Evaluating genetic introgression from hatchery-origin steelhead in the Snake River Basin using advanced grandparentage inference

2025 Pacific Coast Steelhead
Management Meeting
The Riverside Hotel
Thursday, December 11, 2025; 9:00 AM

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Primary Collaborators:
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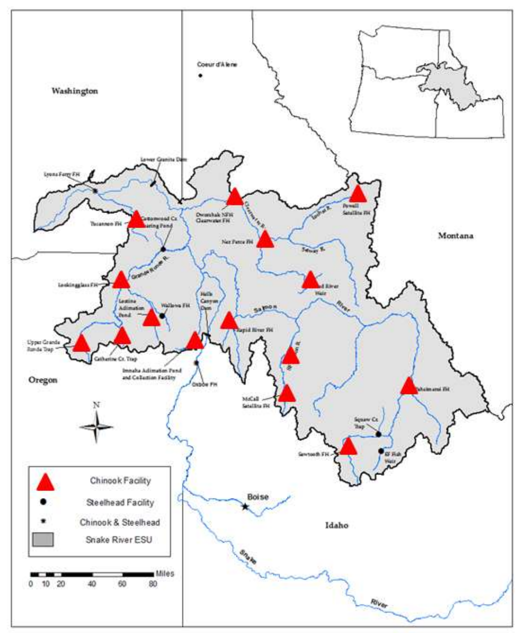
Shawn Narum; Rebekah Horn; Columbia River Inter-Tribal Fish Commission

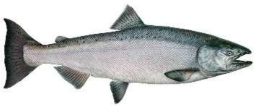
Funding:
Pacific Coast Salmon Recovery Fund

- # Parentage Based Tagging (PBT)

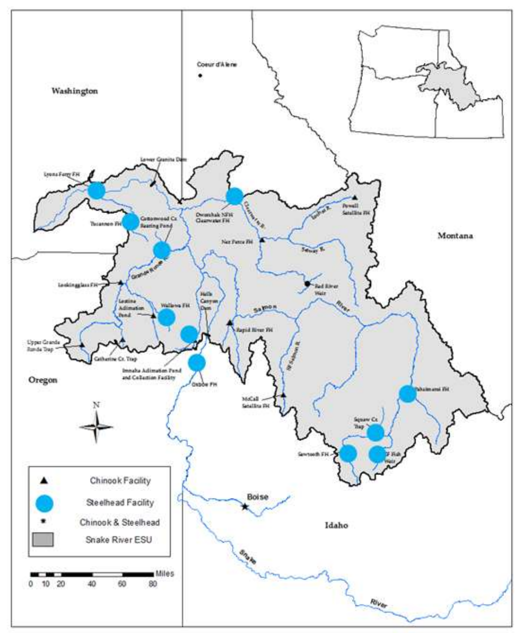
Snake River Chinook Salmon and steelhead

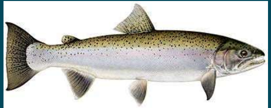
- All Spring/Summer Chinook salmon broodstock sampled since **2008** (~10,000 samples annually)
- All Fall Chinook salmon (Lyons Ferry/NPT) since **2011** (~5,000 samples annually)
- Most Snake River steelhead broodstock sampled in **2008**, all since 2009 (~5,000 samples annually)





Chinook salmon

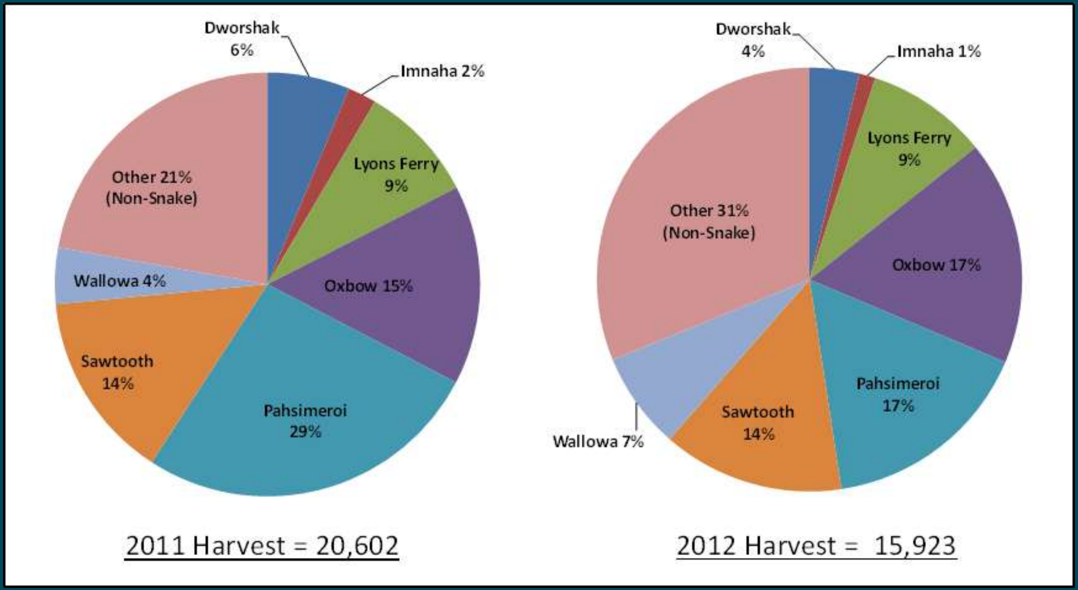




steelhead

• Benefits of PBT technology

- ➢ Better estimation of wild escapement at Lower Granite Dam (8.3% of “wild” adults are actually hatchery; Hargove et al 2021)
- ➢ Better estimation of hatchery escapement at Lower Granite Dam (SAR survival rates were 1.3–2x higher when calculated using PBT compared to PIT tags (Coykendall et al. 2022)
- ➢ Better estimation of out-of-state harvest
- ➢ Better estimation of in-state harvest
- ➢ CRITFC uses throughout the entire Columbia River Basin



A lot of Snake River steelhead are caught in down-river fisheries!!!!!

- # Benefits of PBT technology

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

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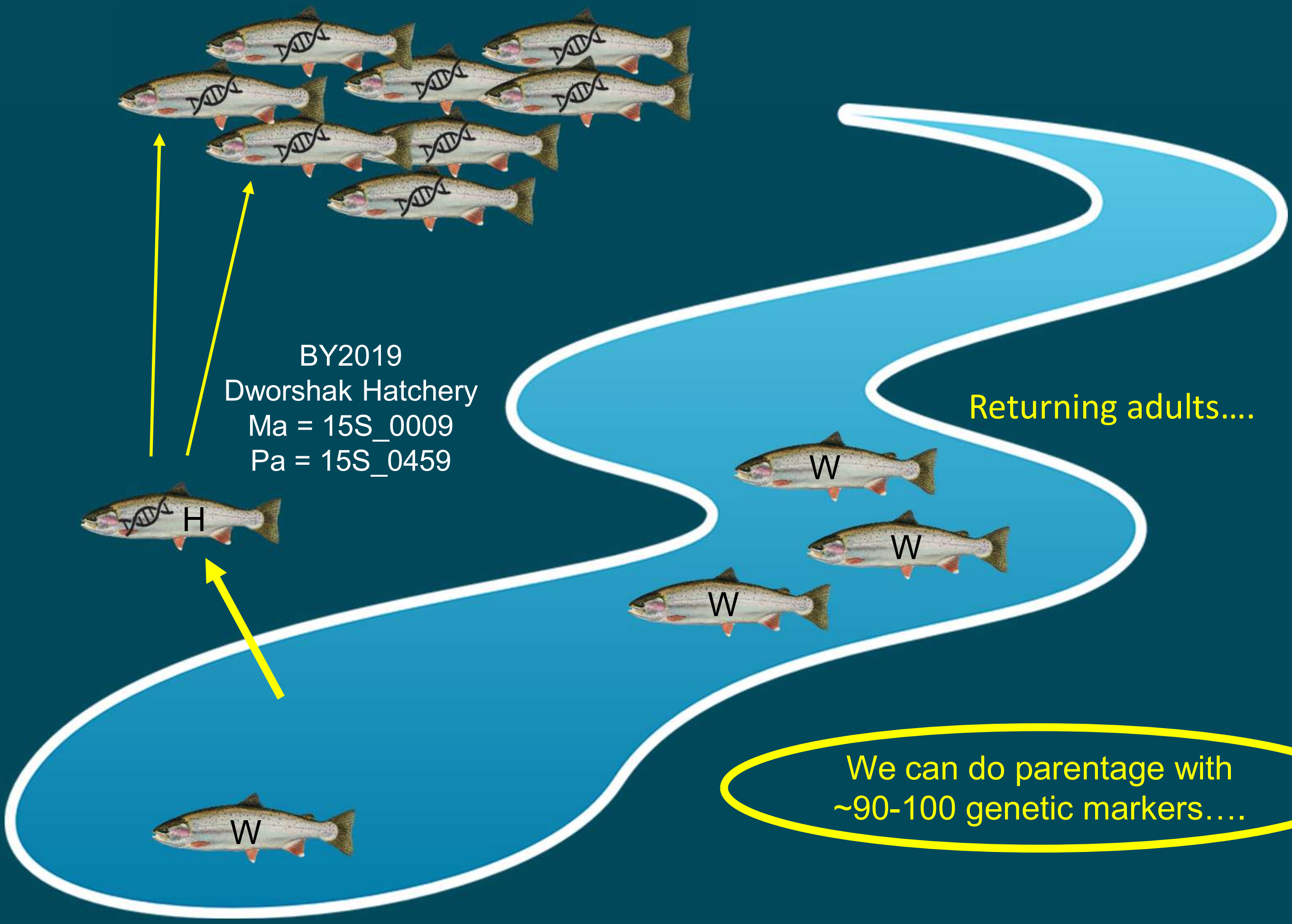
Hinrichsen et al (2016)-"*In the South Fork Salmon River application, there were 340% more PBT recoveries than CWT recoveries, leading to greater precision in release-specific values of p from maximum likelihood estimation.*"

How is this done????

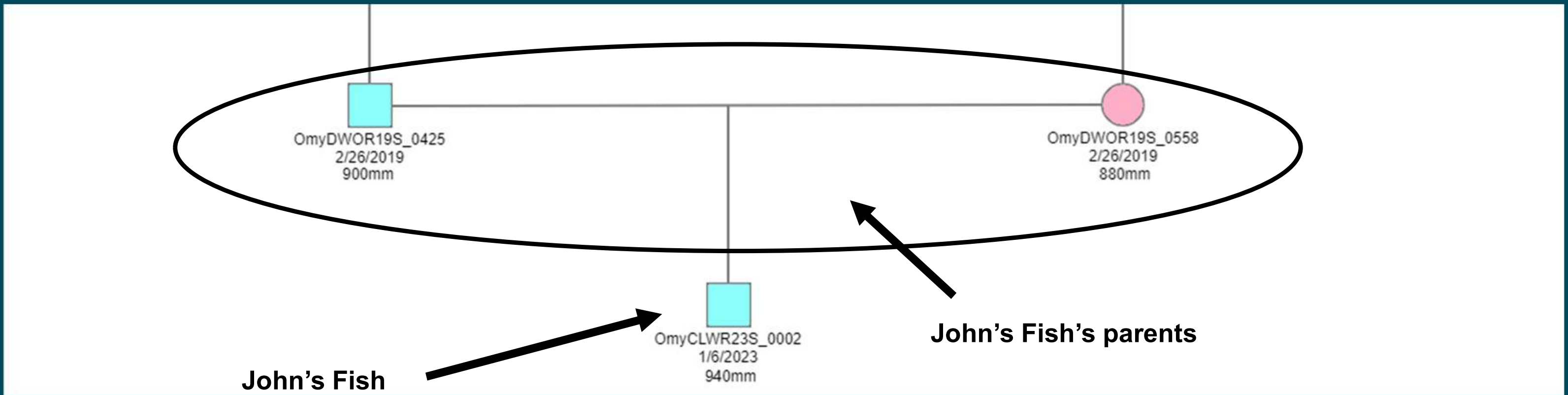


PBT Parent Baseline

BY2019
Dworshak Hatchery
Ma = 15S_0009
Pa = 15S_0459

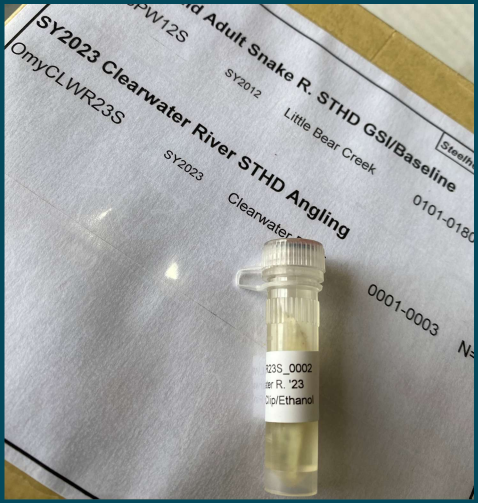
Returning adults….

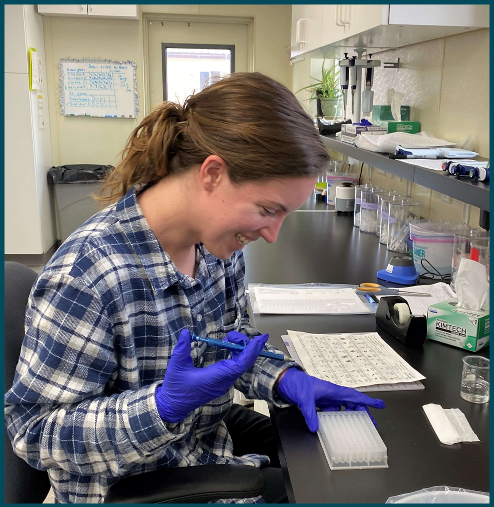
We can do parentage with
~90-100 genetic markers….



John's Fish's parents

John's Fish



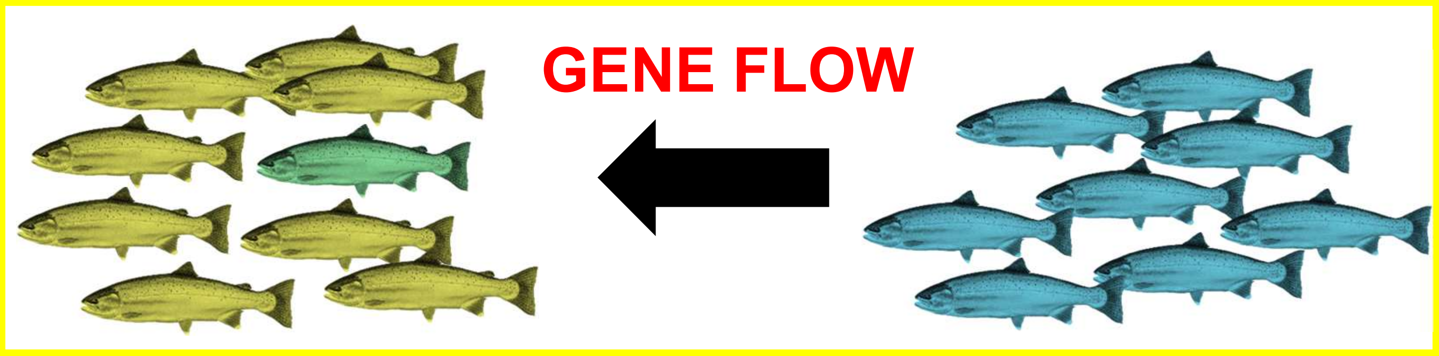


We can do parentage with
~90-100 genetic markers….

- **NOAA wants this information**

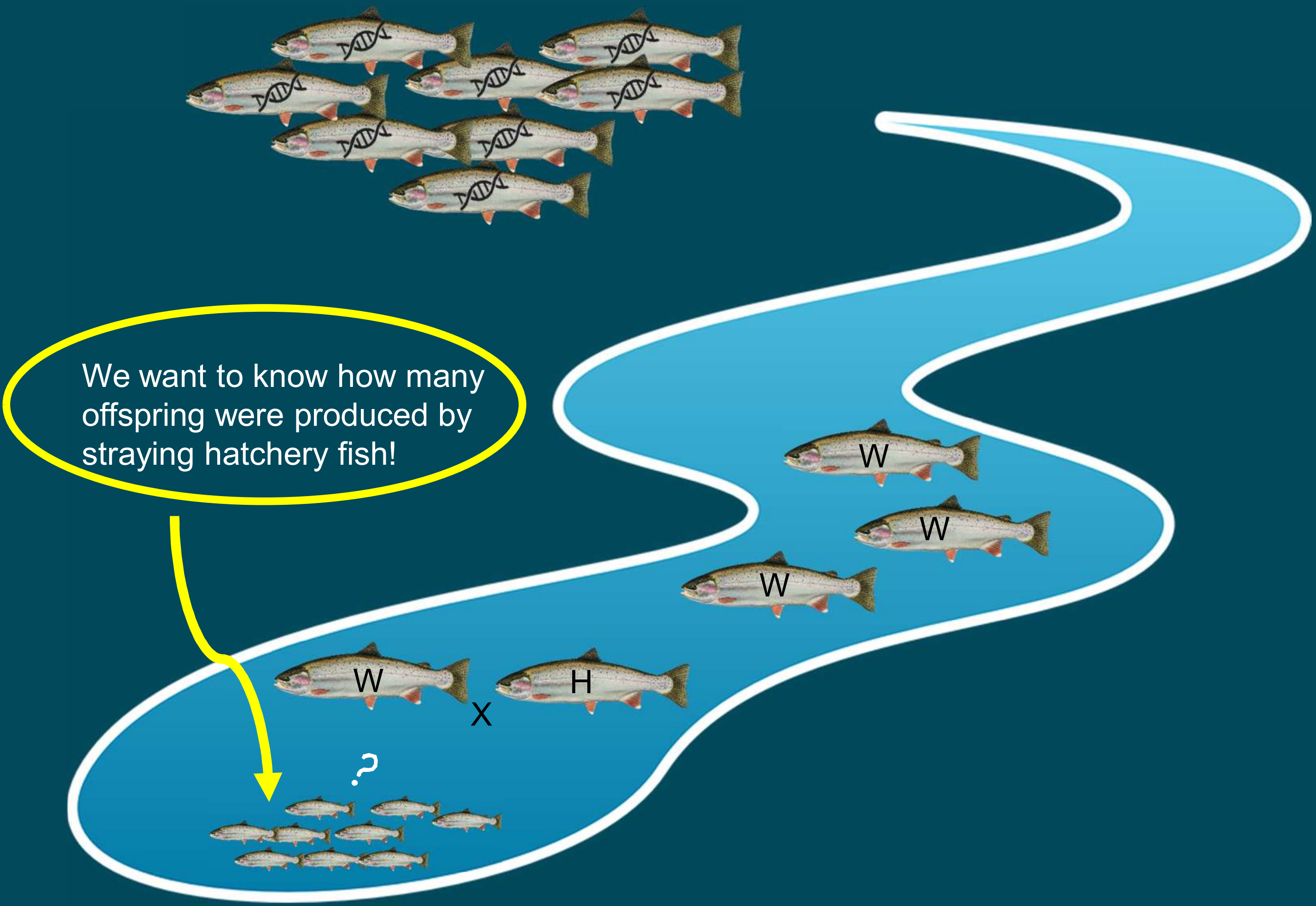
- ➢ Status assessments for ESA-listed salmonid populations in the Snake River and Columbia River basins, require reliable estimates of the proportion of hatchery-origin spawners on the spawning grounds, or pHOS (McClure et al. 2003)

- ➢ pHOS is an important measure, but another thing that geneticists and managers would like to monitor:



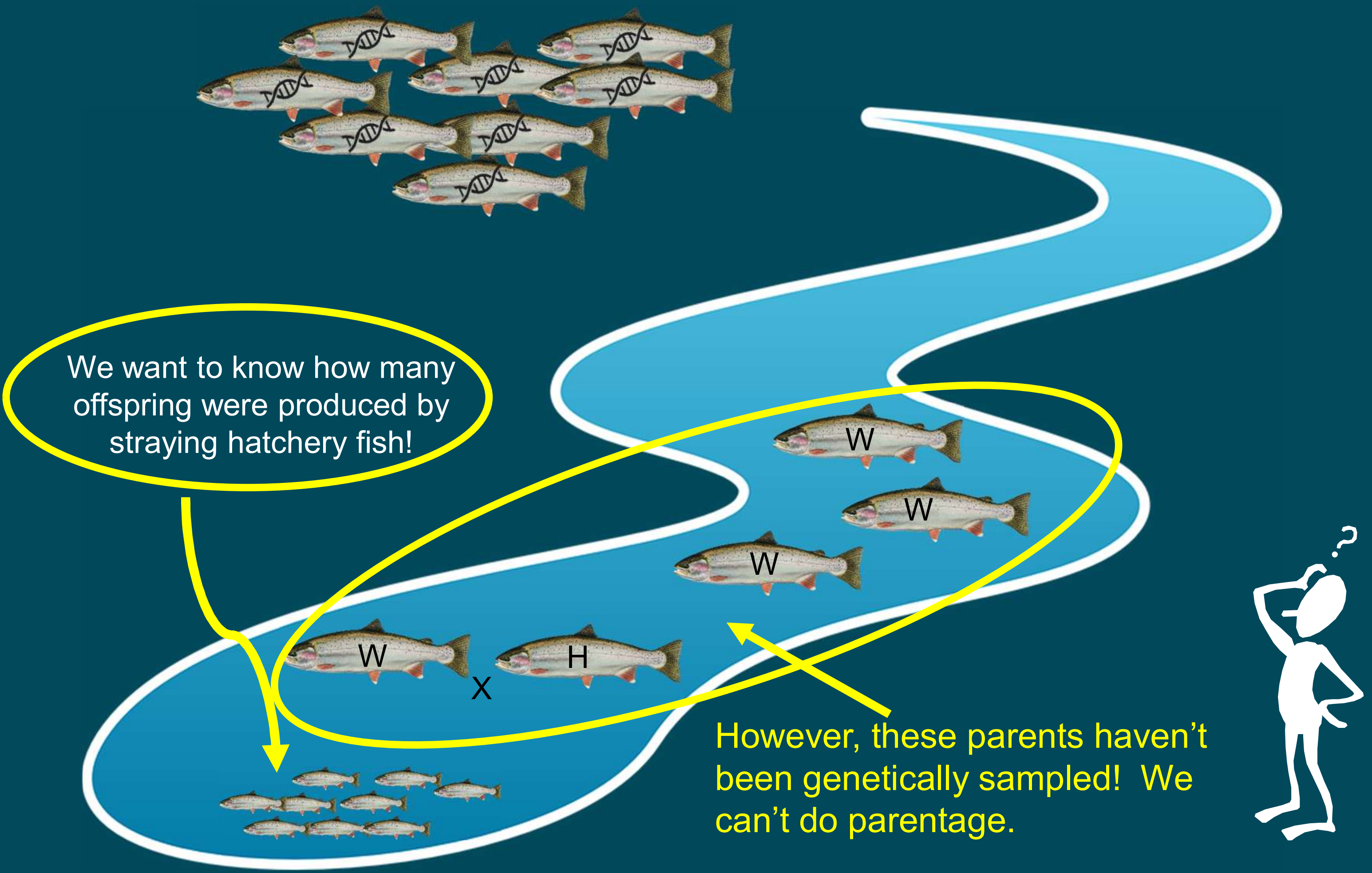
➢Gene flow only occurs if hatchery fish successfully mate with wild fish and produce offspring!

PBT Parent Baseline



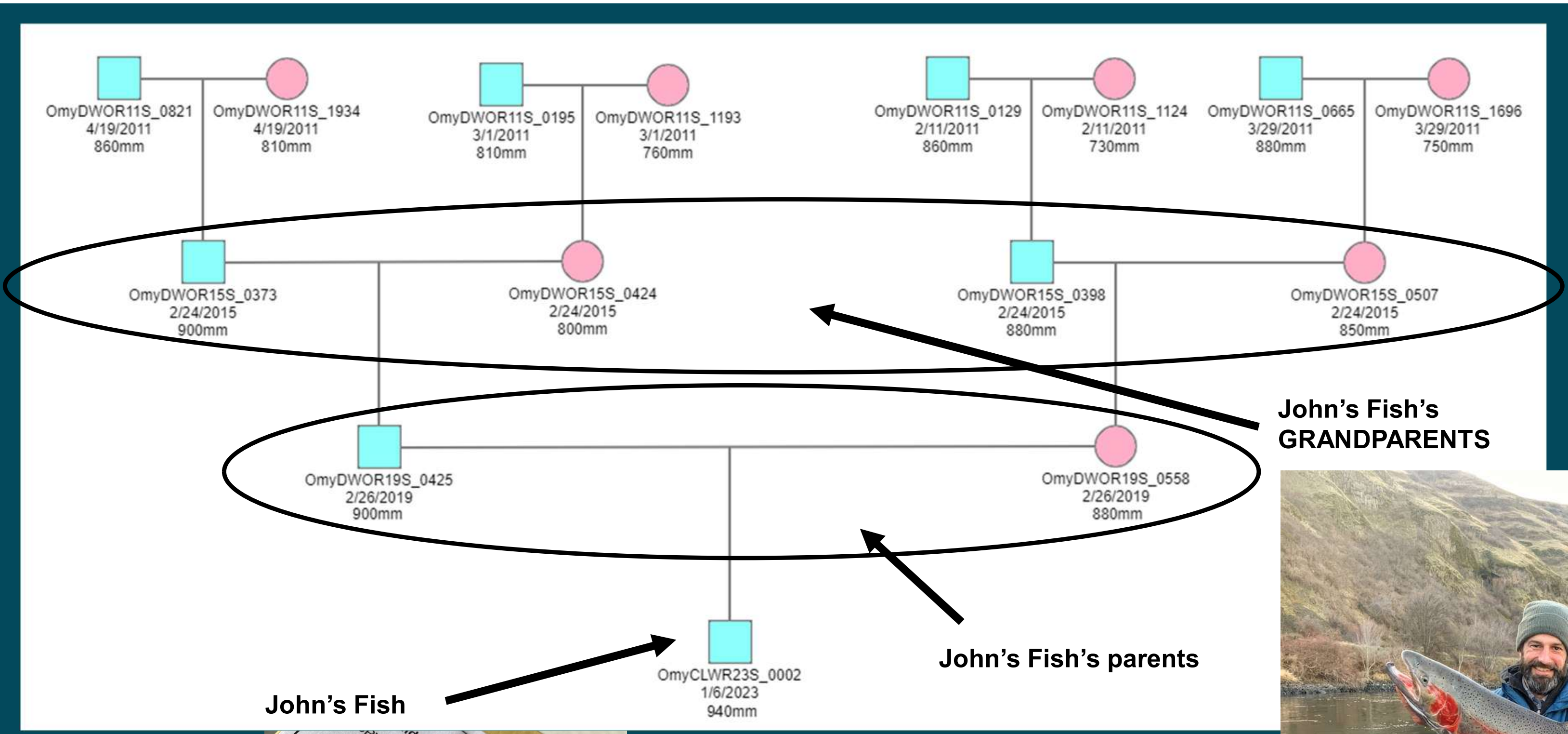
We want to know how many offspring were produced by straying hatchery fish!

PBT Parent Baseline



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

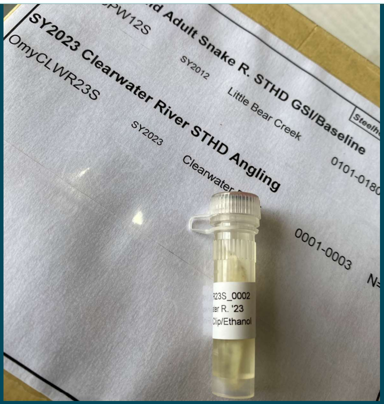
However, these parents haven't been genetically sampled! We can't do parentage.

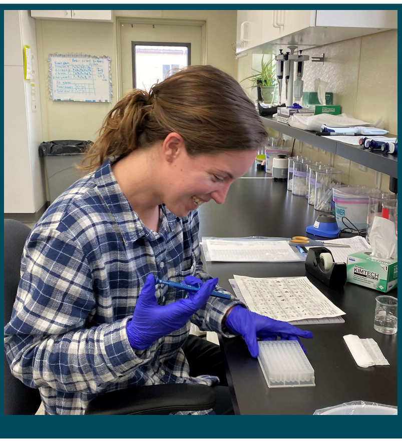


John's Fish's GRANDPARENTS

John's Fish's parents

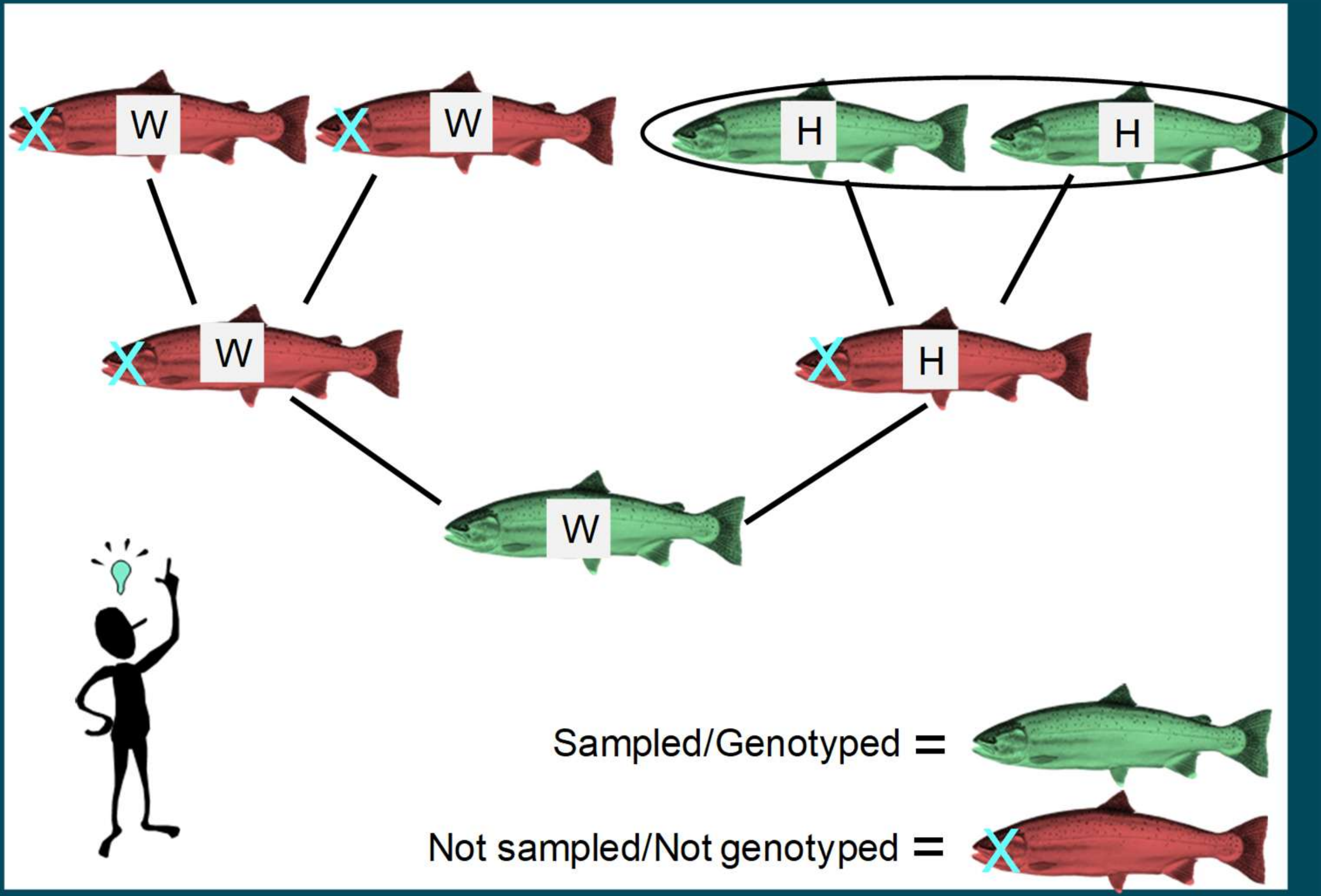
John's Fish





Grandparentage Testing

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



- **History**

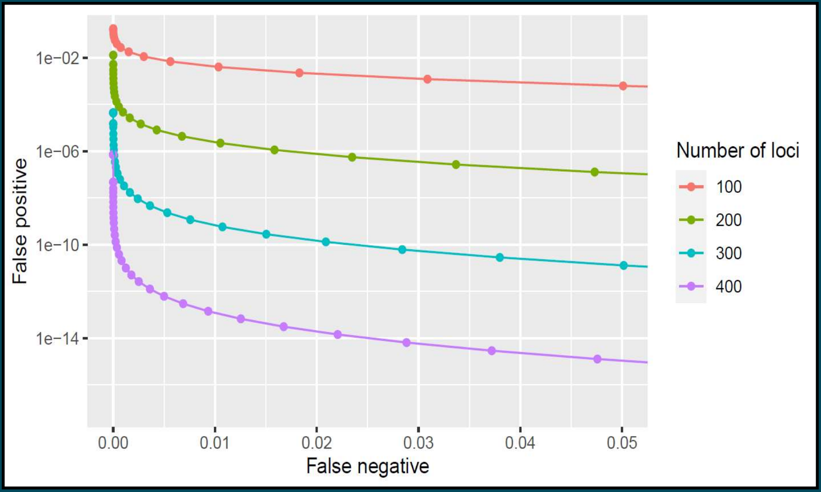
✓ We developed statistical methods for assigning grandparents and estimating error rates for a genetic panel

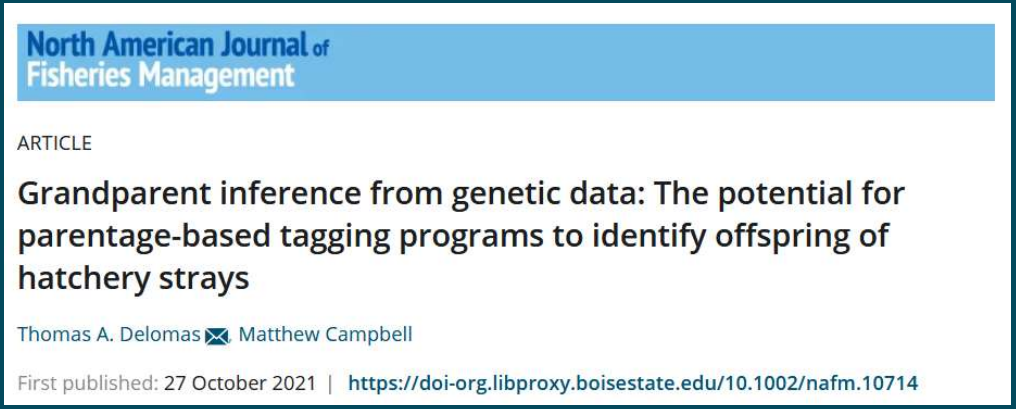
✓ We have implemented these methods in a package for R statistical software at https://github.com/delomast/gRandma

✓ 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

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

- **Next Steps?**

✓ We proposed an empirical proof-of-concept study to validate and demonstrate this new technology in Snake River steelhead (Funded by PCSRF in 2021: 01121SC)

Develop new genetic marker panel

- Identify and test an additional 200-300 markers to add to original 96 markers used to start PBT in the Snake River Basin

DONE (287 new microhaplotypes + 95 SNPs)

Genotype Broodstock & known grandchildren

- All Snake River Basin Hatchery Steelhead Broodstock (spawn years 2012 and 2013; N = 12,242)
- Known grandchildren (identified with PBT) of the 2012 and 2013 hatchery broodstock (spawn year 2019; N = 500)

DONE

Error Testing

- Using samples with known relationships (known unrelated and known grandparent-grandchild trios), we will empirically validate the estimated false positive and false negative rates.

DONE

Genotype wild adults that returned/sampled at LGR Dam (2019 – 2022)

- BY2016; known 3-year olds that returned in 2019 (based on scale ages); N = ~2,000
- Estimate the proportion of natural-origin returning adult steelhead in the 2016 year-class with one or two hatchery-origin pairs

Estimating grandparentage error rates

- Using known grandparentage assignments from multi-generational pedigrees, we can estimate false positive and false negative rates

		Assignment outcome	
		Identified as grandparents	**Not identified as grandparents**
Known relationship	True grandparents (P)	True positive (TP)	False negative (FN) - **Type II error**
	Unrelated grandparents (N)	False positive (FP) - **Type I error**	True negative (TN)

Estimating grandparentage error rates (known pedigrees):

	Assignment outcome	
Known relationship	**Identified as grandparents**	**Not identified as grandparents**
True grandparents (P) **P = 1,198**	True positive (TP)	False negative (FN) - Type II error **FN = 80**
Unrelated grandparent trios (N) **N = 20,107,644**	False positive (FP) - Type I error **FP = 2**	True negative (TN)

$$false\ positive\ rate\ (FPR) = \frac{FP}{N} = \frac{2}{20{,}107644} = 9.95 \times 10^{-8}$$

Driven by the number of **unrelated** grandparent trios considered

Interpretation – for every unrelated comparison we make, there is a 9.95×10^{-8} probability of accepting an incorrect assignment

Estimating grandparentage error rates (known pedigrees):

		Assignment outcome	
Known relationship		**Identified as grandparents**	**Not identified as grandparents**
	True grandparents (P) **P = 1,198**	True positive (TP)	False negative (FN) - Type II error **FN = 80**
	Unrelated grandparents (N) **N = 20,107,644**	False positive (FP) - Type I error **FP = 2**	True negative (TN)

$$false\ negative\ rate\ (FNR) = \frac{FN}{P} = \frac{80}{1198} = 0.067$$

Driven by the number of **true** grandparent trios considered

Interpretation – for every true comparison we make, there is a 0.067 probability of rejecting a correct assignment

Importance of hatchery metadata

- Data collected at hatcheries during spawning can greatly decrease the number of comparisons made during grandparentage analyses by reducing the number of crosses considered
- For the SY2012 steelhead broodstock at Oxbow hatchery, with 477 broodstock and 700 potential grandchildren:

$$\#\ comparisons = \#\ grandparent\ crosses \times \#\ grandchildren$$

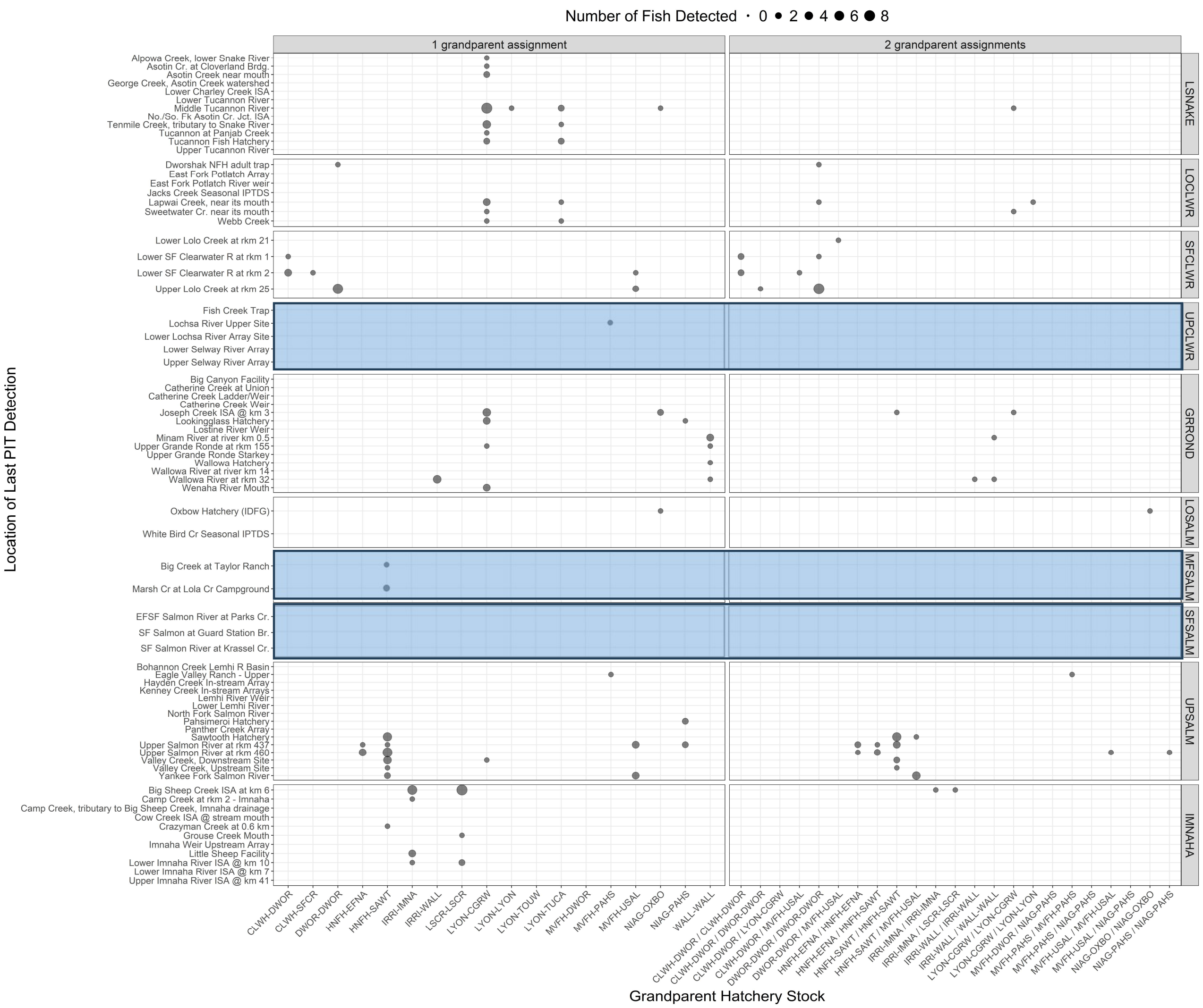
Metadata	# Crosses	# Grandchildren	# Comparisons	# False positives
None	113,526	700	79,486,200	7.94
Phenotypic sex	56,376	700	39,463,200	3.93
Phenotypic sex + spawn date	5,268	700	3,687,600	0.37
Cross records	246	700	172,200	0.02

- # Grandparentage Results (adults):

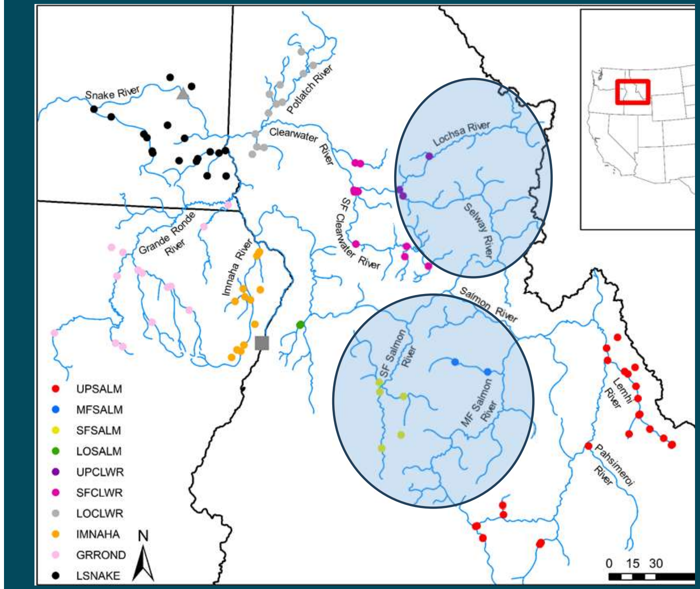
Potential Grandchildren	N =2,009 samples, SY2020-2021 putatively wild fish from Lower Granite ✓ No PBT assignments (i.e. NOT a hatchery no-clip) ✓ BY2016 scale ages
Potential Grandparents	N =10,213 samples, SY2012-2013 broodstock
Assignments	N = 374 **(18.6%)** individuals assigned to grandparents in the SY2012-2013 broodstocks ✓ 81.4% (1635) of individuals assigned to zero sets of hatchery grandparents ✓ 14.3% (288) of individuals assigned to one set of hatchery grandparents ✓ 4.3% (86) of individuals assigned to two sets of hatchery grandparents

- **Grandparentage Results (adults):**

- ✓ **All hatcheries were identified as having some individuals that strayed and spawned successfully**
- ✓ **Using PIT detections of grandchildren indicated that most returned to areas managed for hatchery fish: Upper Salmon, S.F. Clearwater, Grande Ronde (Cottonwood)**
- ✓ **Few grandchildren were identified in areas managed for wild fish (Upper Clearwater, MFSR, SFSR)**



PIT array detected adults:



Natural spawning areas in colored circles

- # Grandparentage Results (juveniles):

Pedigree Name	Location	Group	Life-Stage	N
OmyBGCS18C	Wild Management Area	Big Creek	Juveniles	400
OmyFILW18C	Wild Management Area	Fish Creek	Juveniles	721
OmyHAYW18C	Wild Management Area	Hayden Creek	Juveniles	144
OmyMRST18C	Wild Management Area	Marsh Creek	Juveniles	75
OmyNFSW18C	Hatchery Management Area	N.F. Salmon	Juveniles	198
OmyPAHS18C	Wild Management Area	Pahsimeroi	Juveniles	161
OmyRRHW18C	Wild Management Area	Rapid River	Juveniles	387
OmySAWW18C	Hatchery Management Area	Sawtooth	Juveniles	146

- # Grandparentage Results (juveniles):

Potential Grandchildren	N =2,123 samples, CY2018 wild fish from screw traps throughout the Snake River Basin
Potential Grandparents	N =10,213 samples, SY2012-2013 broodstock
Assignments	N = 131 **(6.2%)** individuals assigned to grandparents in the SY2012-2013 broodstocks ✓ 93.8% (1,992) of individuals assigned to zero sets of hatchery grandparents ✓ 5.0% (106) of individuals assigned to one set of hatchery grandparents ✓ 1.2% (25) of individuals assigned to two sets of hatchery grandparents

Grandparentage Results (juveniles):

- ✓ All grandparent assignments were to Dworshak, Pahsimeroi, and Sawtooth Hatcheries.
- ✓ Most sites managed for wild fish (Big Creek, Fish Creek, Rapid River) exhibited low or no assignments of juveniles to Grandparents in our sample set.
- ✓ Exception: Marsh Creek (16.7% of juveniles receiving at least 1 grandparentage assignment).

Marsh Creek sits at the headwaters of the Middle Fork Salmon River (Wilderness Area) and is managed for wild fish.

While no hatchery juveniles are released in Marsh Creek (or the MFSR) small numbers of straying hatchery fish (Sawtooth Fish Hatchery) have been detected at a PIT-array weir at Marsh Creek.

• Challenges?

- Current technology would require us to run 2 genetic marker panels rather than one. More time and $.

- Large numbers of broodstock would need to be re-genotyped to allow this technology to be used starting in SY2026. More time and $.

- Collection of accurate hatchery metadata is needed!
  - ✓ Without hatchery data, all possible pairs of potential grandparents must be considered for every sampled offspring, resulting in an extremely large number of trio comparisons.
  - ✓ Each comparison carries a small probability of a false-positive error. As the number of comparisons increases, the cumulative likelihood of false positives also increases. Hatchery data (e.g., spawning records, sex, and timing) reduces the total number of plausible pairs by excluding combinations that are biologically or temporally impossible.
  - ✓ This is available in the Snake River Basin. Cross-record information may not currently be collected at hatcheries outside the basin.

Questions???