

Summary:

Matt Campbell, Shawn Narum, and Jon Hess will provide an update on genetic monitoring tools and applications that provide critical information to support fisheries management and conservation in the Columbia River Basin. The presentation will highlight how the region's investment in genetic monitoring has strengthened management by improving stock-specific and origin-specific (hatchery and natural) abundance estimates, enhancing evaluation of hatchery- and natural-origin fish populations, and providing information that can inform management decisions.

Relevance:

The three BPA-funded projects highlighted in this presentation implement measures in the Council's 2026 Columbia River Basin Fish and Wildlife Program. This work is generally aligned with the Program's strategy for Planning, Research, Monitoring, and Evaluation in Support of Multiple Strategies.

The **Program** continues to emphasize research, monitoring, and evaluation to inform adaptive management and improve the effectiveness of Program actions. This presentation provides an opportunity to consider how a long-term investment in genetic monitoring has matured into information that can support management decisions and future Program implementation.

Background:

Marking and tagging fish is one of the region's most important tools for understanding and managing salmon, steelhead, and other fish populations. Tagging and related monitoring allow managers and researchers to track fish from headwater rearing or hatchery release areas, through the mainstem hydrosystem and ocean, and back to spawning grounds and hatchery broodstock collection facilities. The resulting information supports estimates of survival, abundance, migration timing, harvest, hatchery performance, and progress toward conservation and recovery objectives.

Genetic monitoring expanded this toolbox by providing information about the stock, population, and parentage of individual fish. CRITFC and IDFG initially proposed using these approaches to address a fundamental fisheries management need: better information on stock-specific abundance, run timing, and harvest of Columbia Basin salmon and steelhead.

Three BPA-funded projects helped move that concept into implementation: CRITFC's **Genetic Assessment of Columbia River Stocks (2008-907-00)** and two IDFG projects focused on **Genetic Stock Identification (2010-026-00)** and **Parentage-Based Tagging (2010-031-00)**. Together, these investments supported development of genetic resources and methods to identify the origin of fish passing fixed locations, including Bonneville and Lower Granite dams, and fish intercepted in commercial, sport, and tribal mainstem fisheries.

As these genetic approaches were developing, the Council was also working more broadly with the region to improve the effectiveness and efficiency of fish tagging and monitoring. The presentation builds on the Council's role in helping the region improve the effectiveness and efficiency of fish tagging and monitoring. In 2011, the Council chartered the Fish Tagging Forum. The Forum brought together state, tribal, federal, BPA, and other regional experts to evaluate tagging activities, costs, efficiencies, overlaps, and gaps under the Fish and Wildlife Program. The Forum considered emerging tagging approaches and

opportunities to use more efficient technologies where appropriate. The Council's recommendations recognized genetic approaches as an emerging component of the Basin's monitoring toolbox, while associated cost-effectiveness work identified potential advantages as well as the need for continued development of sampling, laboratory, and data-management infrastructure.

More than a decade later, those genetic tools are providing information on stock-specific abundance, harvest, reproductive success, hatchery contributions, and natural-origin populations. Emerging applications, including grandparentage and the use of long-term datasets to examine changes in life-history characteristics, may further extend the value of these investments.

What began as development and proof-of-concept work has evolved into a broadly implemented genetic monitoring program. Parentage-Based Tagging (PBT) uses hatchery broodstock genotypes to identify hatchery-origin offspring, while Genetic Stock Identification (GSI) uses genetic baselines to identify the stock or population of origin of natural-origin fish.

Improvements in genetic baselines, assignment accuracy, analytical methods, and cost efficiency, coupled with more than 15 years of sampling, have expanded the management value of these tools. The program has progressed from asking whether genetic tools could provide information unavailable through conventional monitoring to asking how that information can improve management decisions and biological outcomes.

More information:
Fish Tagging Forum
Project #2008-907-00- Genetic Assessment of Columbia River Stocks
Project #2010-031-00- IDFG Genetic Monitoring of Snake River Salmon and Steelhead Stocks
Project #2010-026-00-Chinook and Steelhead Genotyping for Genetic Stock Identification (GSI) at Lower Granite Dam
2009 Presentation to the Council- Use of Genetic Data to Estimate Salmonid Stock Composition and Migration Patterns
2010 Presentation to the Council-New Genetic Tools and the Management of Columbia River Salmon and Steelhead
2018 Presentation to the Council-Update on Genetic Monitoring Program
2022 Presentation to the FWL Committee- Update on Genetic Monitoring Tools

Recent Publications:

Coykendall, D. K., T. A. Delomas, M. Belnap, and M. R. Campbell. 2022. Improving abundance estimates of spring–summer Snake River Chinook Salmon for fisheries management. *North American Journal of Fisheries Management* 42:1454–1464. https://doi.org/10.1002/nafm.10823

Delomas, T. A., A. C. Harris, J. S. Hargrove, S. R. Narum, J. E. Hess, R. L. Horn, and M. R. Campbell. 2026. Empirical validation of grandparent inference to quantify reproduction of hatchery-origin fish in the wild. *North American Journal of Fisheries Management* 00:1–16. https://doi.org/10.1093/najfmt/vqag051

Hargrove, J. S., M. R. Campbell, A. C. Harris, S. R. Narum, R. L. Horn, and J. E. Hess. 2025. Genetic methods for informing conservation and management of salmonids in the Pacific Northwest, USA. *Journal of Fish Biology*. https://doi.org/10.1111/jfb.70143

Hargrove, J. S., C. A. Camacho, W. C. Schrader, J. H. Powell, T. A. Delomas, J. E. Hess, S. R. Narum, and M. R. Campbell. 2021. Parentage-based tagging improves escapement estimates for ESA-listed adult Chinook salmon and steelhead in the Snake River basin. *Canadian Journal of Fisheries and Aquatic Sciences* 78:349–360. https://doi.org/10.1139/cjfas-2020-0152

Hess, J. E., T. A. Delomas, A. D. Jackson, M. J. Kosinski, M. L. Moser, L. L. Porter, G. Silver, T. Sween, L. A. Weitkamp, and S. R. Narum. 2022. Pacific Lamprey translocations to the Snake River boost abundance of all life stages. *Transactions of the American Fisheries Society* 151:263–296. https://doi.org/10.1002/tafs.10359

Hess, J. E., B. M. Deacy, M. W. Rub, D. M. Van Doornik, J. M. Whiteaker, J. K. Fryer, and S. R. Narum. 2024. Visual and genetic stock identification of a test fishery to forecast Columbia River spring Chinook Salmon stocks 2 weeks into the future. *Evolutionary Applications* 17:e13667. https://doi.org/10.1111/eva.13667

Lewis, D., R. Horn, S. Narum, J. Stephenson, J. McCane, A. C. Harris, M. Campbell, F. Bohlen, and J. Hess. 2026. Utility of parentage-based tagging for research, monitoring, and evaluation of hatchery programs within the Columbia River Basin. Poster presented at the Oregon Chapter of the American Fisheries Society Annual Meeting. critfc.org Poster PDF

Update on Genetic Tools used throughout the Snake/Columbia River Basins

Matthew Campbell (IDFG)
Fisheries Genetics Program Coordinator

Northwest Power and Conservation Council
Wednesday, October 14th - 2026

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

Primary Collaborators: Shawn Narum, Rebekah Horn, 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 (EFGL PSMFC):
Audrey Harris - PBT
John Hargrove - GSI
Katharine Coykendall
Jesse McCane – Database Coordinator
Kelly Heindel
Angie Chia
Yuritzi Calderon
Mark Griffith

Acknowledgements:

Northwest Power and Conservation Council

This is a coordinated regional monitoring effort, not a stand-alone laboratory achievement:

- Bonneville Power Administration
- Columbia River Inter-Tribal Fish Commission
- Idaho Department of Fish and Game
- Idaho Power Company
- Lower Snake River Compensation Plan (USFWS)
- Northwest Power and Conservation Council
- Oregon Department of Fish and Wildlife
- Pacific Coastal Salmon Recovery Fund
- Pacific States Marine Fisheries Commission
- Nez Perce Tribe
- Shoshone Bannock Tribe
- Washington Department of Fish and Wildlife



What did BPA and the Council invest in?

Background

What was the investment?

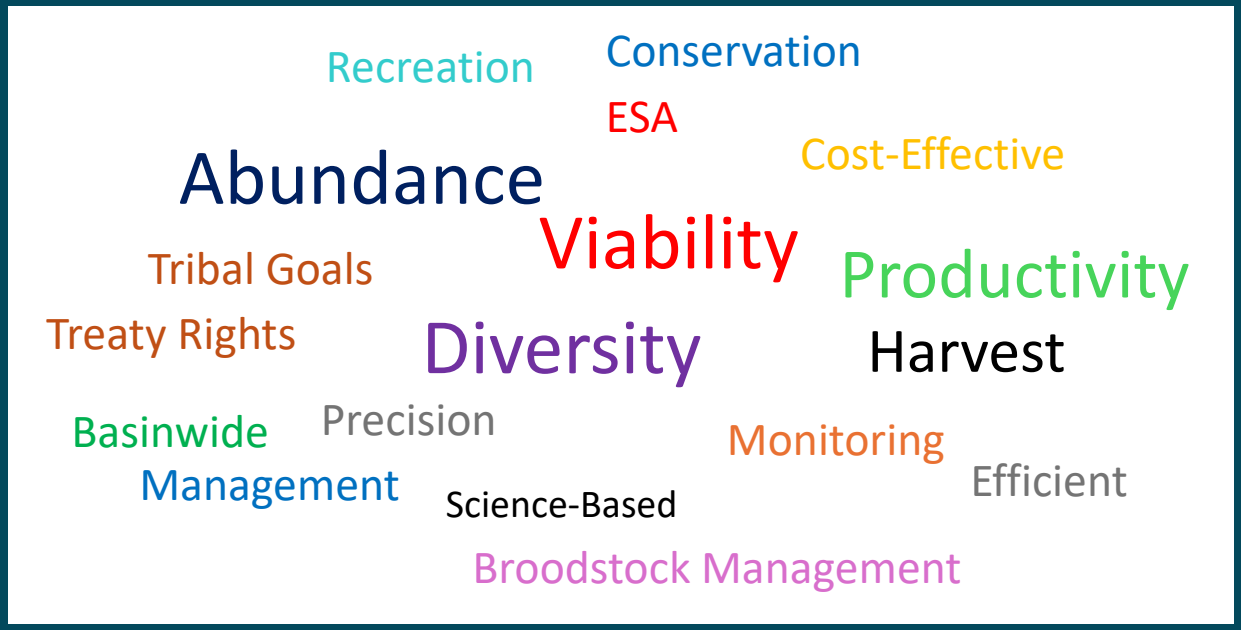
- ✓ ***Since 2010, the BPA has funded a project in the Snake River Basin that utilizes two genetic technologies***

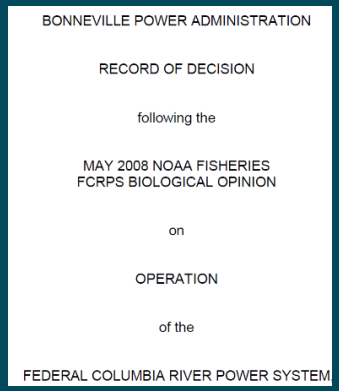
- ➢ **Genetic Stock Identification**
- ➢ **Parentage Based Tagging**

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

Why was the investment made?

- ✓ ***Are there genetic technologies that would be more powerful and efficient for monitoring and managing Salmon and Steelhead in the Snake River Basin?***




BONNEVILLE POWER ADMINISTRATION

RECORD OF DECISION

following the

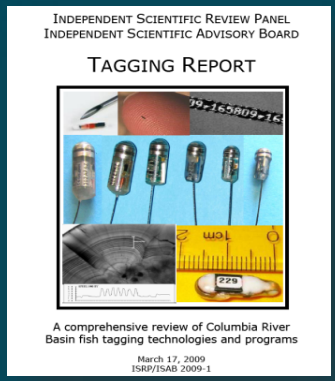
MAY 2008 NOAA FISHERIES
FCRPS BIOLOGICAL OPINION

on

OPERATION

of the

FEDERAL COLUMBIA RIVER POWER SYSTEM


INDEPENDENT SCIENTIFIC REVIEW PANEL
INDEPENDENT SCIENTIFIC ADVISORY BOARD

TAGGING REPORT

A comprehensive review of Columbia River Basin fish tagging technologies and programs

March 17, 2009
ISRP/ISAB 2009-1

What these genetic technologies are and how they work

Parentage-based genetic tagging - PBT (Hatchery Fish)

- Genetic-based fish tagging method that involves genotyping hatchery broodstock
- By genetically sampling the parents, all offspring are genetically "tagged"
- Information obtained similar to CWT, but improved tagging rate of hatchery fish (~95-100%)
- Juvenile handling not required prior to release
- 'Tag' recovery is non-lethal, and possible at all life stages

Hatchery Snake River Steelhead
- All broodstock sampled since 2010
- ~5,000 samples/year

Hatchery Snake River Chinook Salmon
- All Spring/Summer Chinook broodstock sampled since 2008, All Fall Chinook broodstock sampled since 2011;
- ~12,000 samples/year

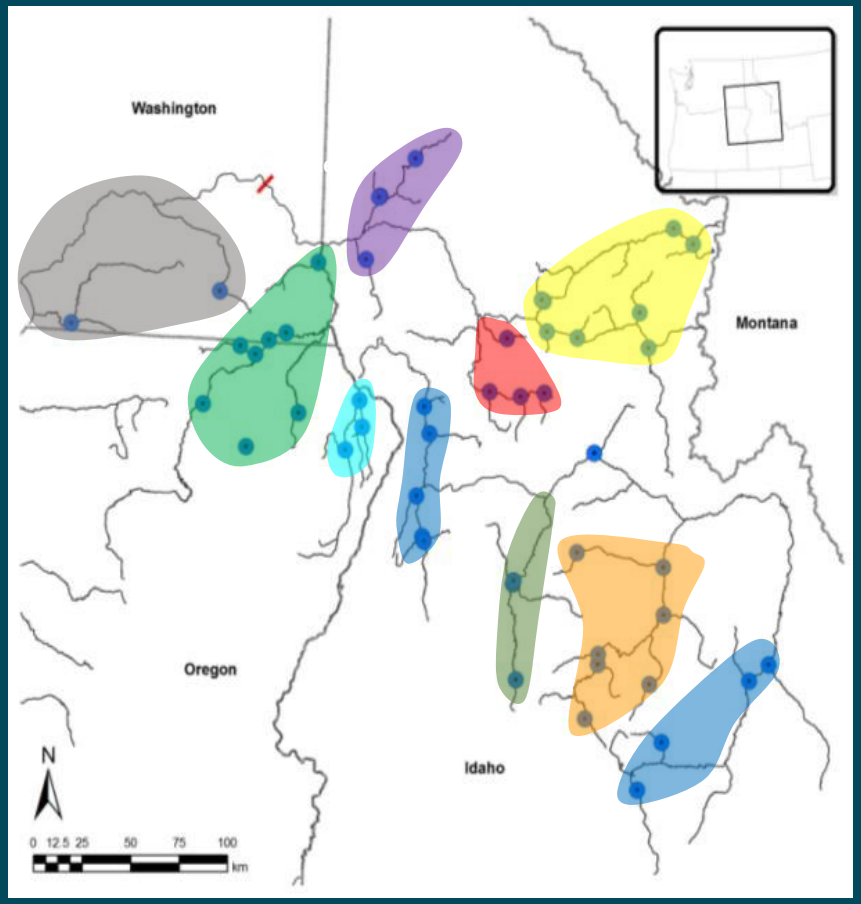


2 = 6,000!!!!

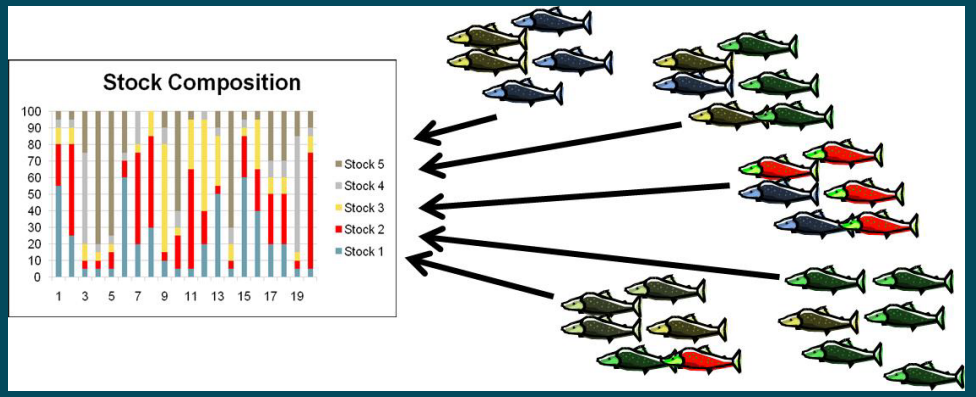
What these genetic technologies are and how they work

Genetic Stock Identification- GSI
(Wild fish)

- Uses genetic profiles from all contributing wild populations to estimate the stock of origin of any unknown fish



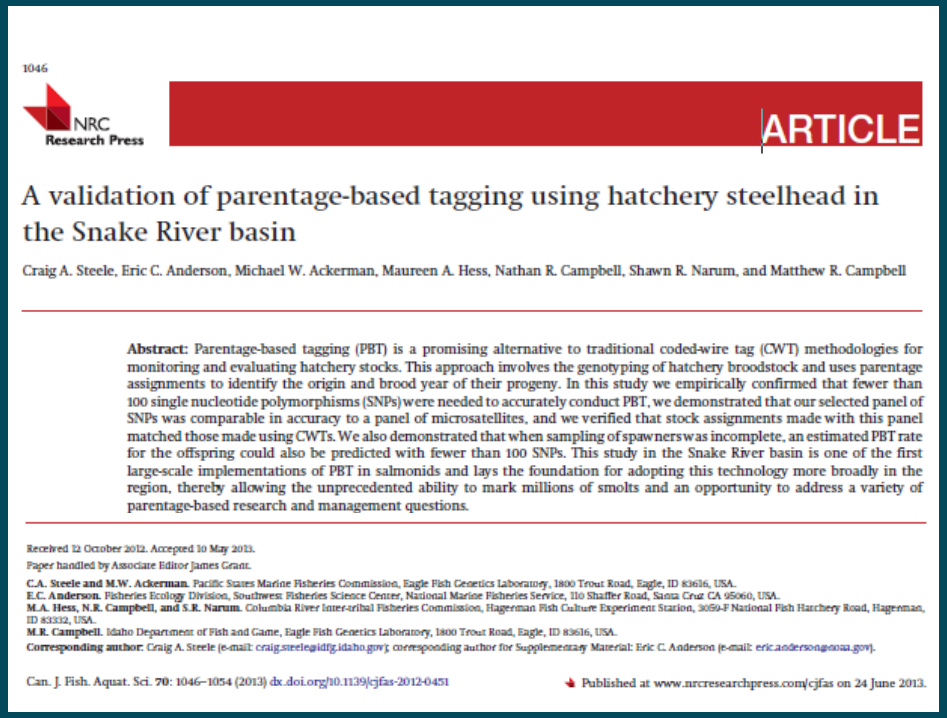




Major achievements early on:

Parentage Based Tagging-

- Accuracy- PBT is accurate and matched CWT assignments (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



1046

NRC Research Press

ARTICLE

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

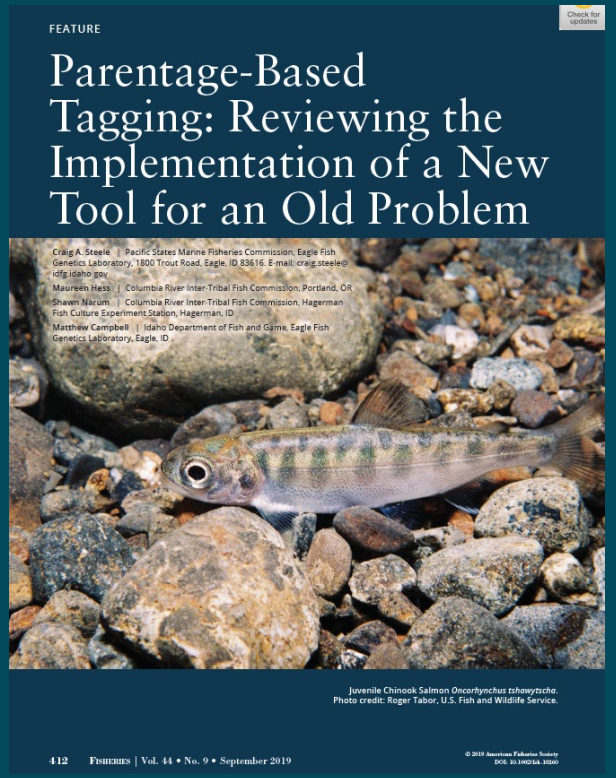
Craig A. Steele, Eric C. Anderson, Michael W. Ackerman, Maureen A. Hess, Nathan R. Campbell, Shawn R. Narum, and Matthew R. Campbell

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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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

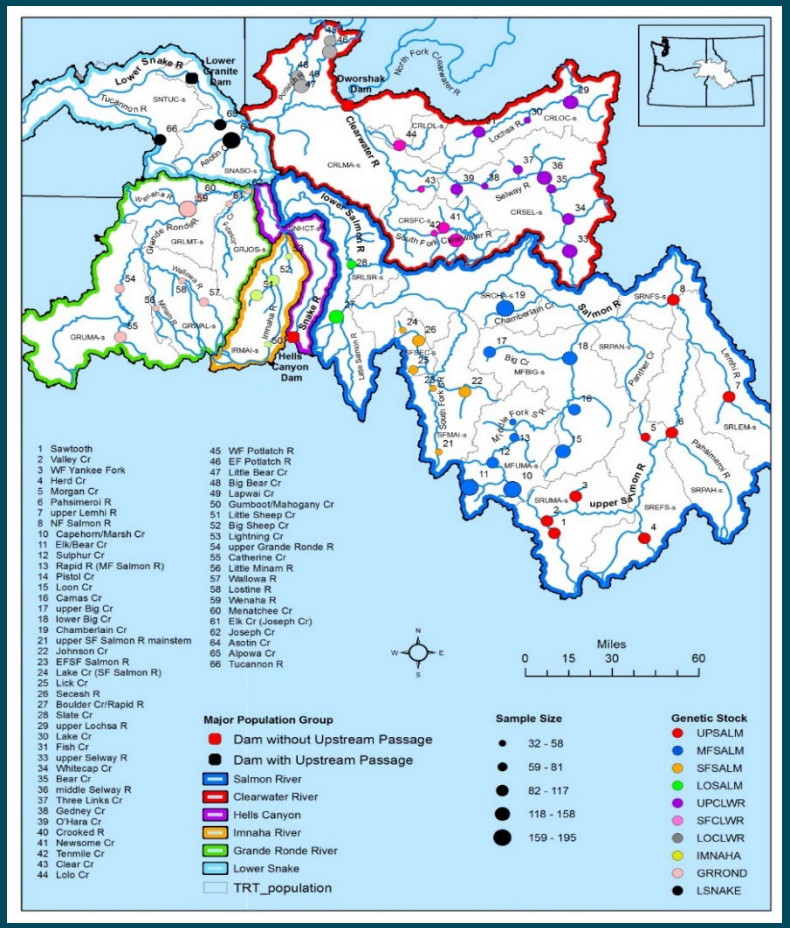
Juvenile Chinook Salmon *Oncorhynchus tshawytscha*. Photo credit: Roger Tabor, U.S. Fish and Wildlife Service.

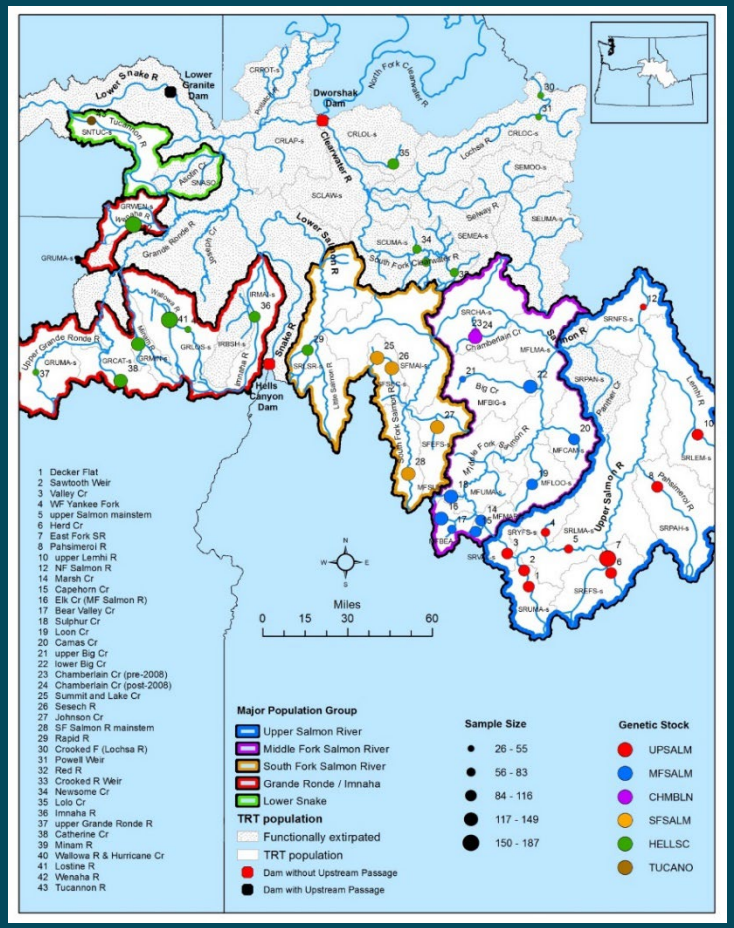
© 2019 American Fisheries Society
DOI: 10.1002/fsh.10260

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)

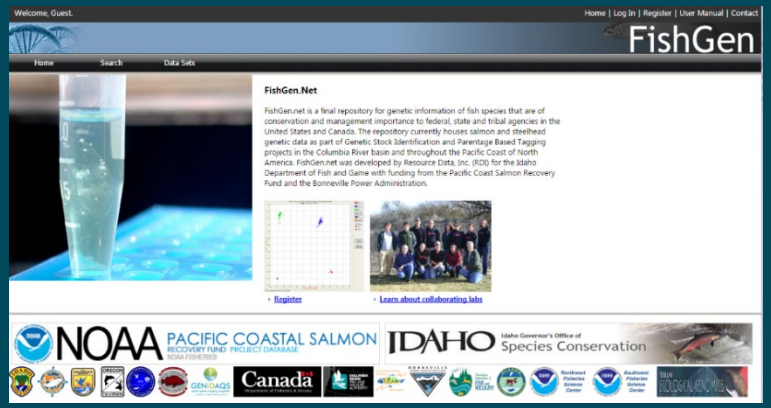


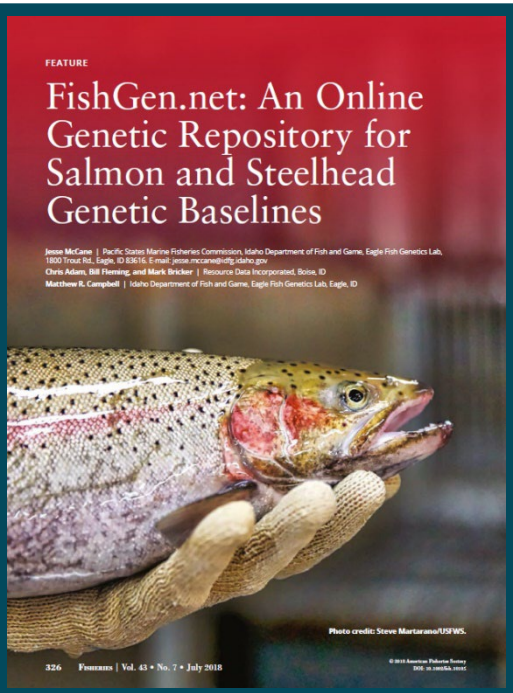


Major achievements:

Both Projects-

- FishGen Database
- Initial funding from PCSRF with annual funding from BPA



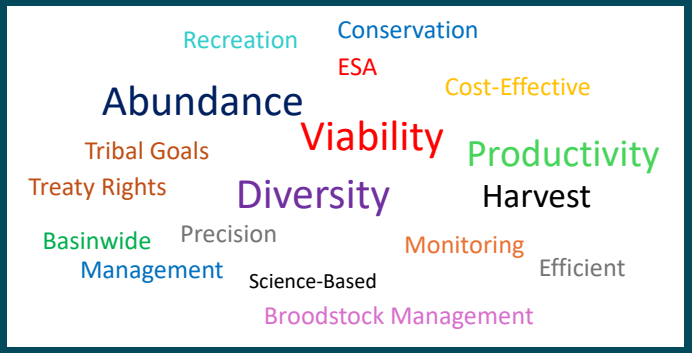


- Current six-year (SY2019-SY2024) combined Snake/Columbia Steelhead PBT Hatchery Baseline is comprised of 34,347 individuals across ~15 hatcheries
- Current six-year (SY2019-SY2024) combined Snake/Columbia Chinook Salmon PBT Hatchery Baseline is comprised of 317,319 individuals across ~45 hatcheries
- These are standardized baselines that are used by our labs and others throughout the Columbia River Basin

Has this investment been realized?

- ✓ ***Are there genetic technologies that would be more powerful and efficient for monitoring and managing Salmon and Steelhead in the Snake River Basin?***

YES!!!



The answer is yes: the investment supports a comprehensive stock-based monitoring program in the Snake River Basin

This genetic project contributes to a comprehensive monitoring and management program for Salmon and Steelhead in the Snake River Basin

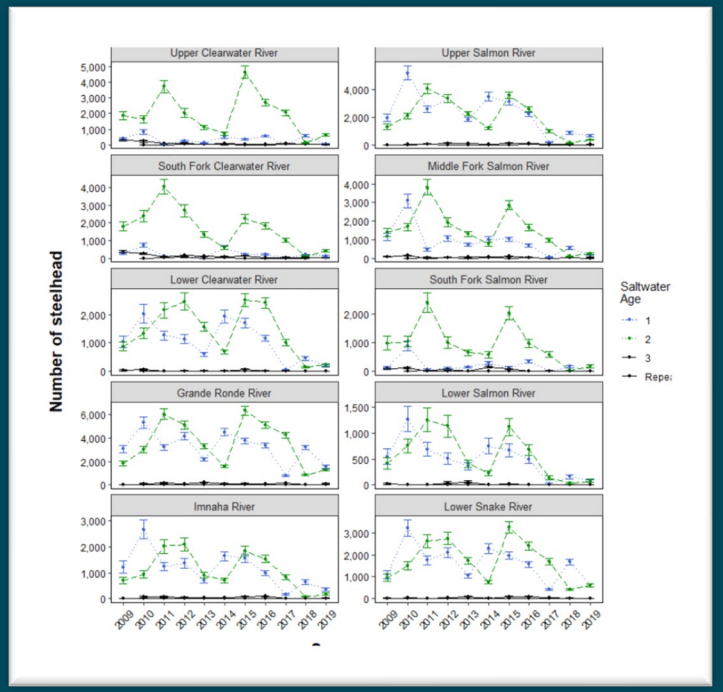




- Lower Granite Dam provides a central location for counting and representatively sampling migrating Snake River Salmon and Steelhead.

✓ PBT identifies hatchery origins
✓ GSI identifies wild genetic stocks

- Combined genetic and biological information describes abundance, age, sex, size, and migration timing



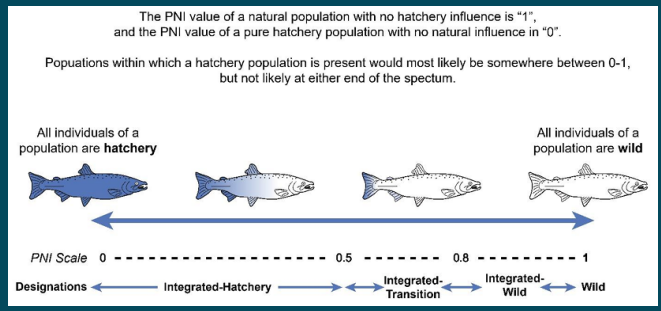
The major achievement is not simply that we can identify fish genetically. It is that we now have an efficient, coordinated program for monitoring individual stocks across the Snake River basin.

That gives managers information at the scale where fisheries and conservation decisions need to be made

The same fish, samples, and baselines can provide information for several purposes-

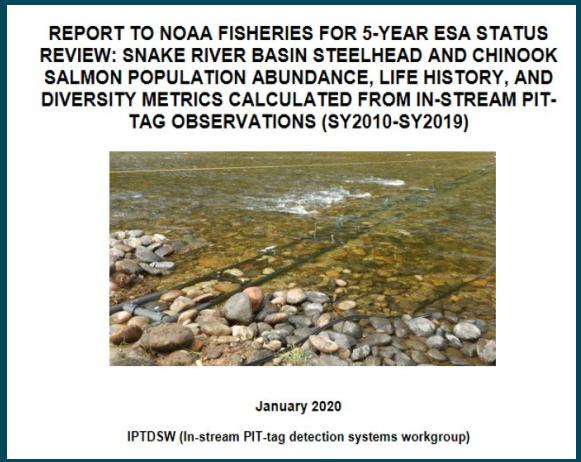
Three applications-

- ***Hatchery influence:*** ***Identify hatchery fish and, with spawning-ground monitoring, estimate the proportion of hatchery-origin spawner-pHOS.***

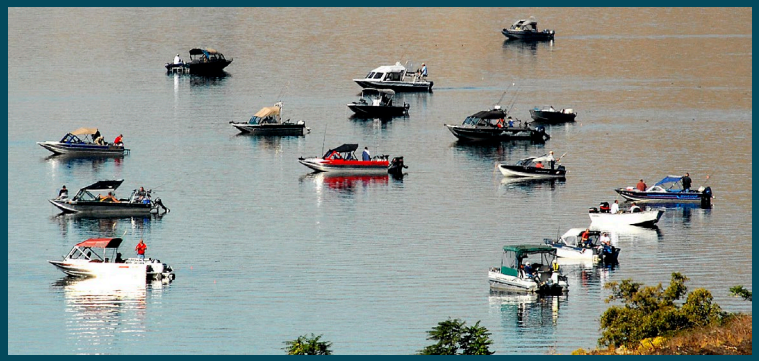


Fisheries and Oceans Canada. 2024. Genetically Based Enhanced Contribution Guidelines for Pacific Salmon Populations. 20 p.

- ***Diversity:*** ***Track genetic and life-history variation, including variation associated with migration timing, size, and age (Tributary-level)***



- ***Fisheries:*** ***Estimate hatchery stock returns and identify contributions to recreational and tribal catches.***



Credit: Tribune/Barry Kough

How has management changed using these technologies?

Two examples:

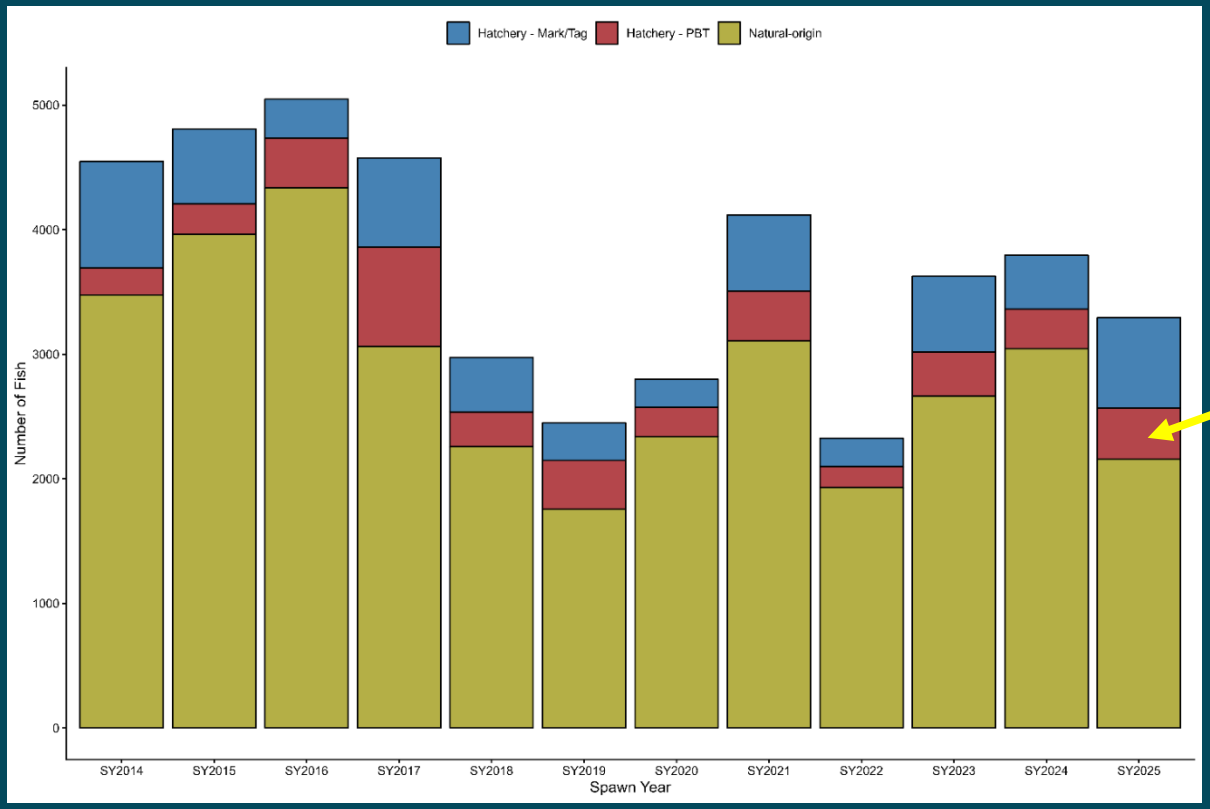
1. More accurate assessments of wild populations
2. More precise management of hatchery fisheries

Management Benefits Realized:
More accurate estimates of wild-fish abundance

- Hatchery fish without identifying marks are no longer automatically counted as wild
- PBT identifies hatchery-origin fish that physical marks and tags miss.
- Those fish are removed from estimates of natural-origin abundance.
- Corrected estimates strengthen the information used to evaluate population viability and recovery.

Is this a wild fish or an unmarked hatchery fish???





Not all hatchery fish are adclipped or mechanically tagged (CWT/PIT)!!!
PBT makes a difference!!!!!!

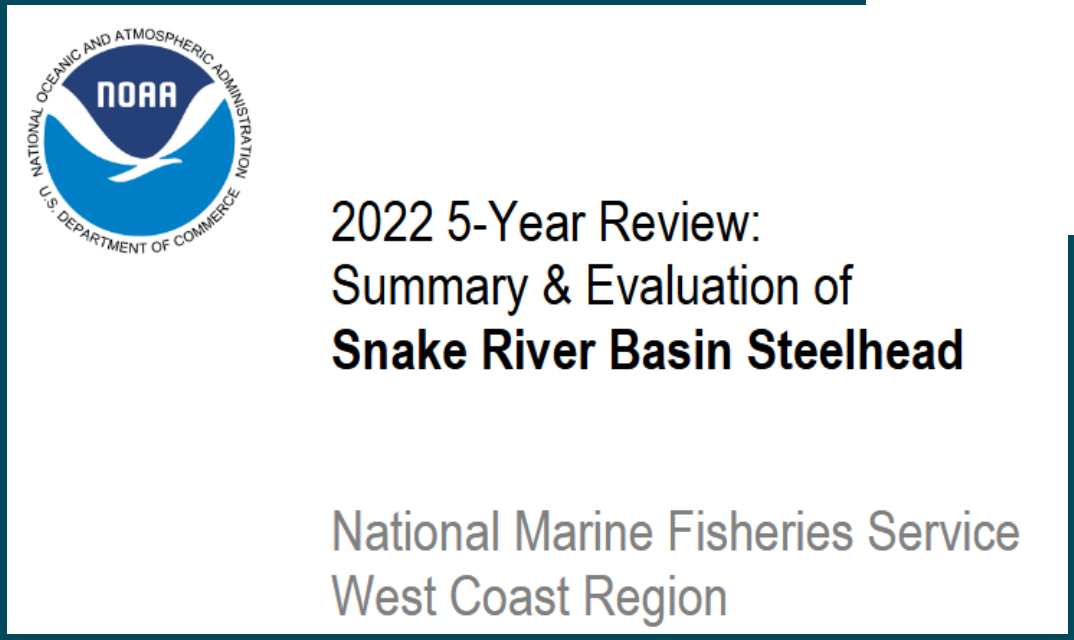
18.9%

Red bars represent the number of fish that would have been counted as wild without PBT

The number of adipose-intact adult steelhead sampled

Management Benefits Realized:
More accurate estimates of wild-fish abundance

- Corrected counts matter because they feed into status and viability assessments





Management Benefits Realized:
More accurate estimates of hatchery abundance by stock

- Hatchery abundance estimates based on returning fish that were PIT-tagged as juveniles can underestimate hatchery returns.
- Managers can use PBT estimates from representative sampling of returning adults to adjust harvest shares while meeting conservation and hatchery spawning objectives.

North American Journal of Fisheries Management

Article | Open Access

Improving Abundance Estimates of Spring–Summer Snake River Chinook Salmon for Fisheries Management

D. Katharine Coykendall, Thomas A. Delomas, Matthew Belnap, Matthew R. Campbell

First published: 09 August 2022 | https://doi-org.libproxy.boisestate.edu/10.1002/nafm.10823

"Across all years, PIT tag estimates accounted for 65% of the PBT-based estimates at Lower Granite Dam across all age-groups and release sites combined"

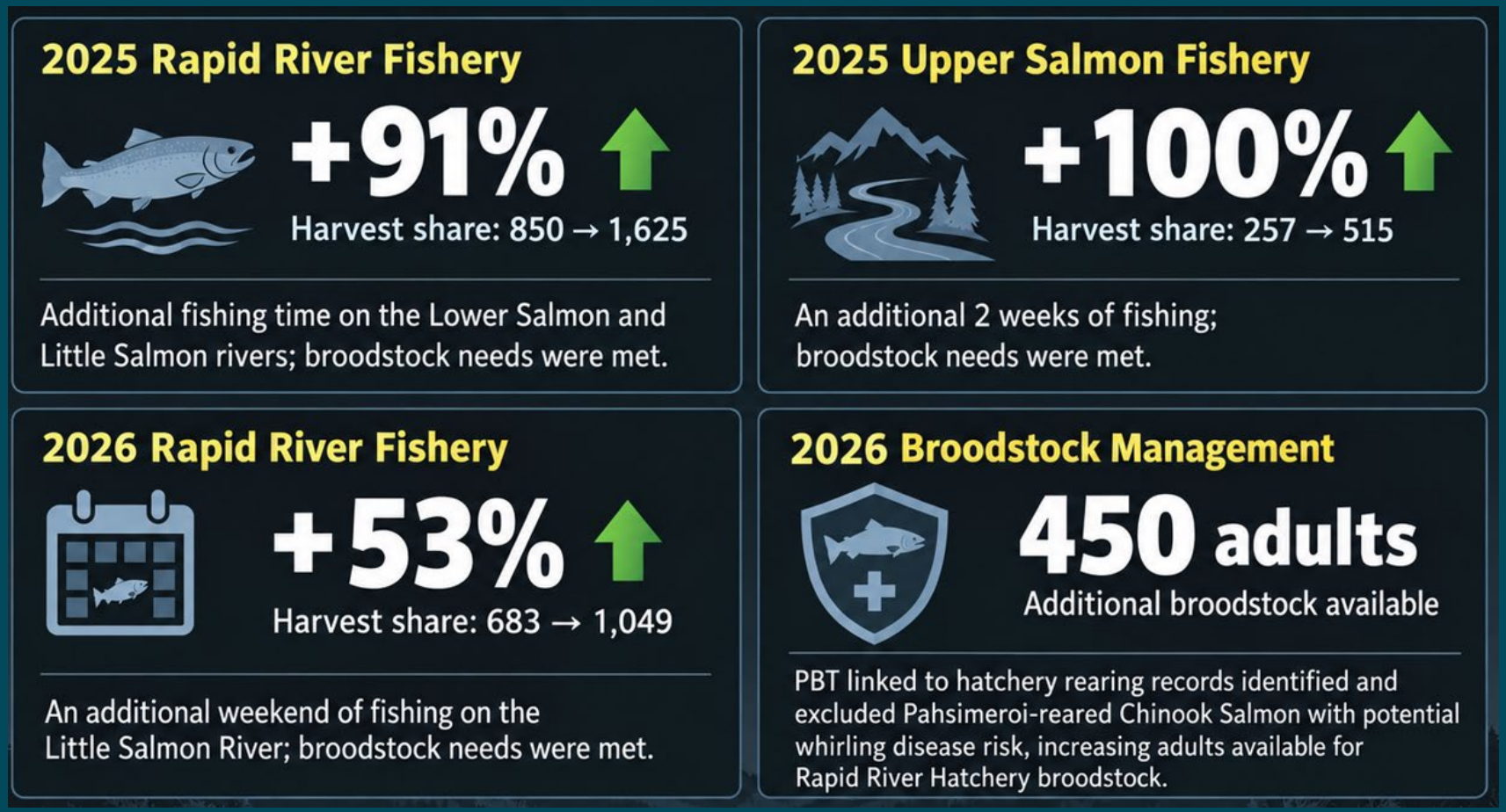




Examples from last 2 years:

Management Benefits Realized-

More accurate estimates of hatchery Chinook Salmon abundance by stock:



What comes next?



Grandparentage Testing

- **Grandparentage!!!**
- **Reminder: Benefits of PBT technology**

➢ PBT can be used to identify the origin of hatchery fish spawning in the wild







Transactions of the American Fisheries Society 145:671–686, 2016
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ISSN: 0002-8487 print / 1548-8659 online
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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Hinrichsen Environmental Services, 9034 45th Avenue Northeast, Seattle, Washington 98115, USA

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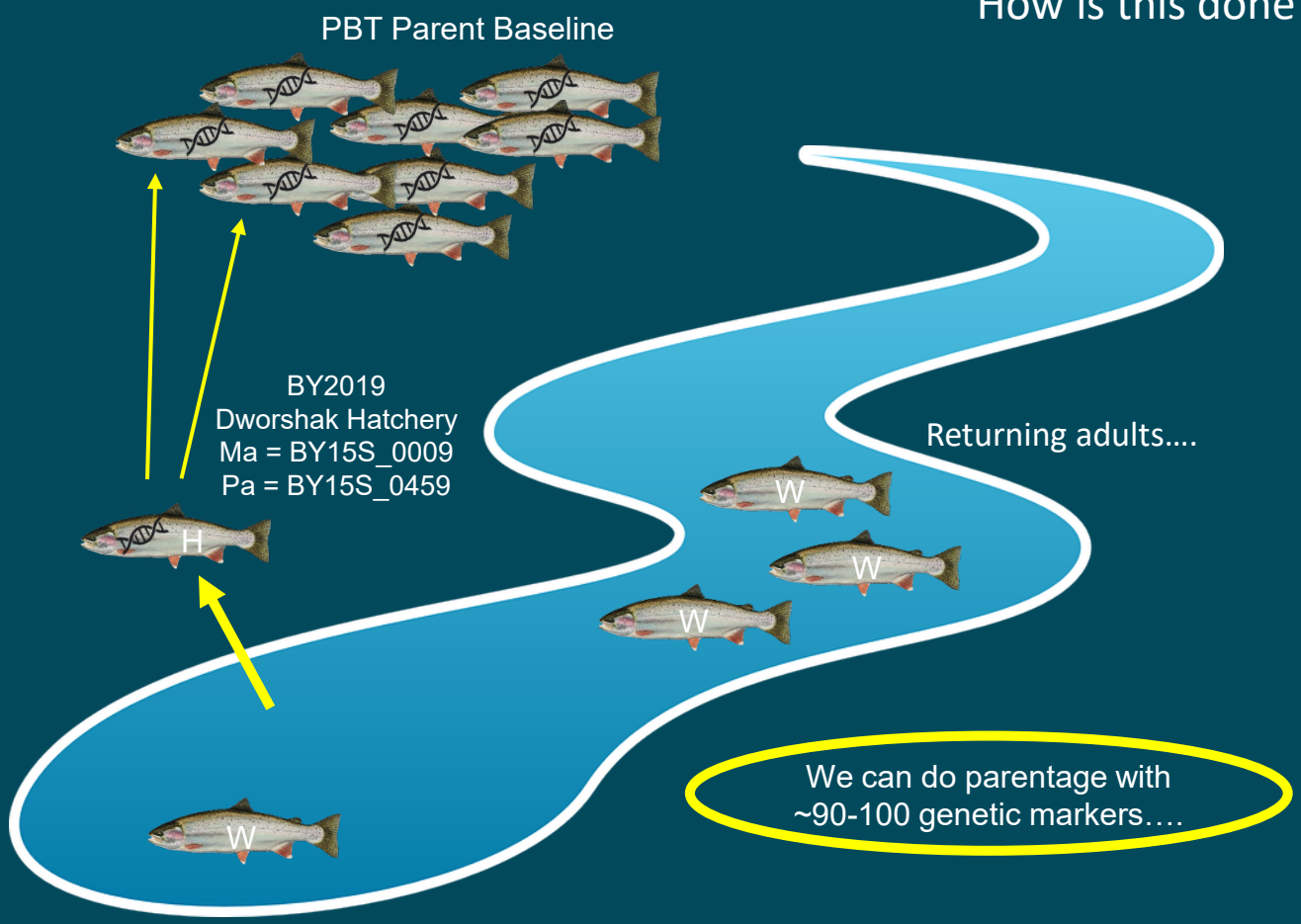
William P. Young
Nez Perce Tribe, Department of Fisheries Resources Management, 14054 Burr Road, McCall, Idaho 83638, USA

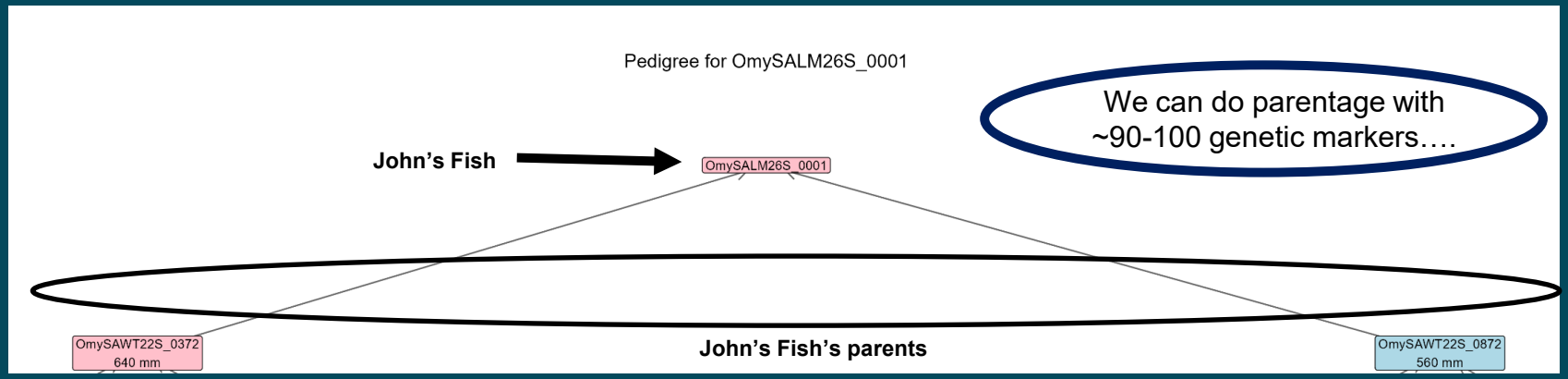
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Brian L. Maschhoff
Salmonetics, 7813 1st Avenue Northwest, Seattle, Washington 98117, USA

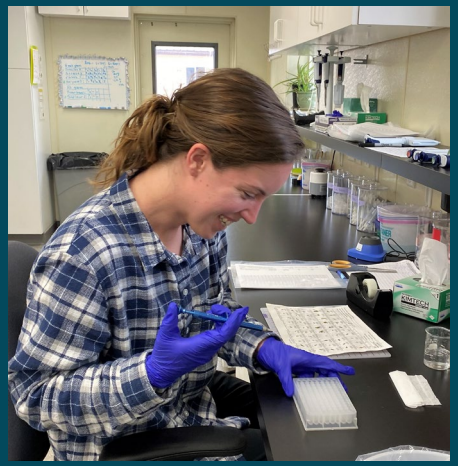
Hinrichsen et al (2016)-”*In the South Fork Salmon River application, there were 340% more PBT recoveries than CWT recoveries, leading to greater precision in release-specific values of p from maximum likelihood estimation.*”

How is this done????




Pedigree for OmySALM26S_0001
We can do parentage with ~90-100 genetic markers….
John's Fish
OmySALM26S_0001
OmySAWT22S_0372
640 mm
John's Fish's parents
OmySAWT22S_0872
560 mm


Genetic Sample
Date: 10, 4x, 26
Species: omy
Sex: M F U
Field Number: Salmon-01
Location: Upper Salmon R
Collector Info: JH
Fork Length: (mm) 58
Comments:





PBT Parent Baseline

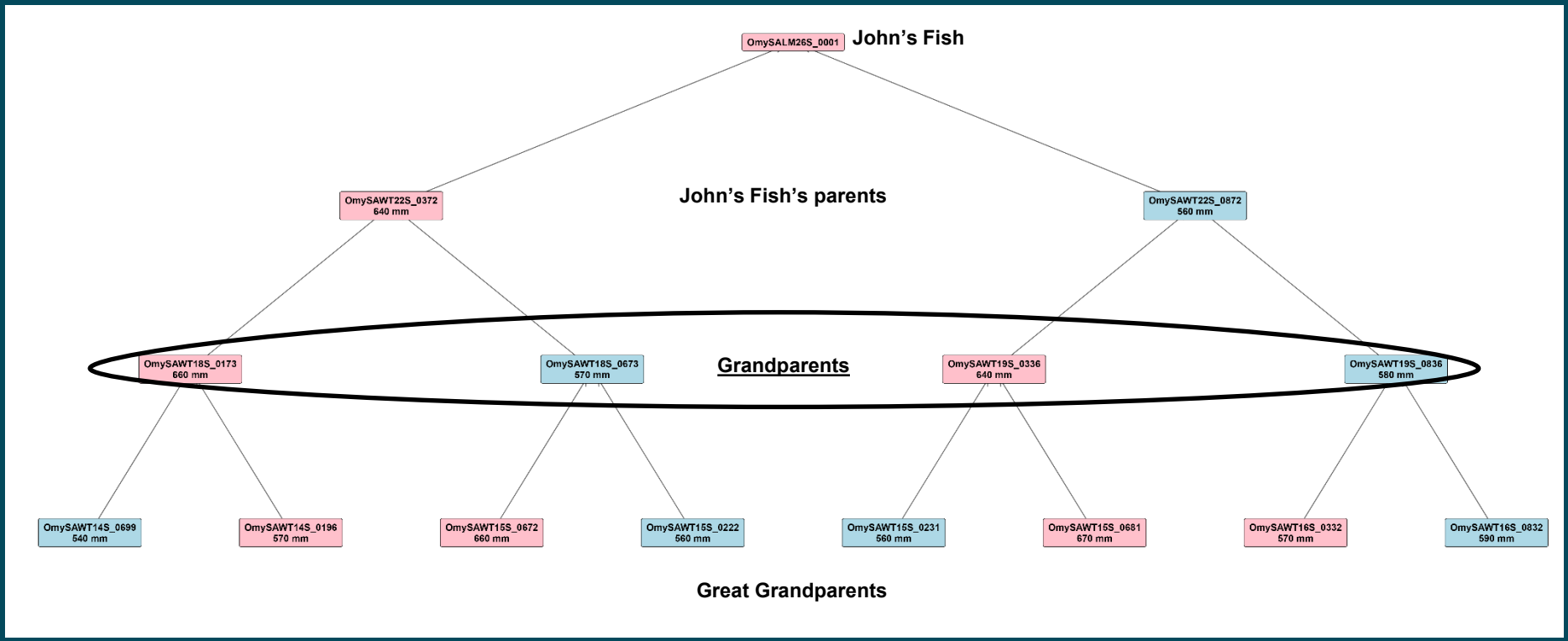


We want to know how many offspring were produced by hatchery fish spawning in the wild!

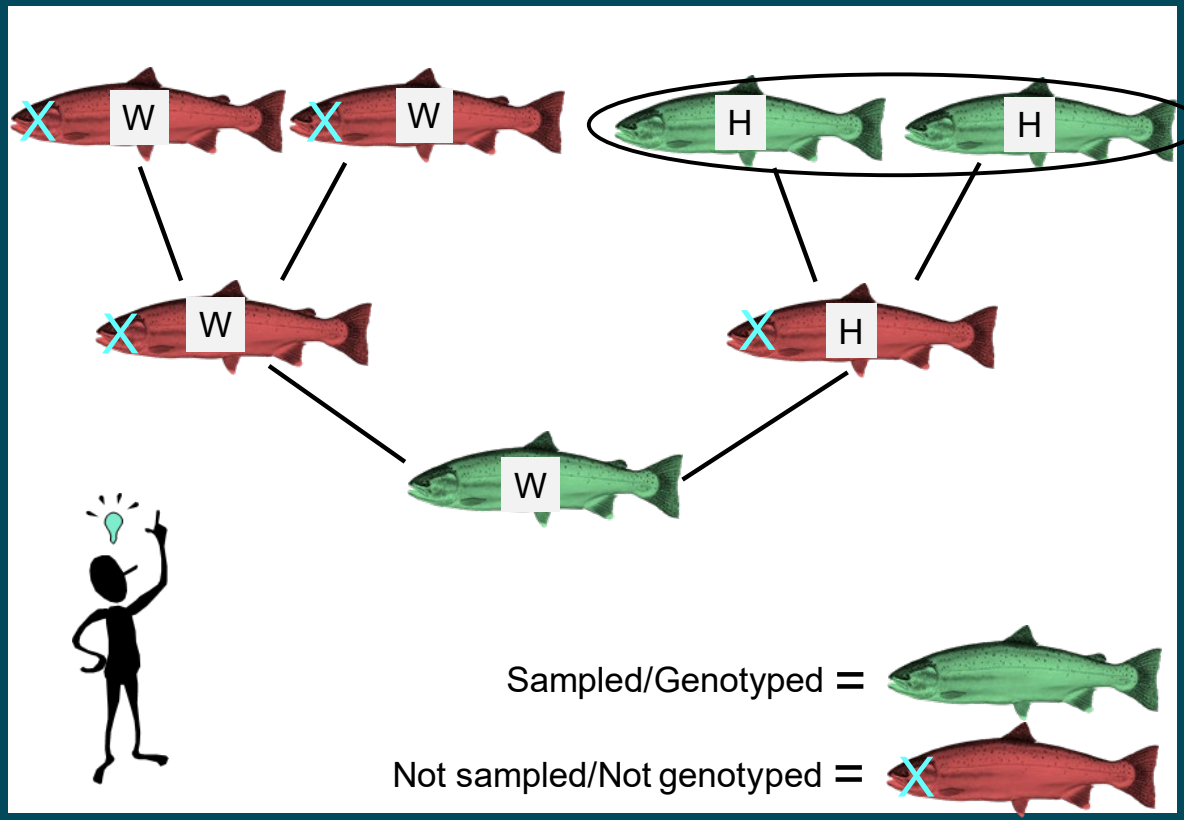
However, these parents haven't been genetically sampled! We can't do parentage.



We have very deep, very complete pedigrees!!!



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



- **History**

✓ We developed statistical methods for assigning grandparents and estimating error rates for a genetic panel

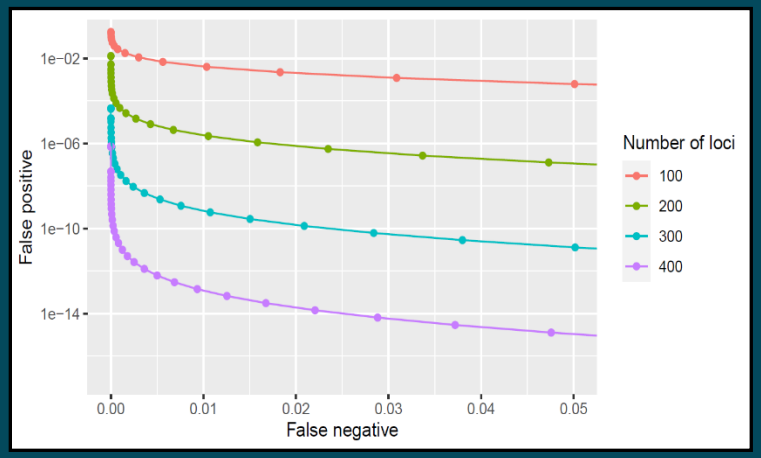
✓ We have implemented these methods in a package for R statistical software at https://github.com/delomast/gRandma

✓ Preliminary analysis shows that 300 – 500 genetic markers are sufficient to accurately assign grandparents basin-wide

✓ We proposed an empirical validation and demonstration of this new technique (POC studies, funded by BPA and PCSRF)



Tom Delomas



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

North American Journal of Fisheries Management, 2026, **00**, 1–16
https://doi.org/10.1093/najfmt/vqag051
Published: 15 September 2026
Feature Article

American Fisheries Society

Empirical validation of grandparent inference to quantify reproduction of hatchery-origin fish in the wild

Thomas A. Delomas[1,6,*], Audrey C. Harris[2], John S. Hargrove[2], Shawn R. Narum[3], Jon E. Hess[4], Rebekah L. Horn[3], and Matthew R. Campbell[5]

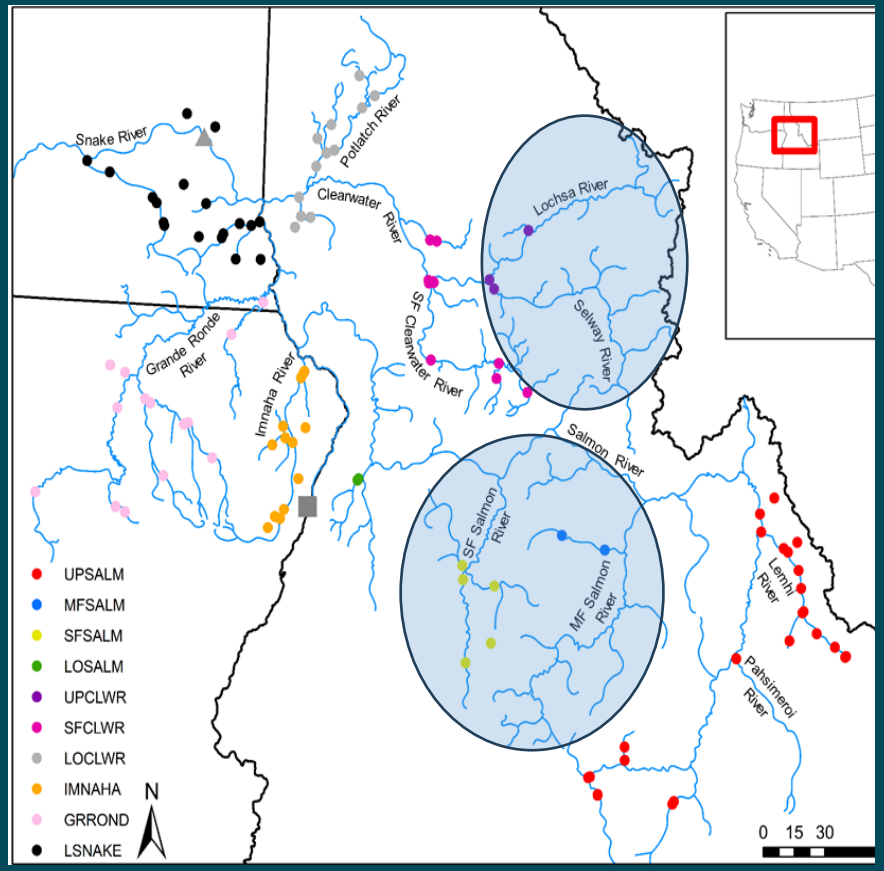
[1]U.S. Department of Agriculture, Agricultural Research Service, National Cold Water Marine Aquaculture Center, Kingston, Rhode Island, USA
[2]Pacific States Marine Fisheries Commission, Eagle, Idaho, USA
[3]Columbia River Inter-Tribal Fish Commission, Hagerman Genetics Lab, Hagerman, Idaho, USA
[4]Columbia River Inter-Tribal Fish Commission, Portland, Oregon, USA
[5]Idaho Department of Fish and Game, Eagle, Idaho, USA

*Corresponding author: Thomas A. Delomas. Email: tdelomas@aquatechcenter.com.
[6]Present address: The Center for Aquaculture Technologies, San Diego, California, USA

- Two POC studies completed
- New larger genetic marker panels used
- Extremely low rates of incorrect and missed assignments
- Grandparentage can work even at very large scales (Snake River Basin)

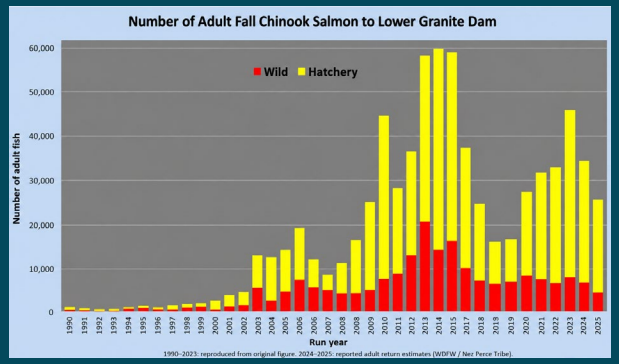
What do managers want to use Grandparentage for?
Snake River Steelhead

- A dominant management strategy that Idaho Department of Fish and Game uses to protect ESA-listed wild steelhead and Chinook Salmon is to maintain large core areas of the highest habitat where no hatchery fish are released.
- Has this management strategy worked?
- We can look for hatchery fish in wild spawning areas, but their presence doesn't mean they are contributing to spawning.



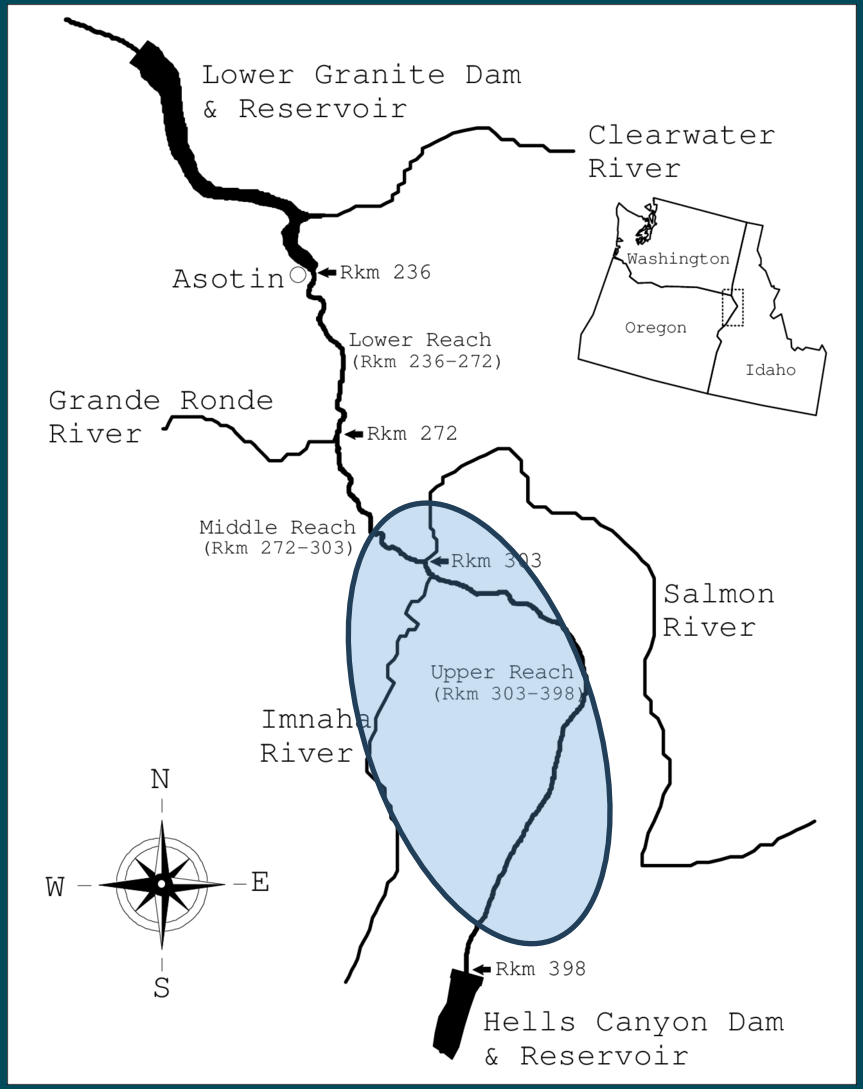
What do managers want to use Grandparentage for?

Snake River Fall Chinook



- Hatchery supplementation helped rebuild Snake River Fall Chinook Salmon
- Natural production emphasis areas are needed to achieve recovery.
- The intent is to manage where hatchery fish reproduce while retaining the benefits of an integrated hatchery program.

- Has this management strategy worked?



What did we do?

- Developed new larger genetic marker panels for both species
- Reran a subset of hatchery grandparents (could have offspring that spawned in the wild)
  - 12,242 steelhead from 2012/2013
  - 8,260 Fall Chinook Salmon from 2012 – 2014
  - Sampled wild steelhead (2020/2021; N = 2,035) and hatchery and natural-origin Fall Chinook Salmon (2021; N = 2,546) at Lower Granite Dam and ran them with the larger genetic marker panels and looked for hatchery grandparent contributions.



Audrey Harris





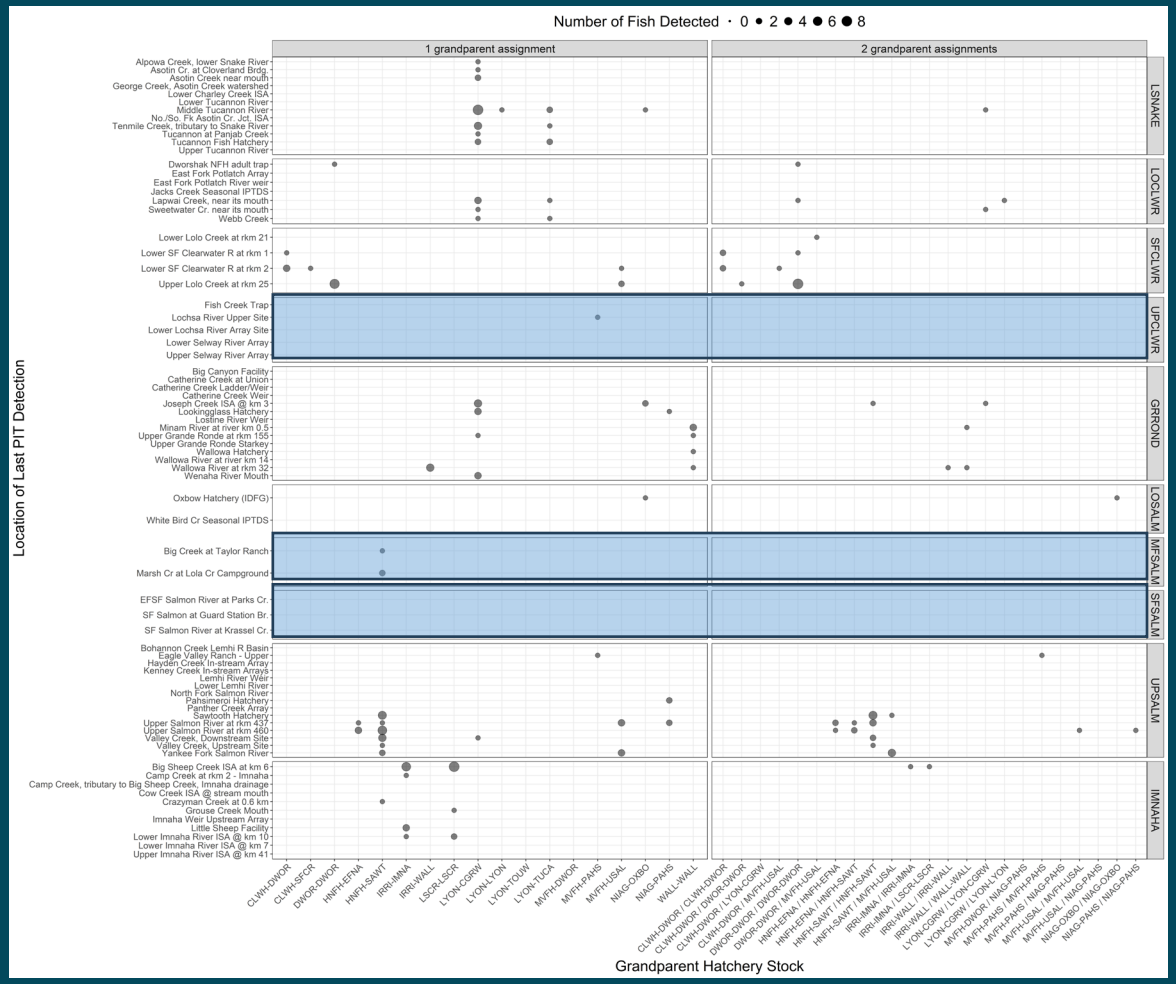




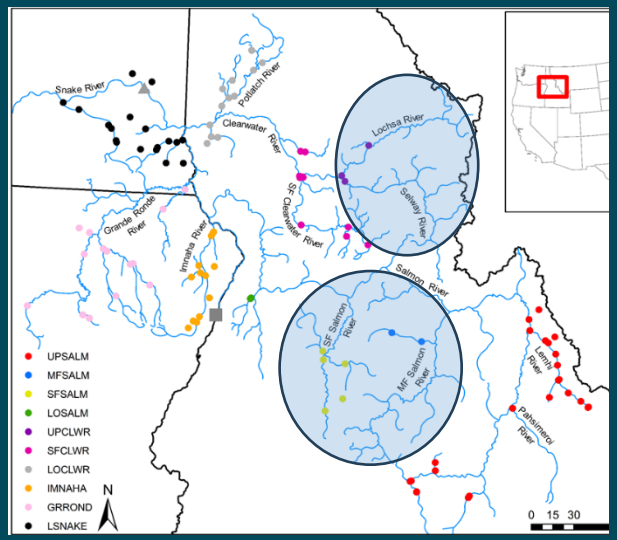
Steelhead- What did we observe?

Findings are consistent with management objectives!

- From a sample of N = ~2,000 wild adults
  - 81.4% (1,635) had no hatchery grandparents assigned
  - 14.3% (288) of individuals assigned to one set of hatchery grandparents
  - 4.3% (86) of individuals assigned to two sets of hatchery grandparents



PIT array detected adults:



Natural spawning areas in colored circles

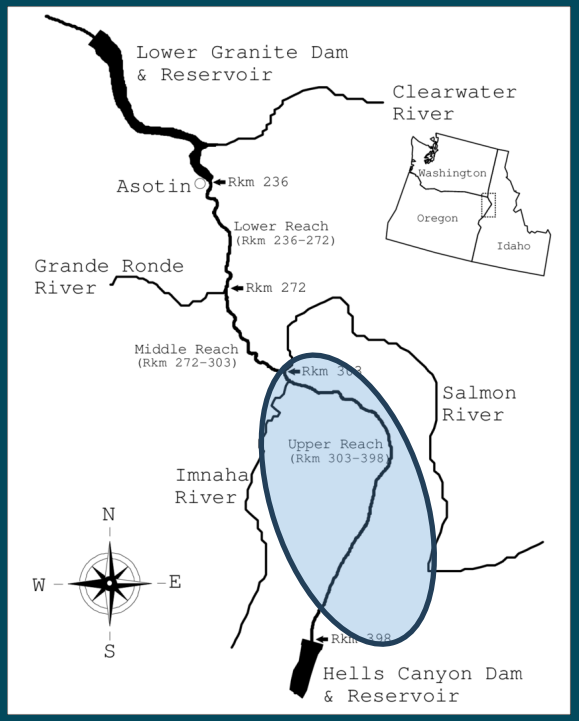
Little evidence of wild-born adults with hatchery Grandparents detected in wild spawning areas

Fall Chinook Salmon - what did we learn?

- About 70% of unclipped adults passing Lower Granite in 2021 were hatchery-raised.
- Grandparentage estimated that hatchery fish supplied about 40% of the parental contribution to wild-born adult returns, a conservative upper-bound estimate.

- While the pattern we observed could be explained by reduced reproductive success of hatchery fish, it is consistent with management limiting hatchery spawning and overlap with natural-origin spawners.

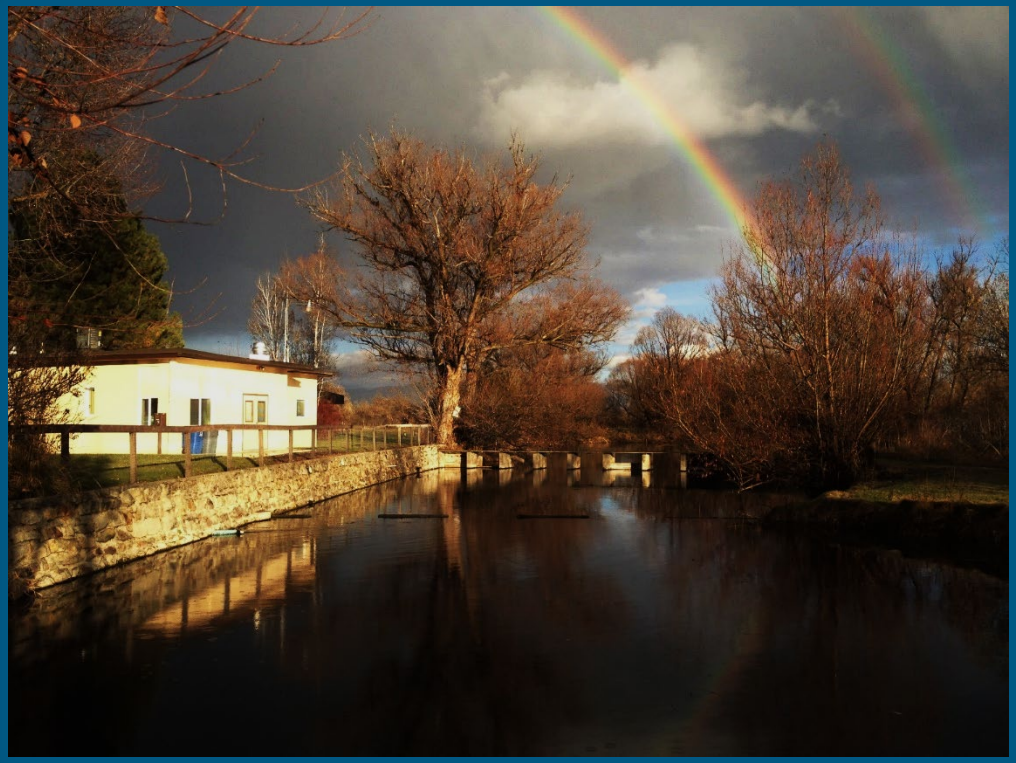
- Future work could focus on specific areas and ages:
  - ✓ Applying grandparentage to juveniles sampled from designated spawning areas could help evaluate where hatchery reproduction occurs and distinguish management effects from fitness differences.
  - ✓ Repeating those assessments would allow managers to track hatchery contribution over time.



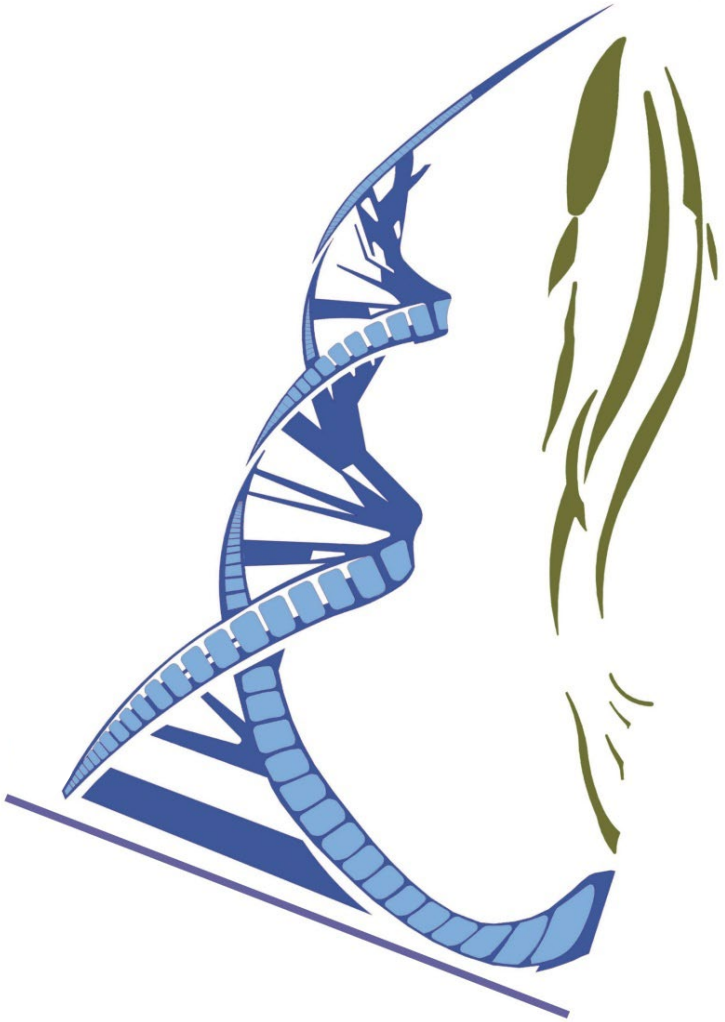
Natural production emphasis area is in shaded blue



Questions???



Genetic Monitoring of Anadromous Fish in the Columbia River Basin



Shawn Narum & Jon Hess

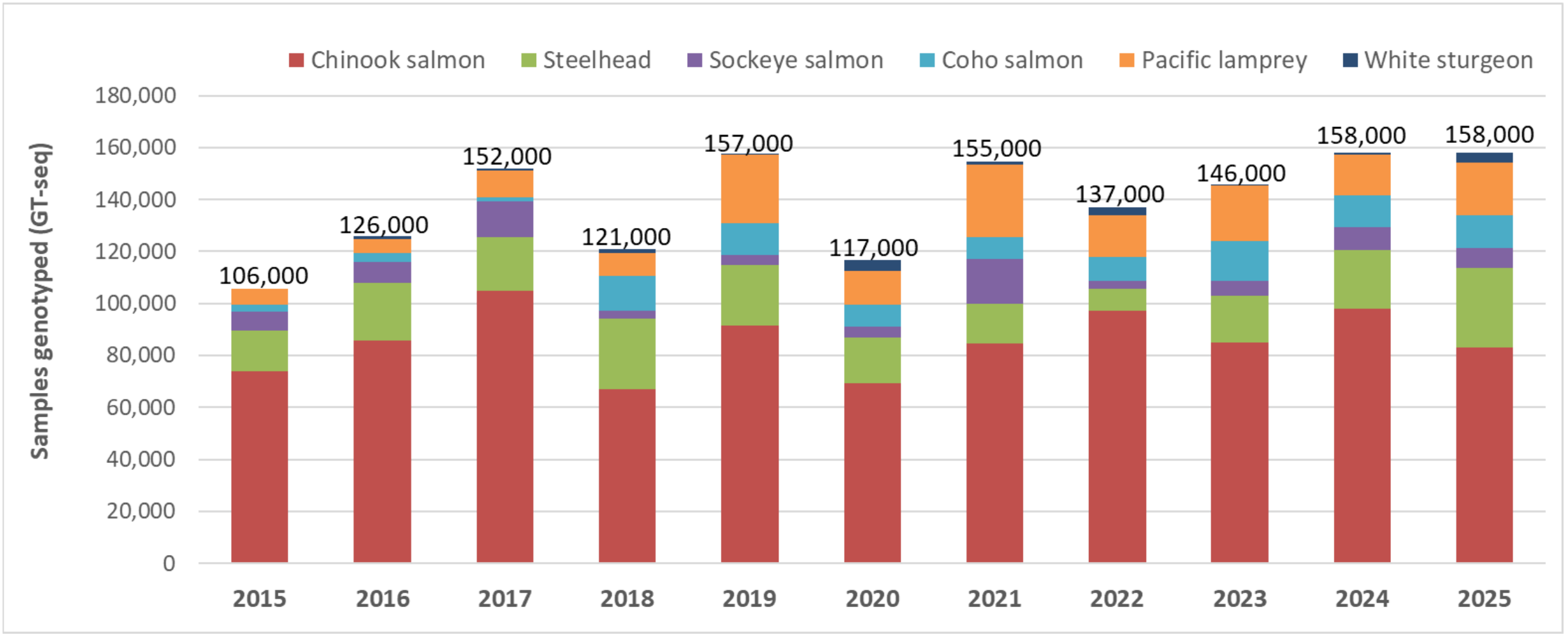
Columbia River Inter-Tribal Fish Commission (CRITFC)



Applied Genetics Research & Monitoring

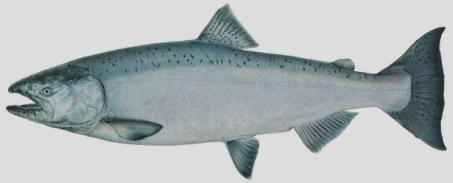
- **Genetic monitoring of distinct stocks**
  - Return timing and abundance of stocks (hatchery & natural)
  - Estimating harvest of stocks (hatchery & natural)
- **Effects of hatchery programs on wild stocks**
  - Estimate fitness with genetic pedigrees
  - Monitor effects on heritable phenotypic variation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

Fish Genotyped Annually by CRITFC with GT-seq



Genetic monitoring in the Columbia River

Chinook salmon



Steelhead

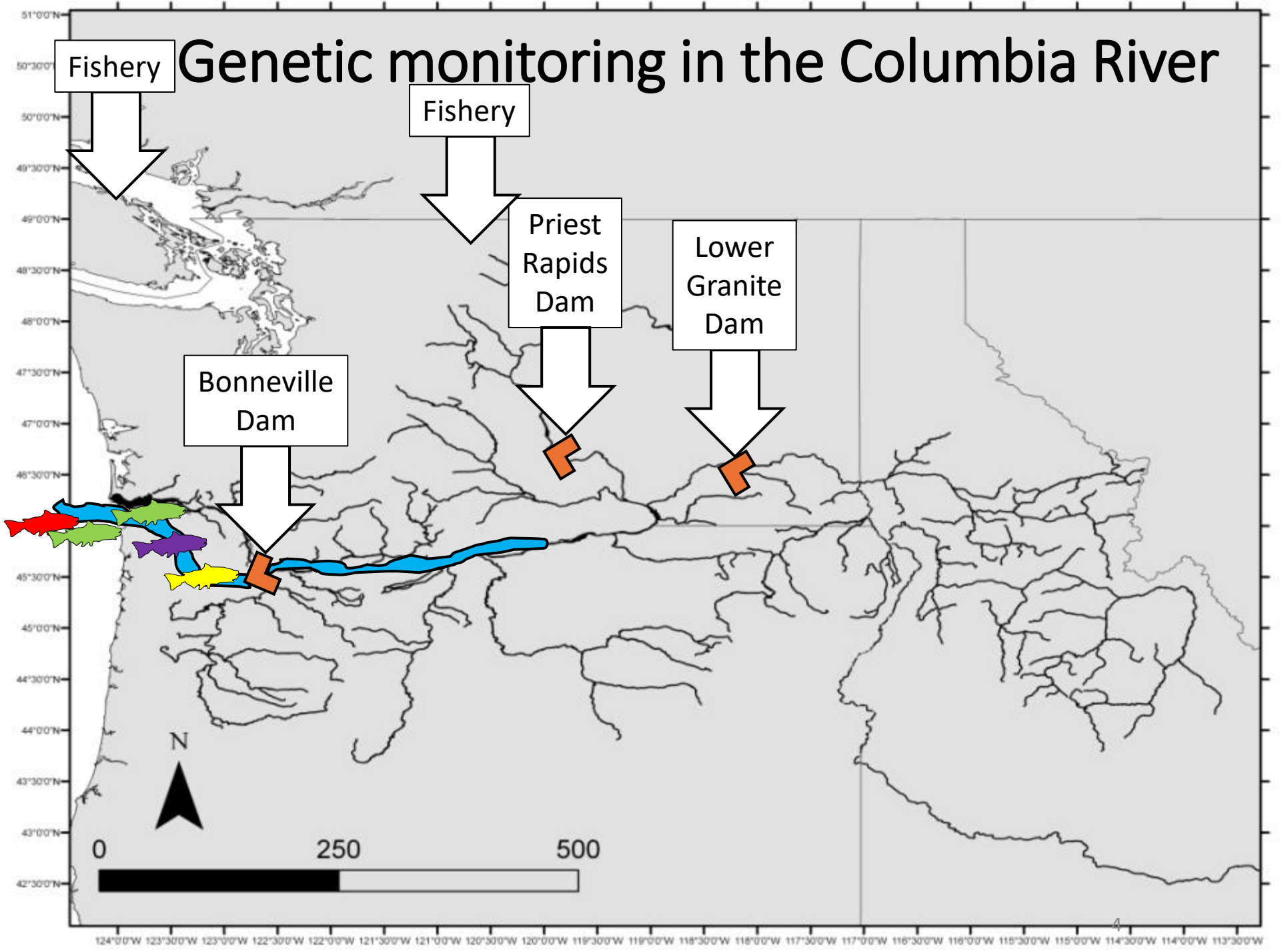


Sockeye salmon



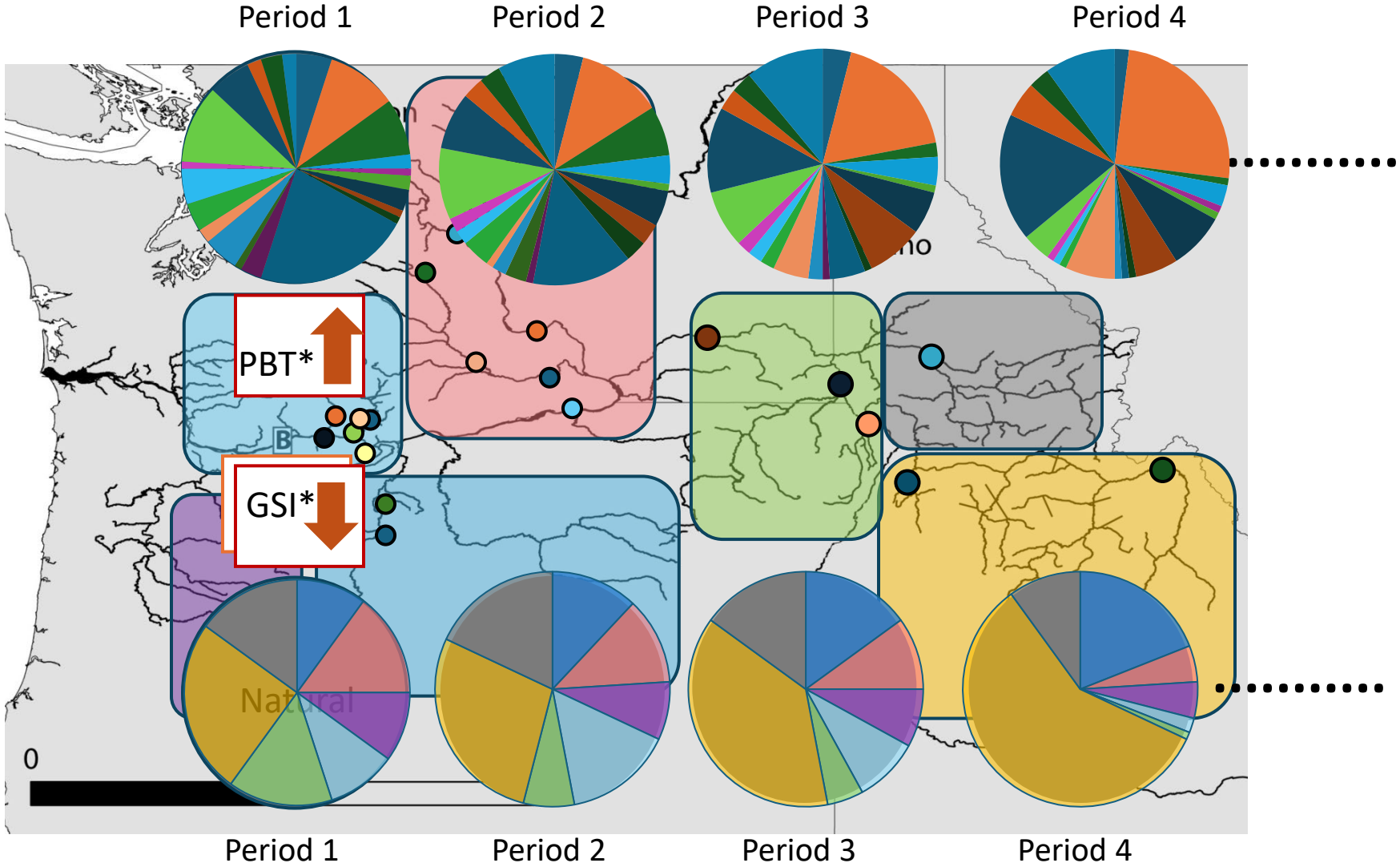
Coho salmon





Bonneville Dam:

In-season estimates of abundance/timing at Bonneville Dam for specific stocks of Chinook, steelhead, sockeye; updated reports sent to co-managers every 2 weeks



*PBT = Parentage Based Tagging

*GSI = Genetic Stock Identification

What if we bring the lab to them?

CRITFC Mobile Genetics Lab



Designing a Mobile Genetics Lab

Lanie Galland



Ben Fredericksen



2025: Test deployments
2026: Active Reporting of PBT/GSI

Lab Bed Living Space/Bathroom Bed



44’ trailer

F350 truck (GSA lease)




Chelex
PCR 1
index 40
charm 90
BSS <40
Qubit 15
Kit 10

Innovation & Fisheries Recovery

“Whether you think you can, or you think you can't--*you're right*.”

— Henry Ford

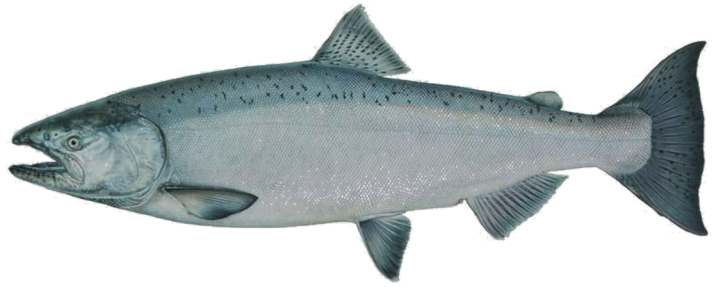
Whether you think:

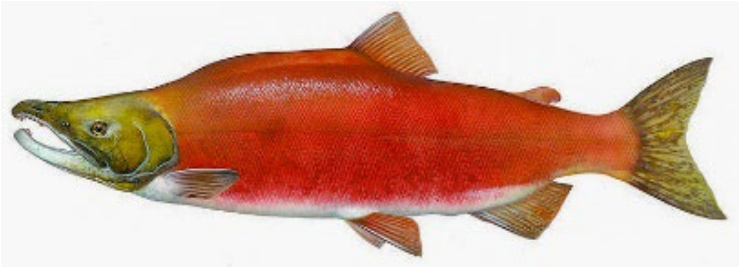
The CWT program can’t be replaced as salmon populations continue to be lost,

OR

You think innovative PBT can help with salmon recovery;

You’re right.







Using PBT, GSI, and Sibship Tools to Improve Management Outcomes Across the Columbia Basin

CRITFC Applications in Spring Chinook, Sockeye, and Pacific Lamprey

What CRITFC's Program Was Designed to Answer



IDENTIFY HATCHERY-ORIGIN AND NATURAL-ORIGIN FISH AT SCALES NOT ACHIEVABLE BEFORE.



MONITOR STOCK CONTRIBUTIONS IN MIXED-STOCK FISHERIES (ESPECIALLY AT BONNEVILLE).



QUANTIFY BROODSTOCK COMPOSITION AND EVALUATE HATCHERY PRACTICES.

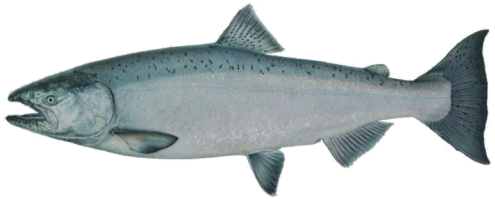


TRACK PERFORMANCE AND ABUNDANCE OF NATURAL-ORIGIN STOCKS.



EXPAND GENETIC MONITORING TO NON-SALMONIDS (PACIFIC LAMPREY).

Example A — Spring Chinook at Bonneville (PBT + GSI)



Why Spring Chinook at BON Matters

- BON is the major monitoring choke point for upriver spring Chinook.
- Mixed-stock passage includes ESA-listed and hatchery populations.
- Harvest managers seek accurate in-season abundance and stock-specific forecasts.

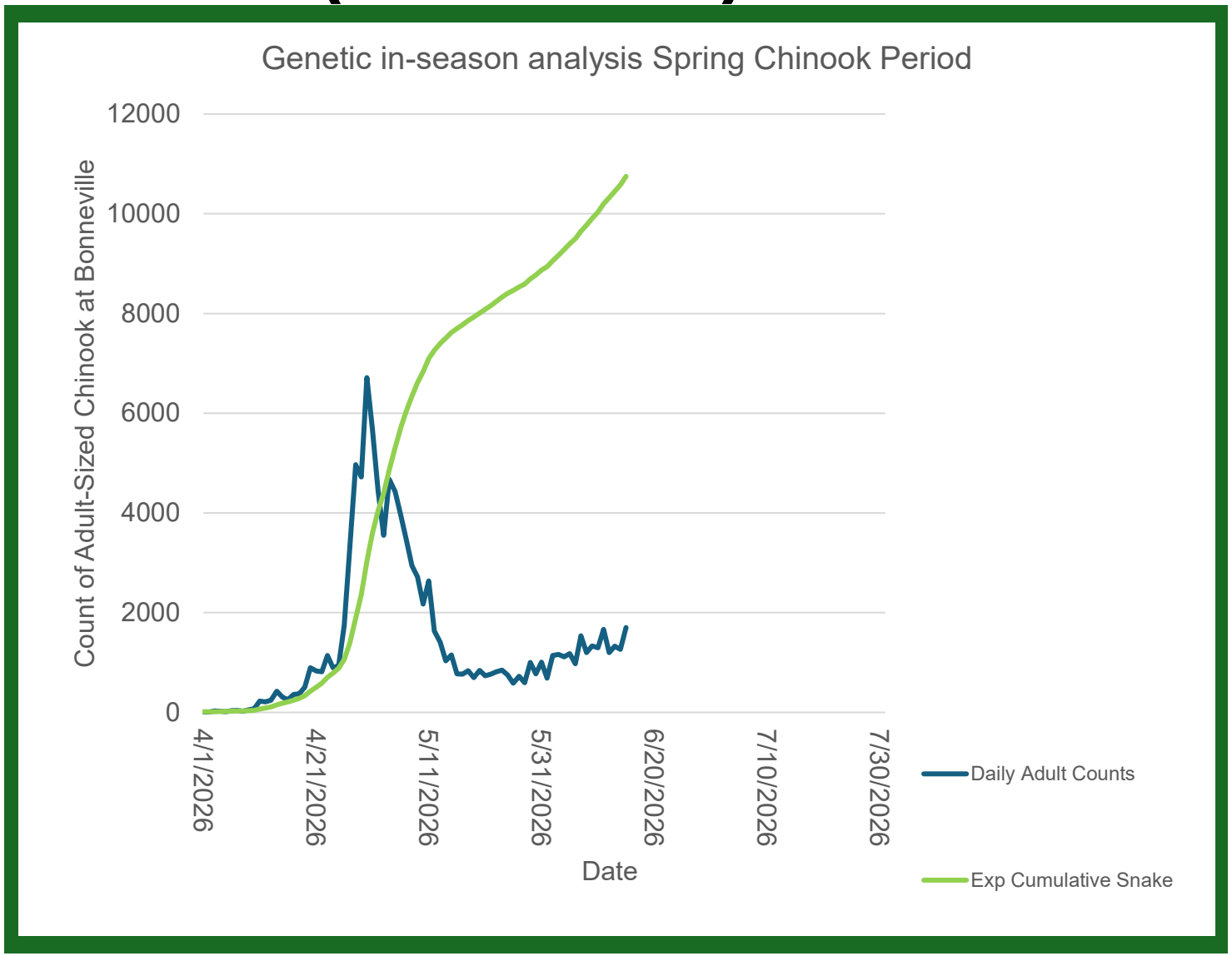




Example A — Spring Chinook at Bonneville (PBT + GSI)

What We Can Answer Now

- **In-season genetic stock identification (GSI)** – near real-time updates of stock composition.



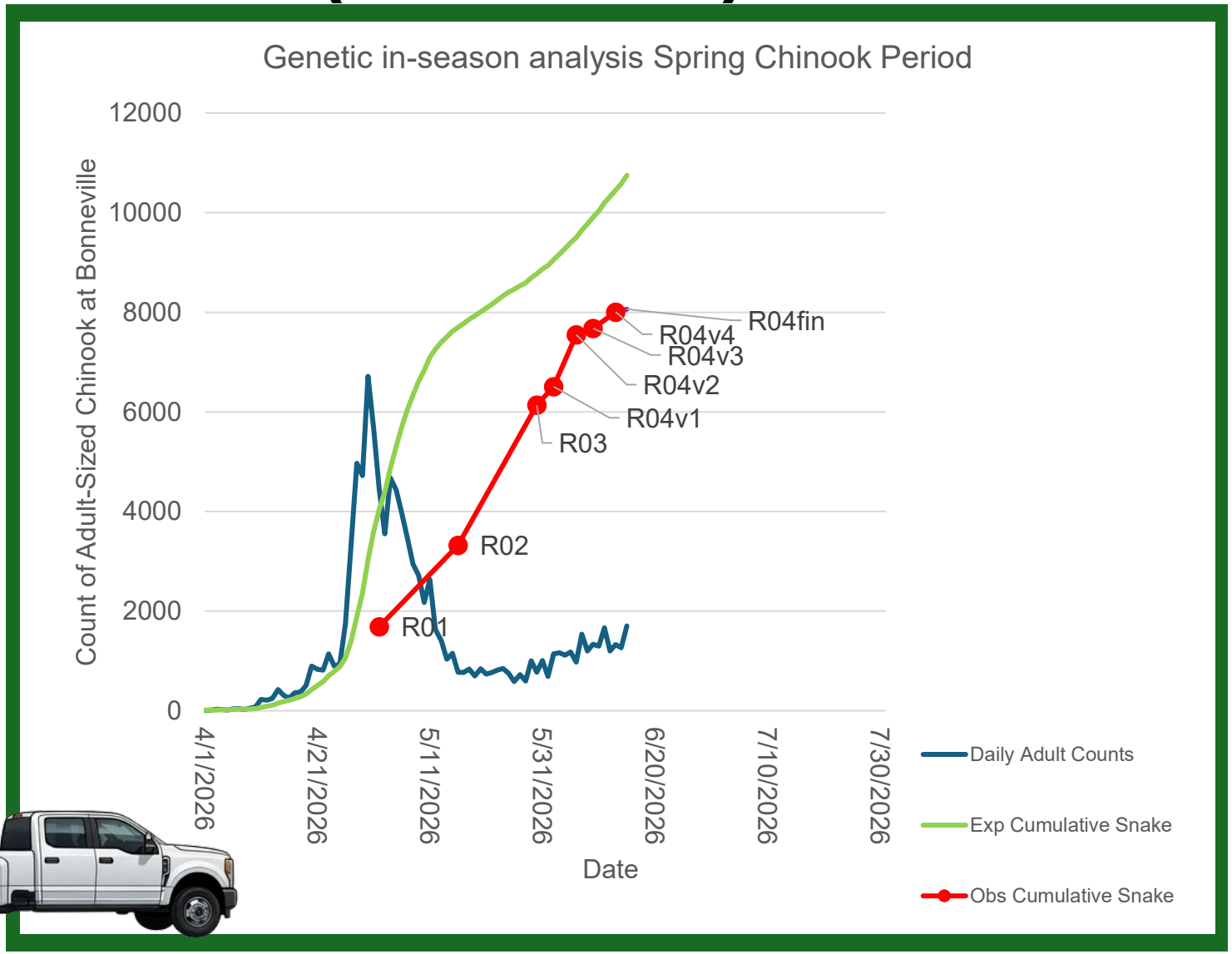
Example A — Spring Chinook at Bonneville (PBT + GSI)

What We Can Answer Now

- **In-season genetic stock identification (GSI)** – near real-time updates of stock composition.

CRITFC Mobile Genetics Lab





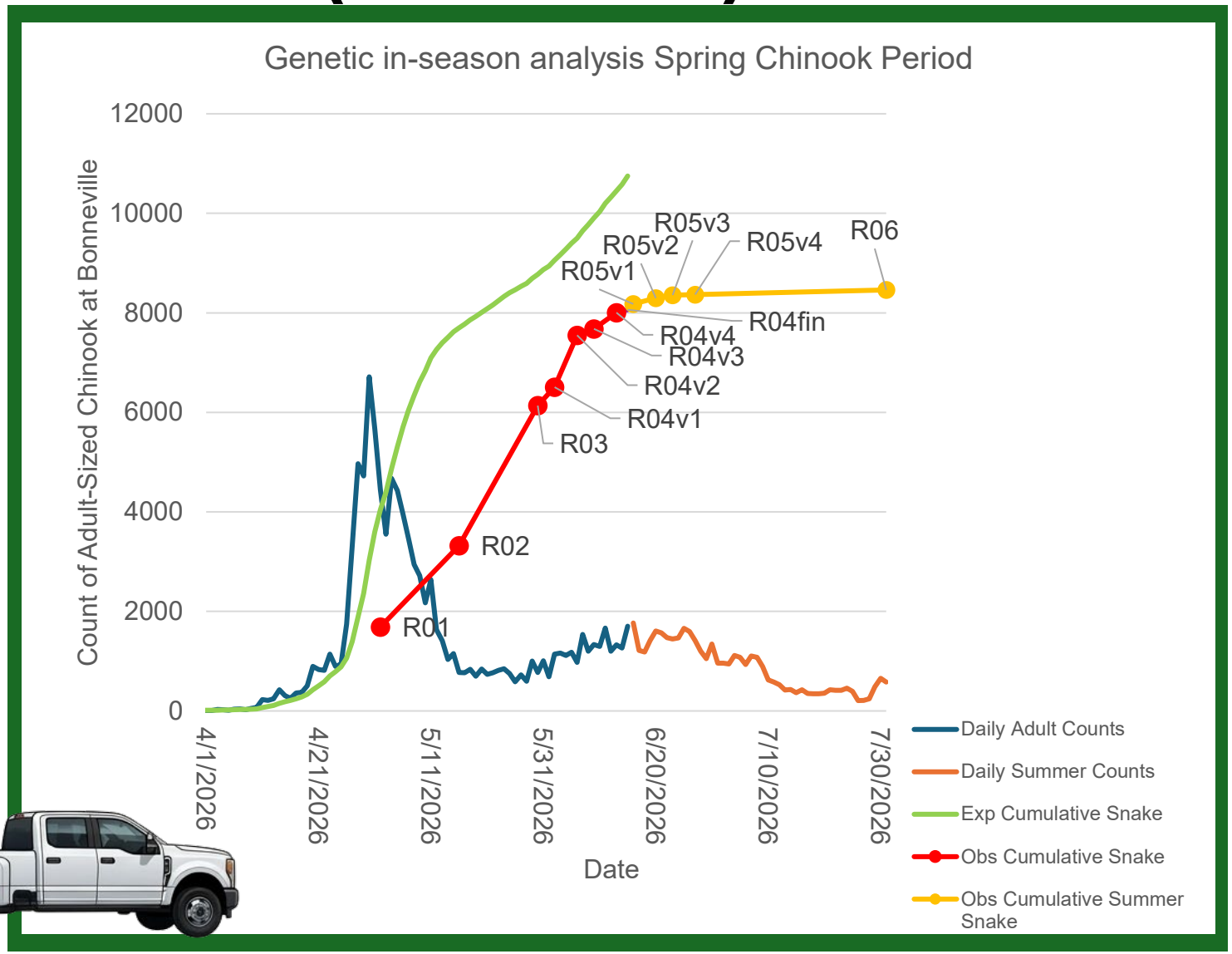
Example A — Spring Chinook at Bonneville (PBT + GSI)

What We Can Answer Now

- **In-season genetic stock identification (GSI)** – near real-time updates of stock composition.

CRITFC Mobile Genetics Lab



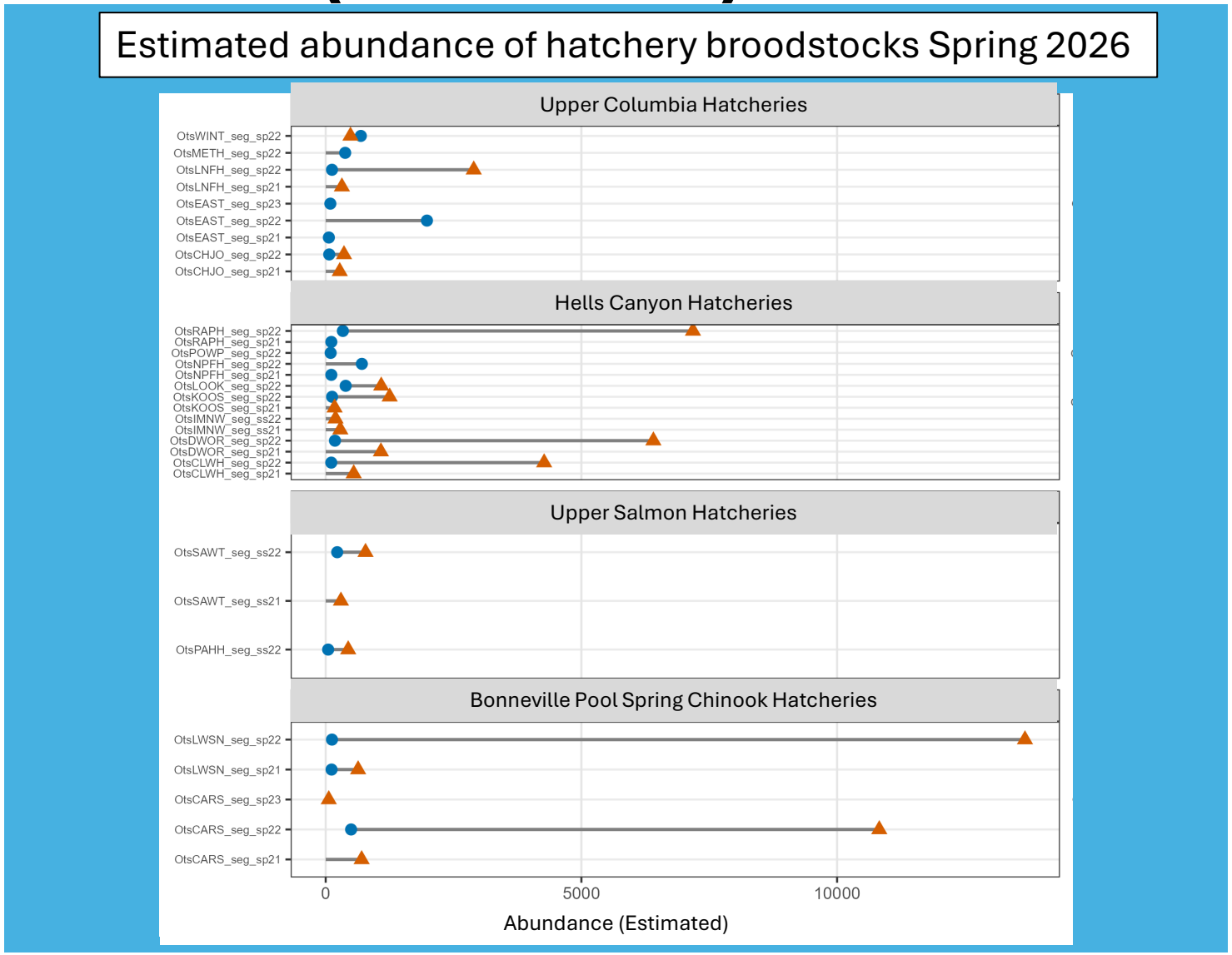


Example A — Spring Chinook at Bonneville (PBT + GSI)

What We Can Answer Now

- **In-season genetic stock identification (GSI)** – near real-time updates of stock composition.
- **PBT-based identification of hatchery-origin fish** – broodstock status & post-season performance.

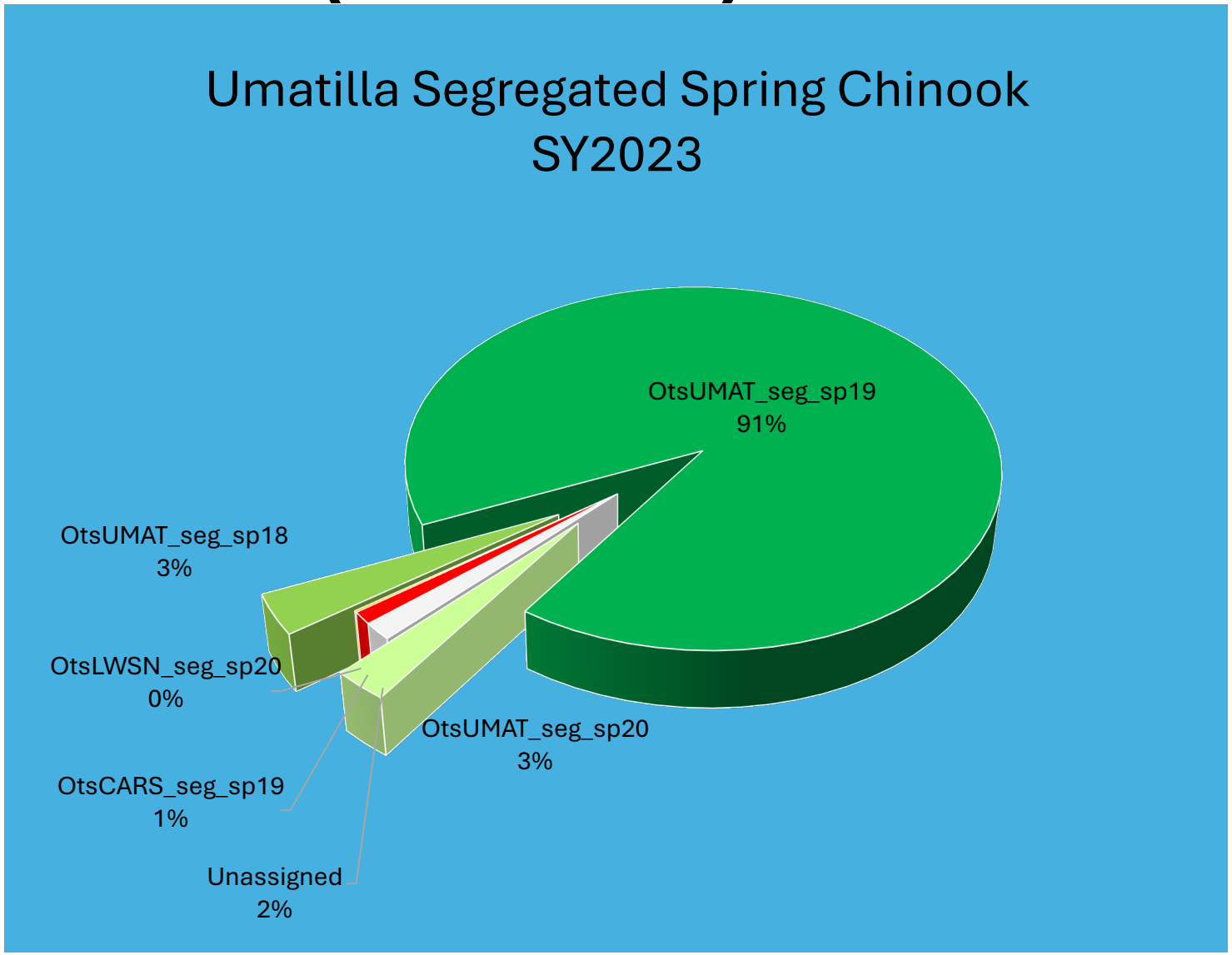
Clipped Unclipped



Example A — Spring Chinook at Bonneville (PBT + GSI)

What We Can Answer Now

- **In-season genetic stock identification (GSI)** – near real-time updates of stock composition.
- **PBT-based identification of hatchery-origin fish** – broodstock status & post-season performance.
- **Custom hatchery manager reports** – broodstock composition.

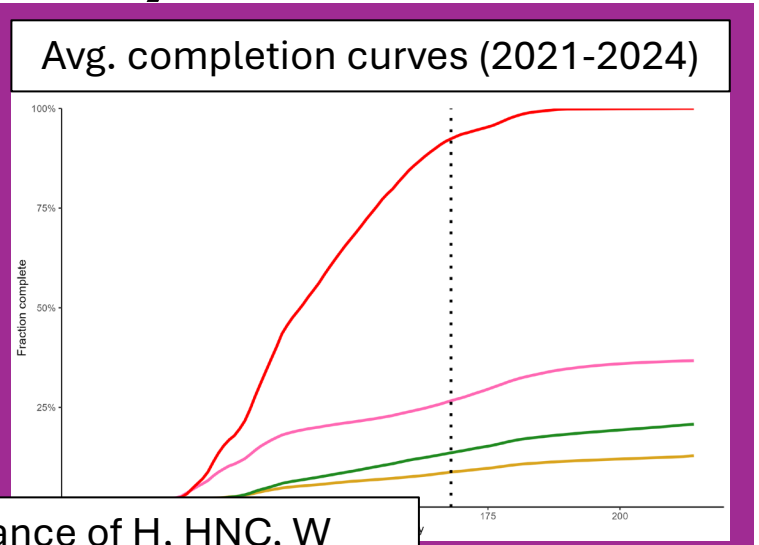


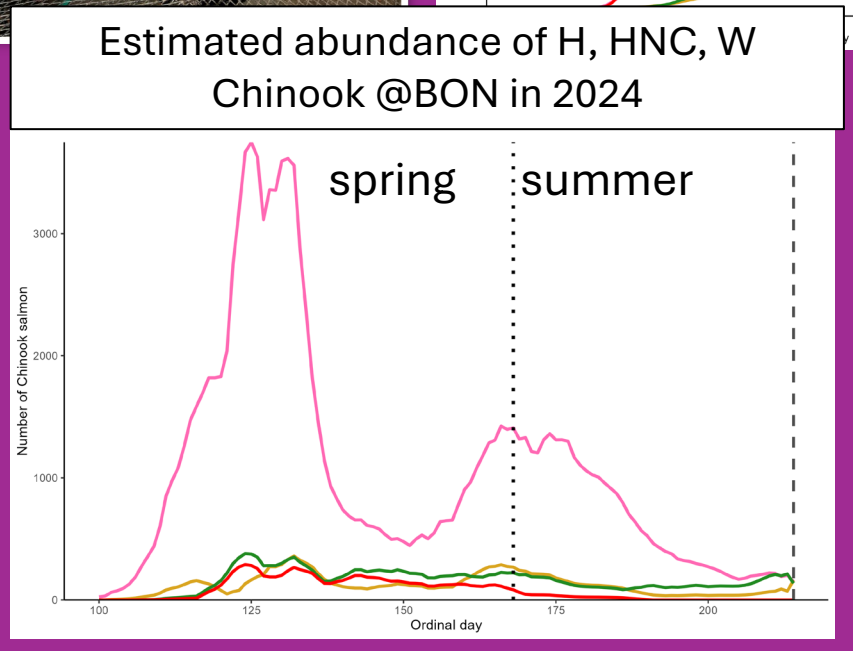
Example A — Spring Chinook at Bonneville (PBT + GSI)

Management Outcomes

- **Hatchery managers learned true broodstock composition** → adjustments to protocols the following year.
- **In-season GSI informed stock timing curves** → data to evaluate harvest opportunity in near real time.
- **Postseason PBT/GSI accurate stock-specific abundance estimates** → hatchery and natural stock reports.







Clipped (H)

Unclipped (HNC)

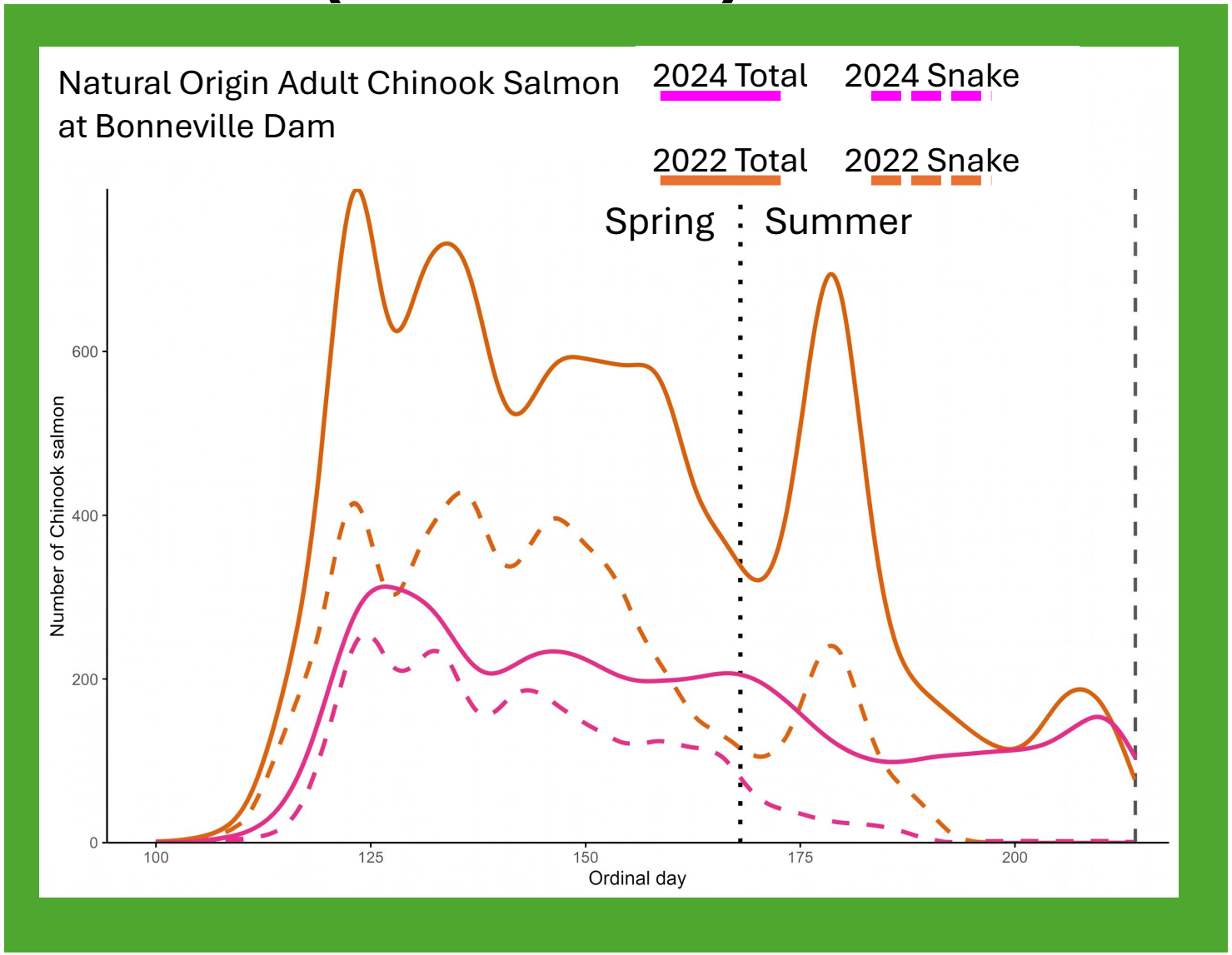
Natural Origin (W)

W-Snake

Example A — Spring Chinook at Bonneville (PBT + GSI)

Where This Can Go Next

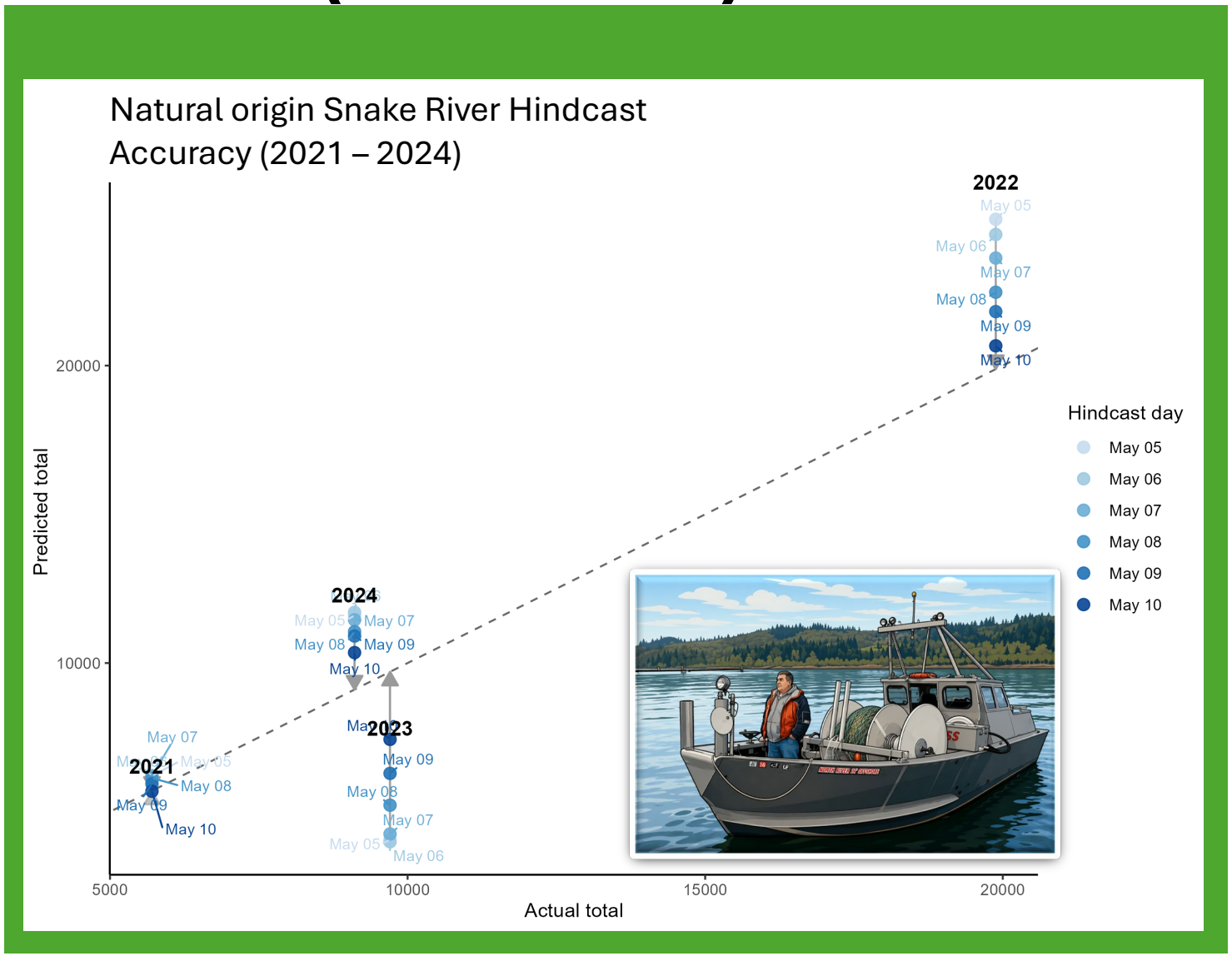
- **Near-real-time run-size updating** using PBT/GSI samples early in the run to infer postseason abundance with actionable precision.



Example A — Spring Chinook at Bonneville (PBT + GSI)

Where This Can Go Next

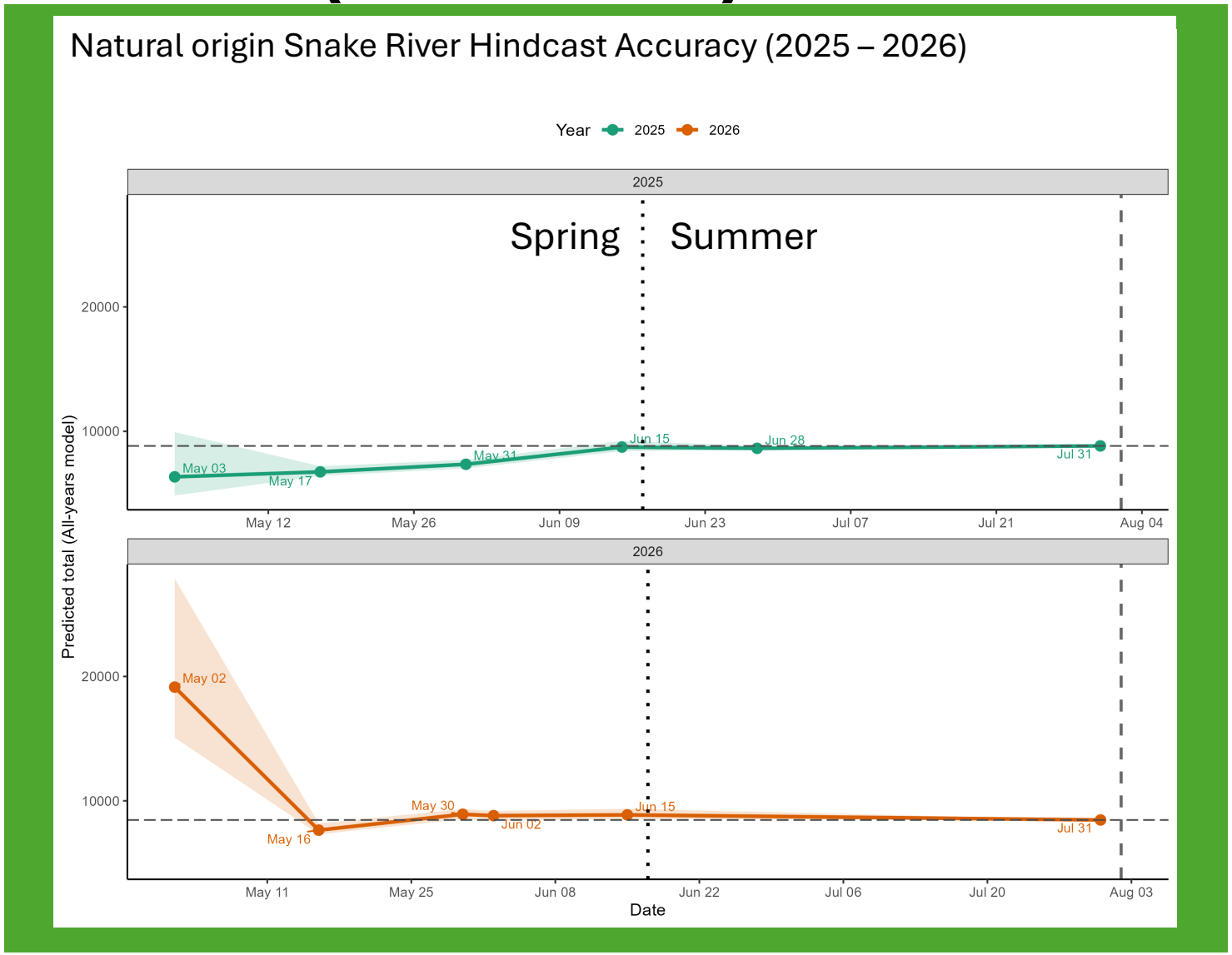
- **Near-real-time run-size updating** using PBT/GSI samples early in the run to infer postseason abundance with actionable precision.
- **Ability to fine-tune harvest decisions** earlier than current models allow.



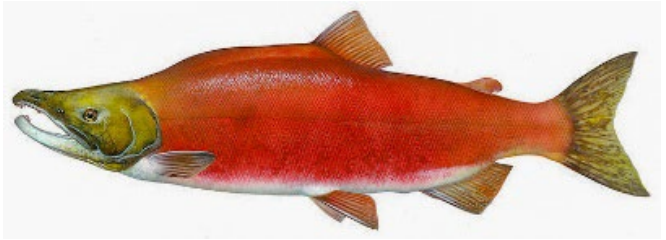
Example A — Spring Chinook at Bonneville (PBT + GSI)

Where This Can Go Next

- **Near-real-time run-size updating** using PBT/GSI samples early in the run to infer postseason abundance with actionable precision.
- **Ability to fine-tune harvest decisions** earlier than current models allow.
- **Early detection of anomalies** (e.g., stock failing to appear when expected, unusually early/late timing).

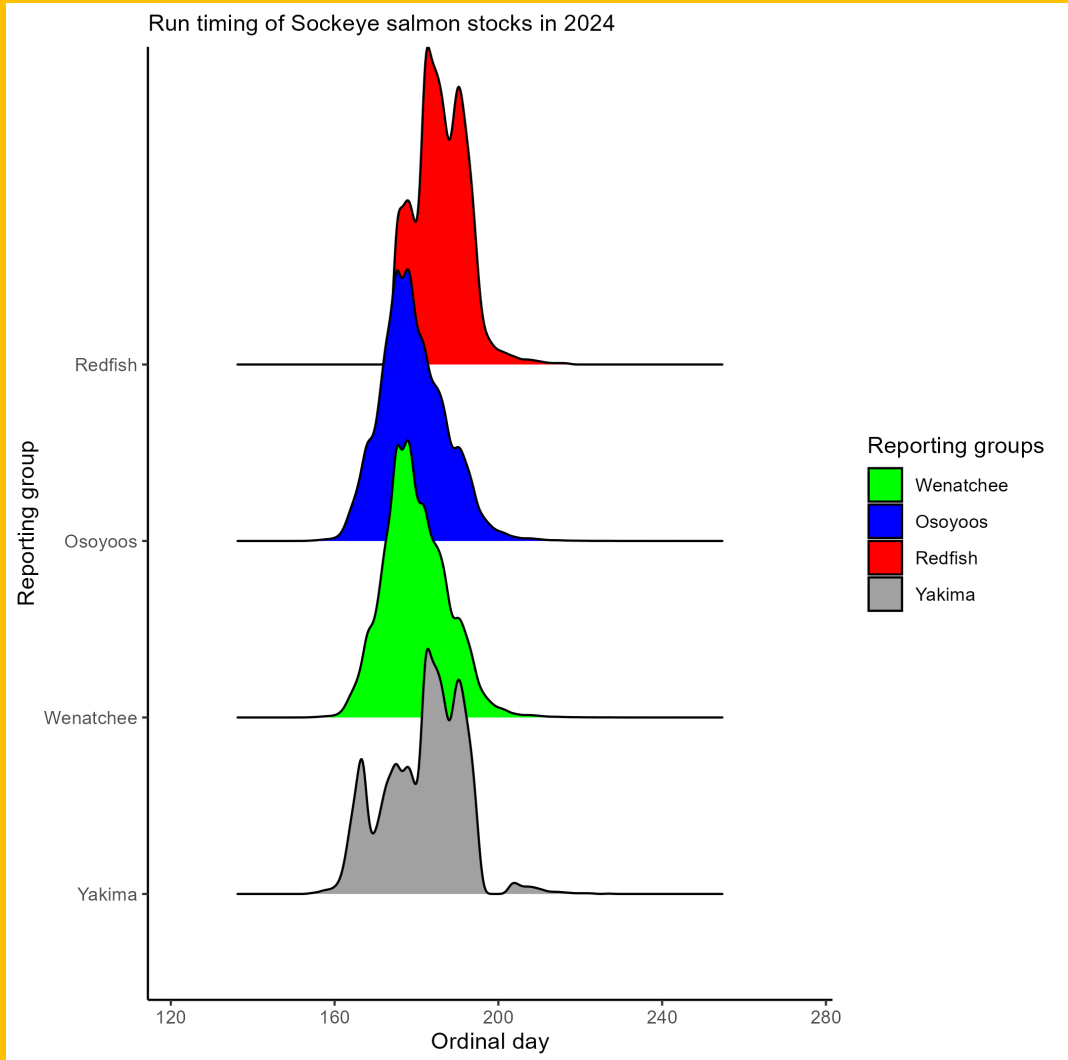


Example B — Sockeye at Bonneville (PBT + GSI)



What We Can Answer Now

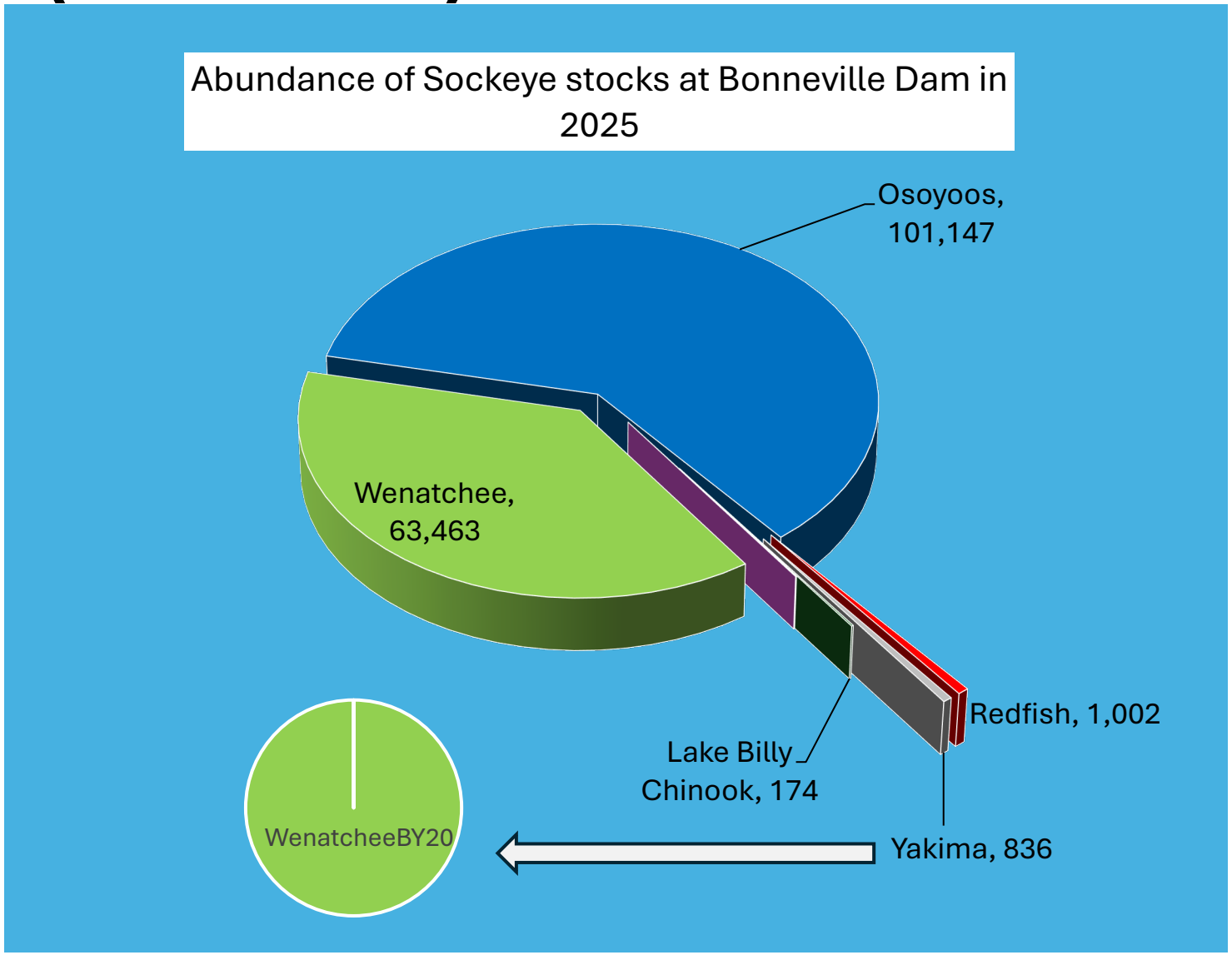
- Dual PBT and “single-parent” PBT methods can identify:
- Offspring of known hatchery releases
- Reintroduced Yakima stock (Yakama Nation) within a complex mixed-stock migration
- No other method can separate this reintroduction stock reliably at BON



Example B — Sockeye at Bonneville (PBT + GSI)

Management Outcomes

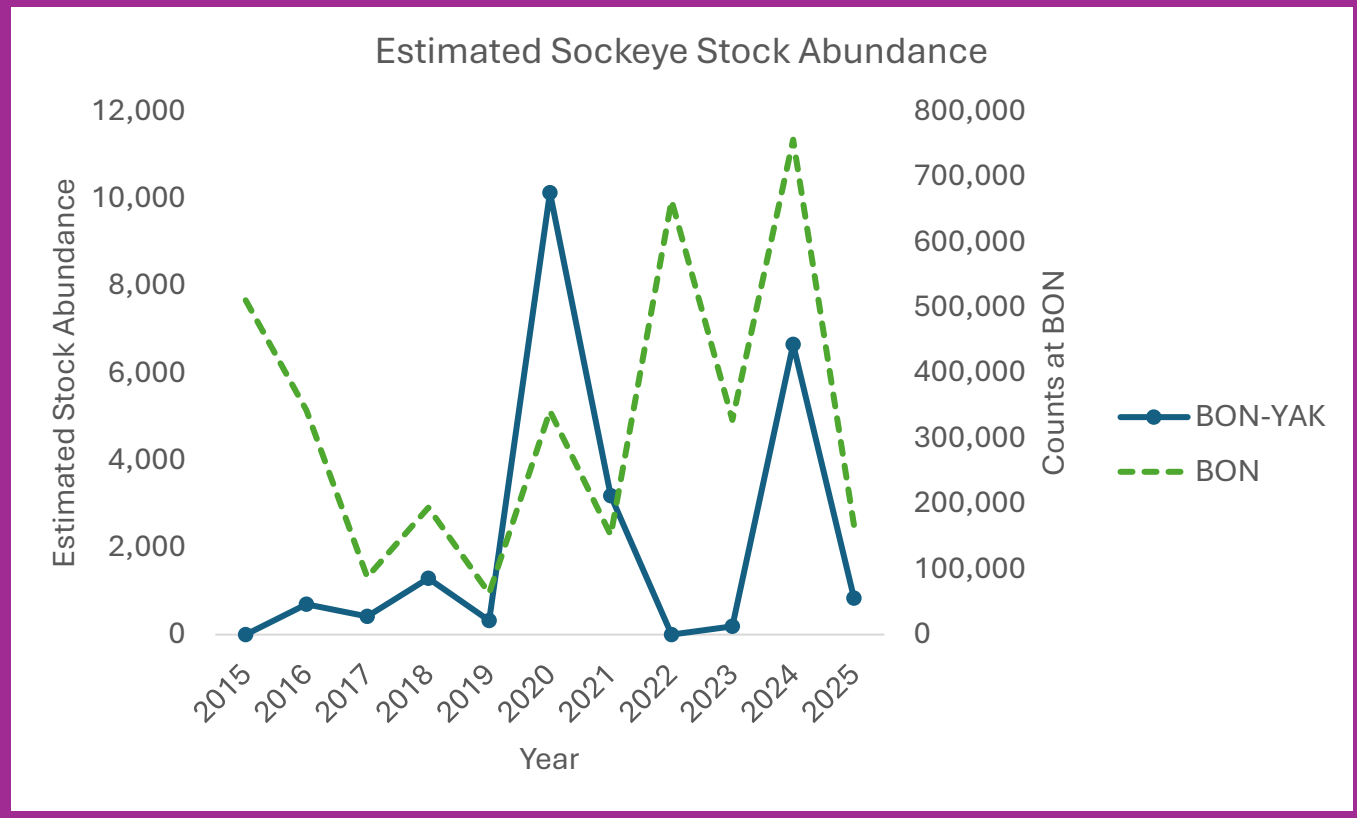
- Estimate mixed-stock sockeye components → Wenatchee, Okanogan, Redfish Lake, LBC, and reintroduction stocks (Yakima).
- Within stock components→ informs supplementation evaluations.
- Stock-specific abundance → harvest managers can evaluate ESA effects and forecast runs.



Example B — Sockeye at Bonneville (PBT + GSI)

Where This Can Go Next

- Abundance trends for each reintroduction component to measure long-term establishment success.
- Rapid identification of reintroduced stocks to aid transport.



CRITFC Mobile Genetics Lab



Example C — Pacific Lamprey (PBT + Sibship)



Why Lamprey Natal Origin Matters

- Cultural importance and ecological role.
- Translocation and artificial propagation are major restoration tools.
- Until recently, no way to track success of larvae or adults from these programs.

Translocation



Photo credit: Aaron Jackson



Photo credit: Conrad Gowell

Harvest



Artificial Propagation







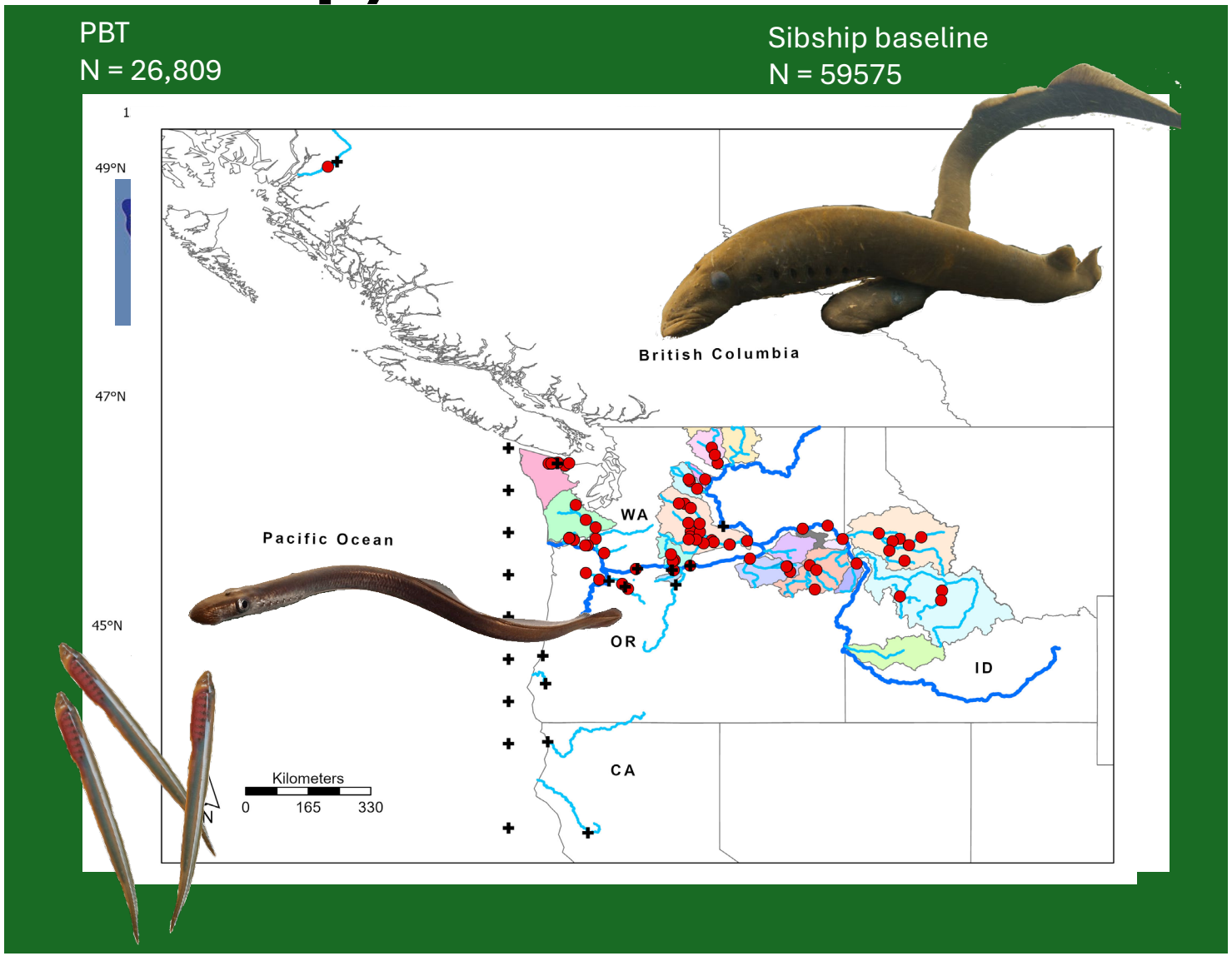
Ecosystem



Example C — Pacific Lamprey (PBT + Sibship)

What We Can Answer Now

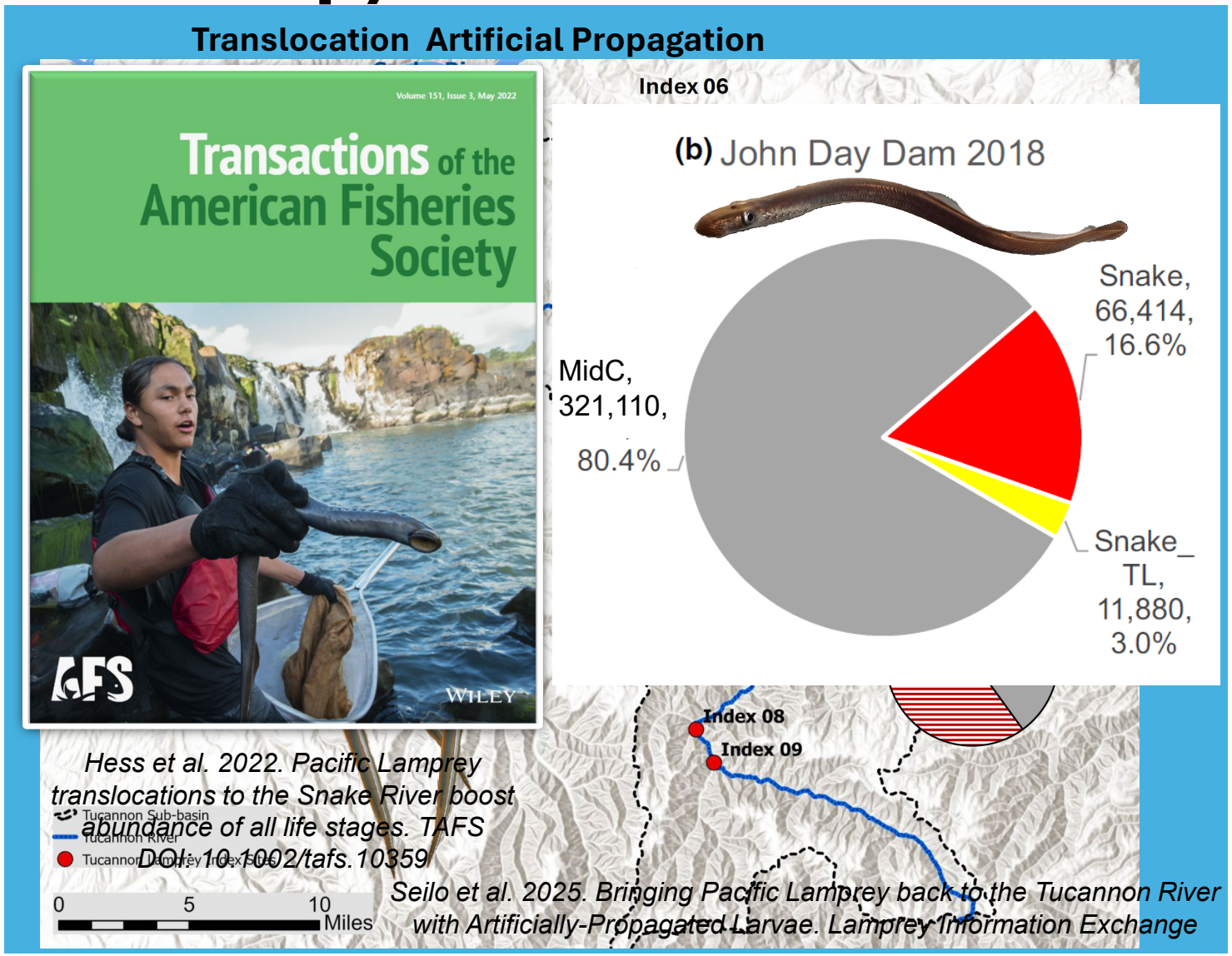
- PBT can assign offspring back to translocation release groups or assign hatchery-produced larvae back to parents.
- Sibship analyses identify family groups and survival of individual cohorts.
- Ability to track life stages through time and evaluate contributions to adult returns.



Example C — Pacific Lamprey (PBT + Sibship)

Management Outcomes

- Demonstrated that translocations increase larval and juvenile abundance in targeted tributaries.
- Showed that artificial propagation releases survive to age-4 and contribute to out-migration.
- These insights have supported funding and program expansion by demonstrating biological benefit across life stages.



Example C — Pacific Lamprey (PBT + Sibship)

Where This Can Go Next

- Identifying which restoration actions produce the strongest demographic responses.
- Evaluating the effectiveness of different treatment strategies

Direct-Release



Over-Winter







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The Return of the Adult Pacific Lamprey Offspring from Translocations to the Columbia River

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