

# Genetics 101 for Managers – An Introduction to GSI and PBT Technologies in Fisheries

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# Genetics in Fisheries Management

Long history of using genetic tools to study salmonids

- Determine distinct population segments and ESUs
- Evaluate hatchery impacts on wild stocks
- Determine genes underlying specific traits
- Stock Assessment
  - ✓ **Genetic stock identification (GSI)**
  - ✓ **Parentage based tagging (PBT)**

# GSI has been in use for several decades

GSI studies began in the 1970's

Many on-going projects using GSI:

- Ocean fisheries (project CROOS, Oregon State University)
- Juvenile survival in the estuary and ocean (NOAA)
- In-river harvest and dam passage (IDFG, CRITFC)

# Genetic Stock Identification

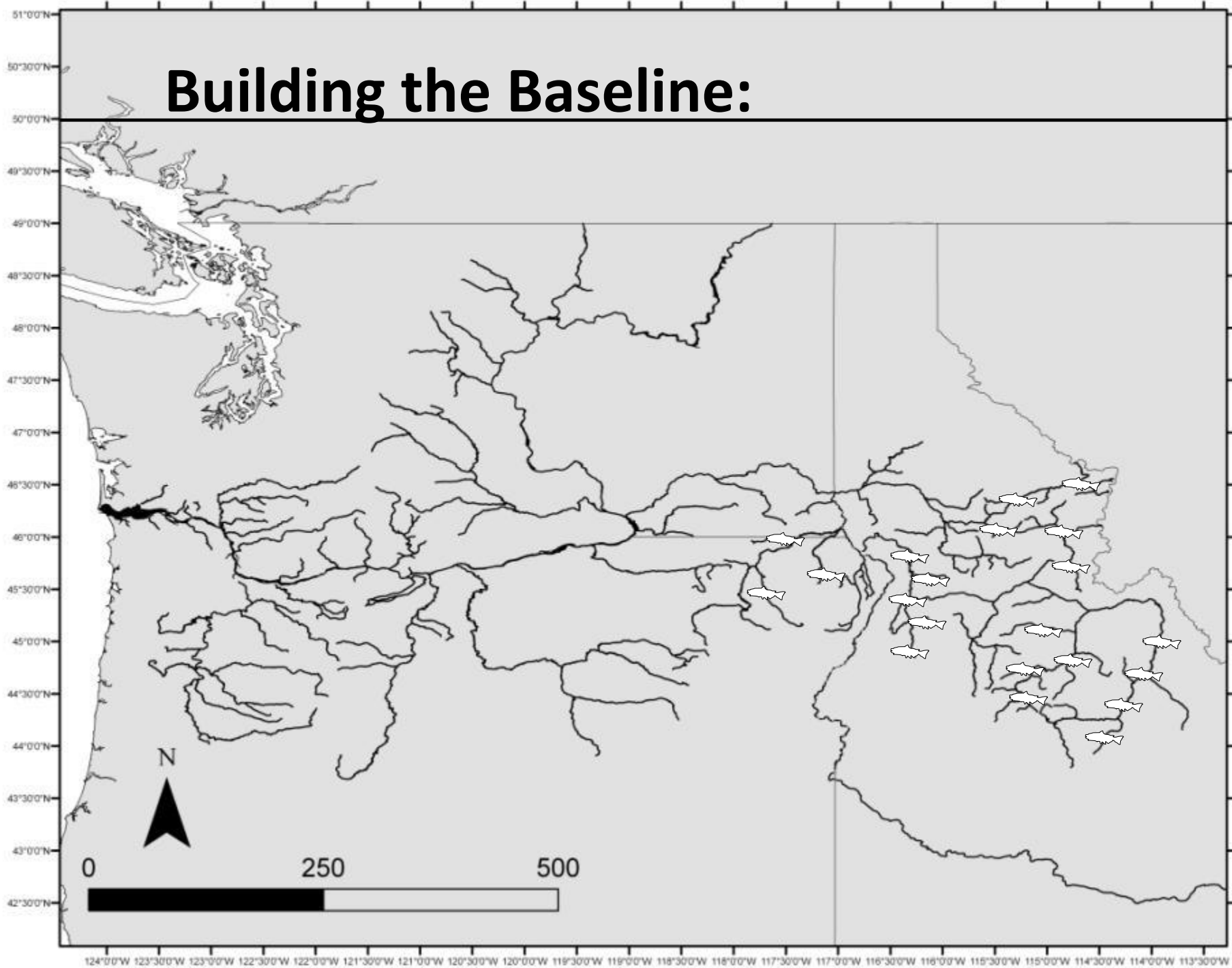
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GSI is a two-step process:

- 1. Generate baseline**

- Characterize genetic profile of the contributing stocks (i.e. wild steelhead populations)

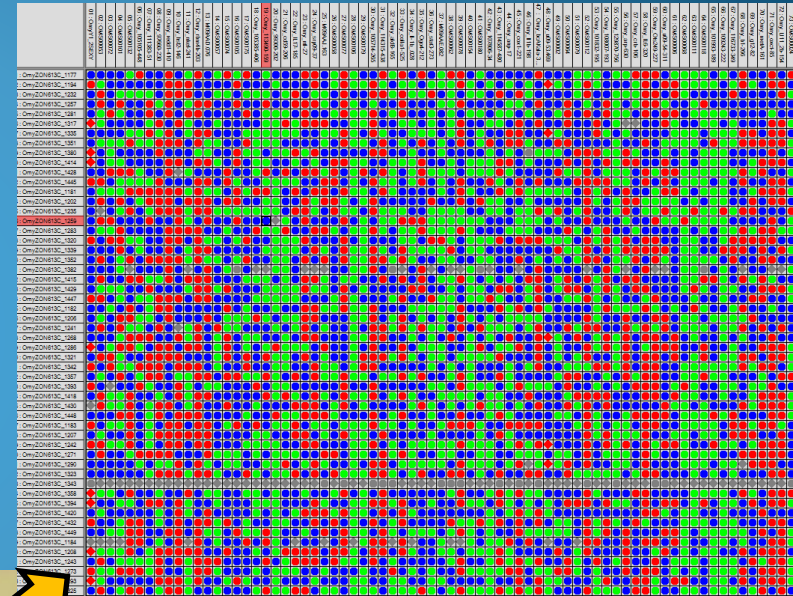
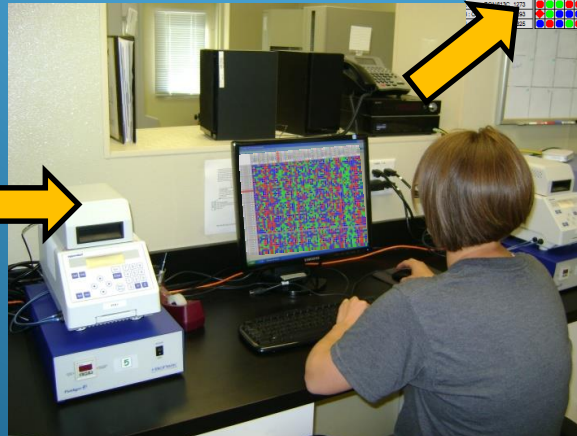
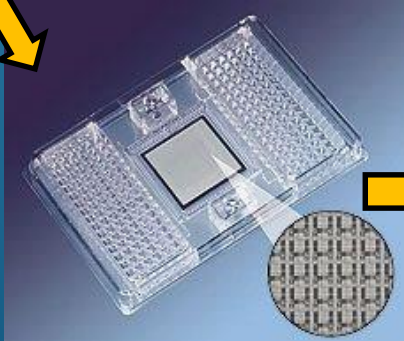
# Building the Baseline:



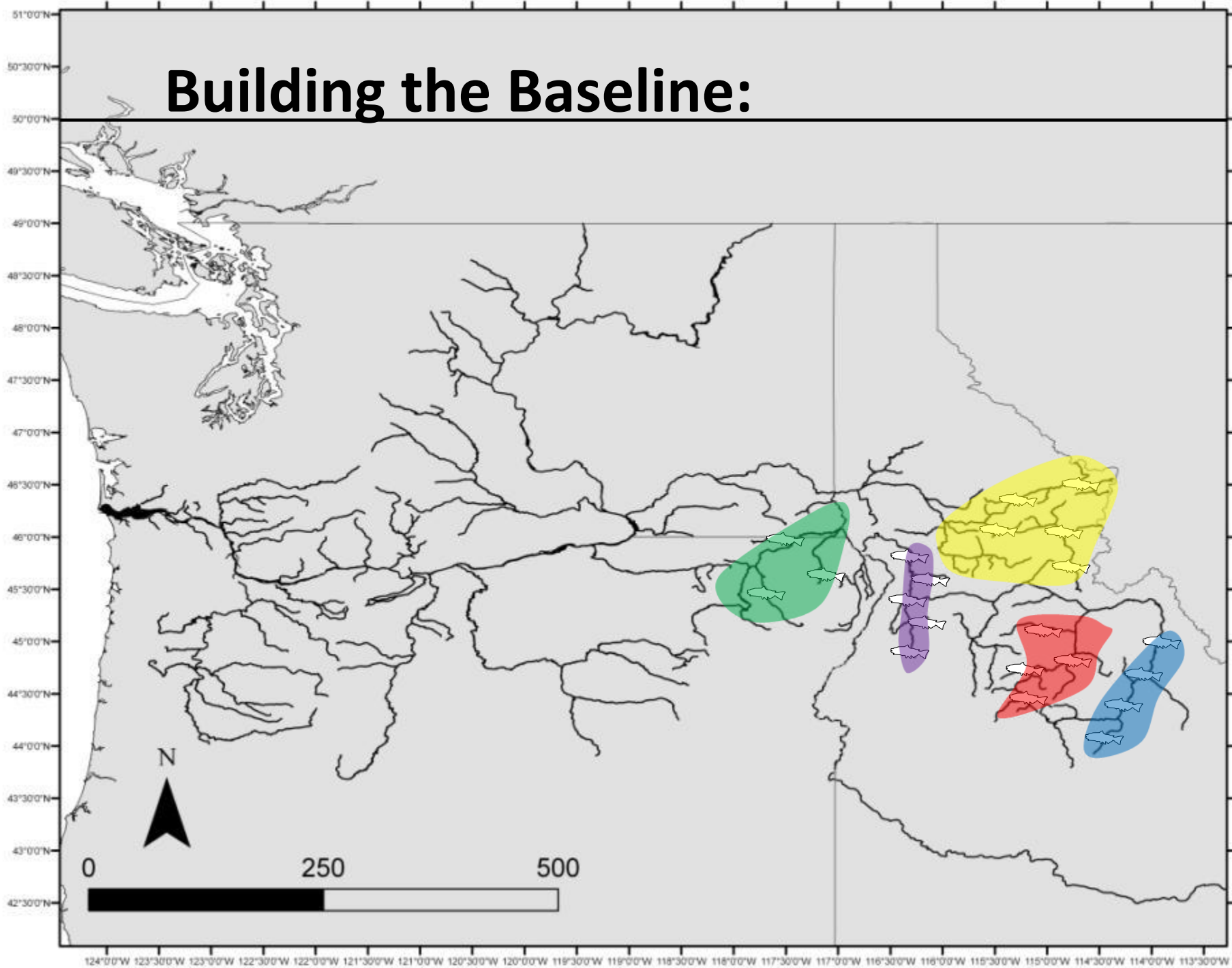
# Building the Baseline:

Samples genotyped at 192 genetic markers

- Single Nucleotide Polymorphisms (SNPs)



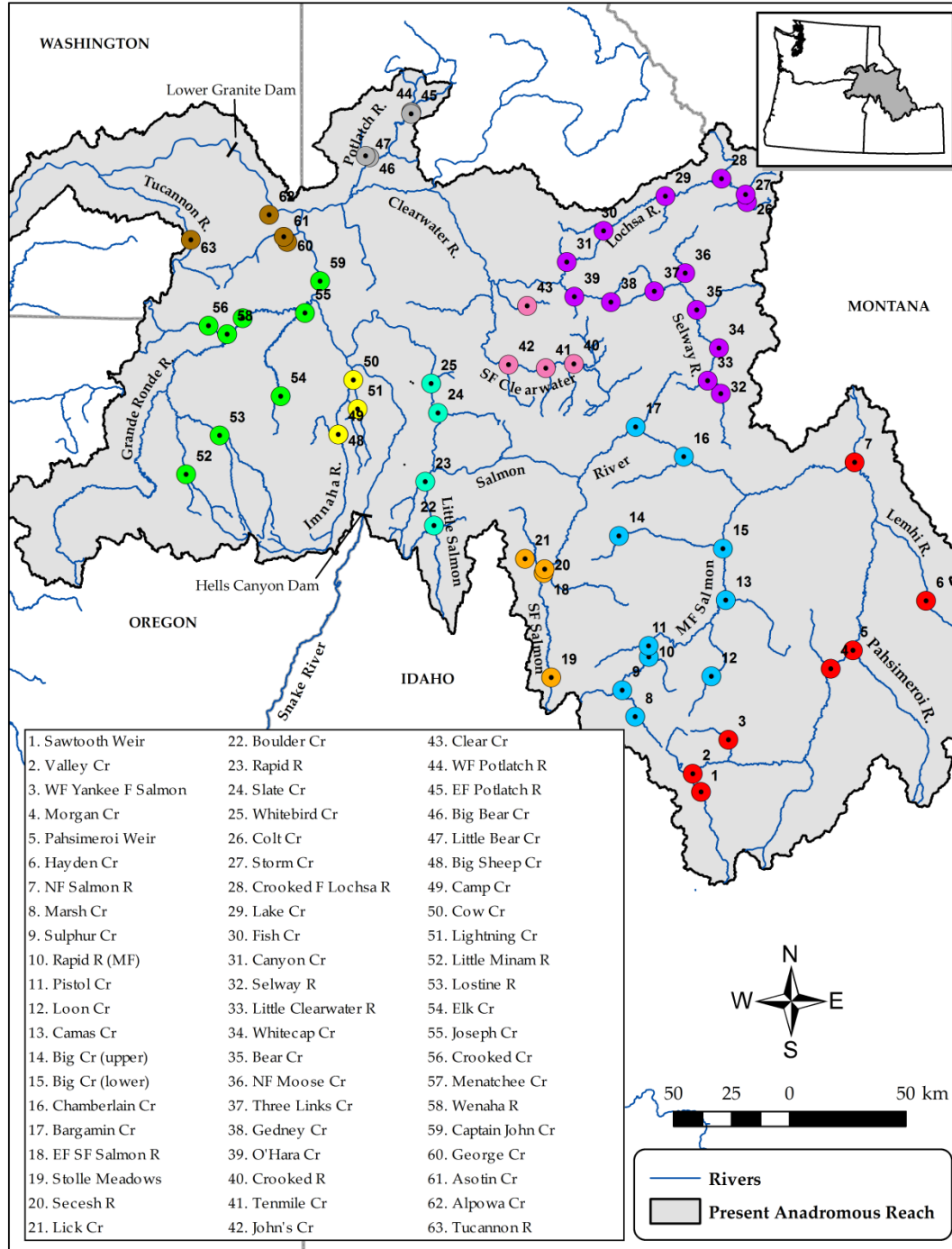
# Building the Baseline:



# Steelhead Baseline v2.0

- 4,145 samples
- 63 locations
- 10 genetic stocks

- UPSALM
- MFSALM
- SFSALM
- LOSALM
- UPCLWR
- SFCLWR
- PTLTCH
- IMNAHA
- GRROND
- LSNAKE



From Ackerman et al. 2013



# Genetic Stock Identification:

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GSI is two-step process:

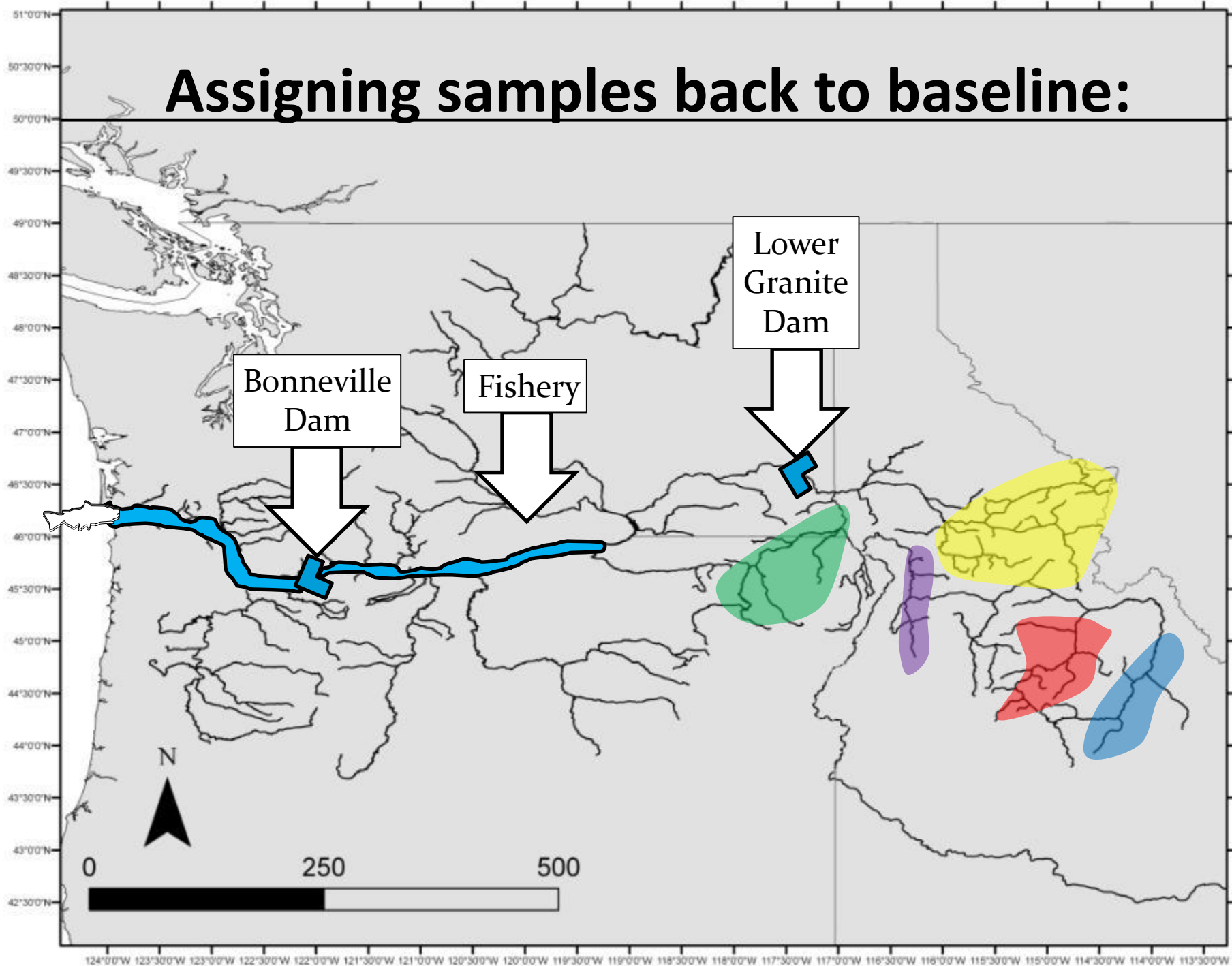
**1. Generate baseline**

- Characterize genetic profile of the contributing stocks (i.e. wild steelhead populations)

**2. Estimate composition of mixture**

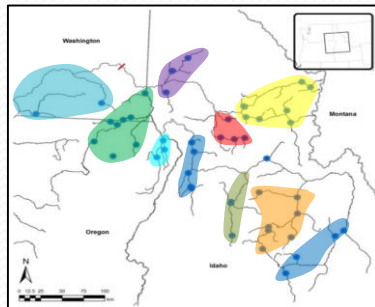
- Obtain genotype data from mixture samples to estimate contribution (e.g. fishery, juveniles, or escapement samples)

# Assigning samples back to baseline:



# Projects using GSI baselines

- **Adult Stock Composition:**
  - Columbia River Fisheries (Alan Byrne, IDFG)
  - Escapement at Bonneville Dam (Jon Hess, CRITFC)
  - Escapement at Lower Granite Dam (Bill Schrader, IDFG)
- **Juvenile Stock Composition at:**
  - Lower Granite Dam (Bill Schrader, IDFG)
  - Bonneville Dam (Jon Hess, CRITFC)

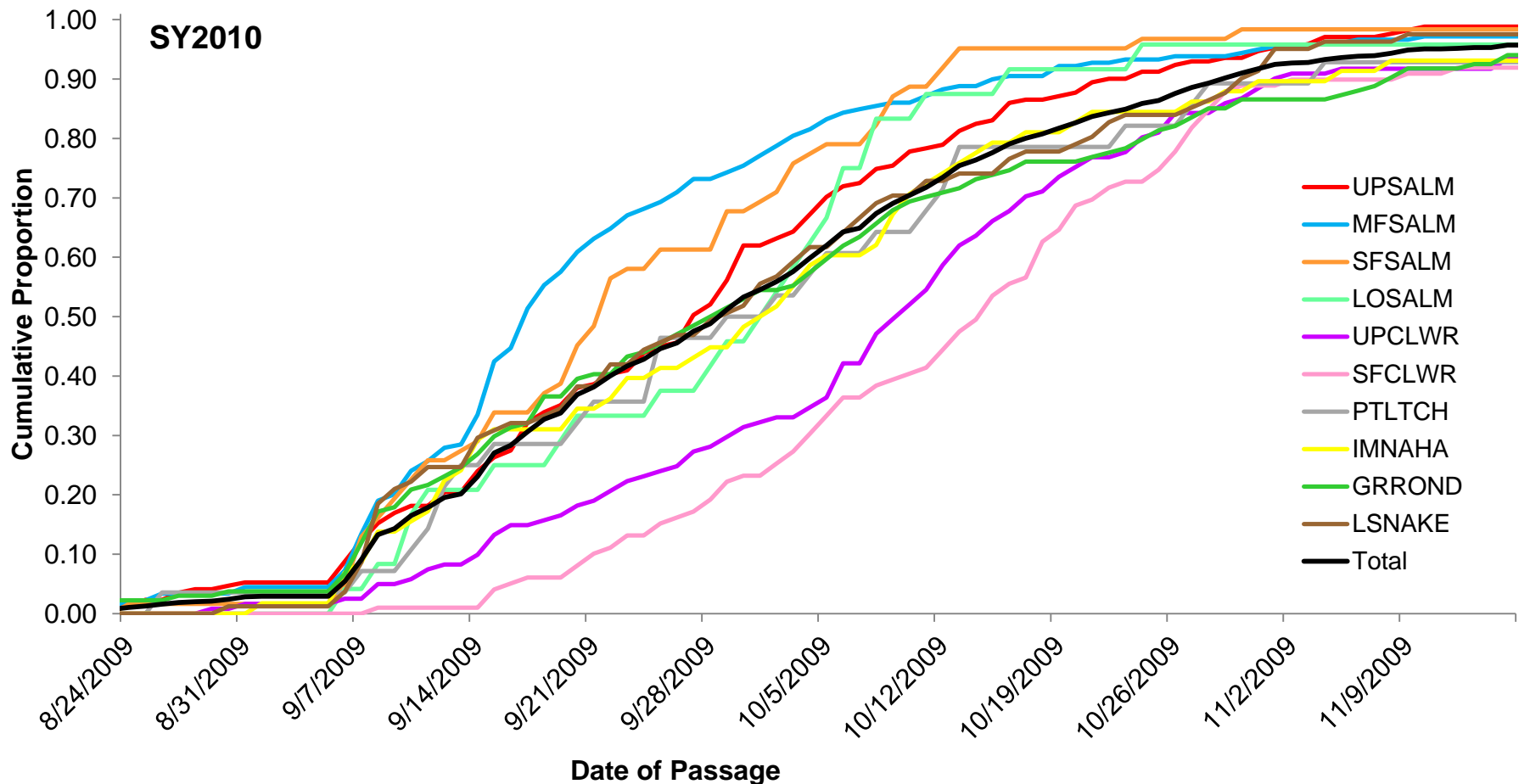


# Run-Timing of Different Genetic Stocks

- Median fall passage dates

Mid. Frk. Salmon and S.F. Salmon: mid-September

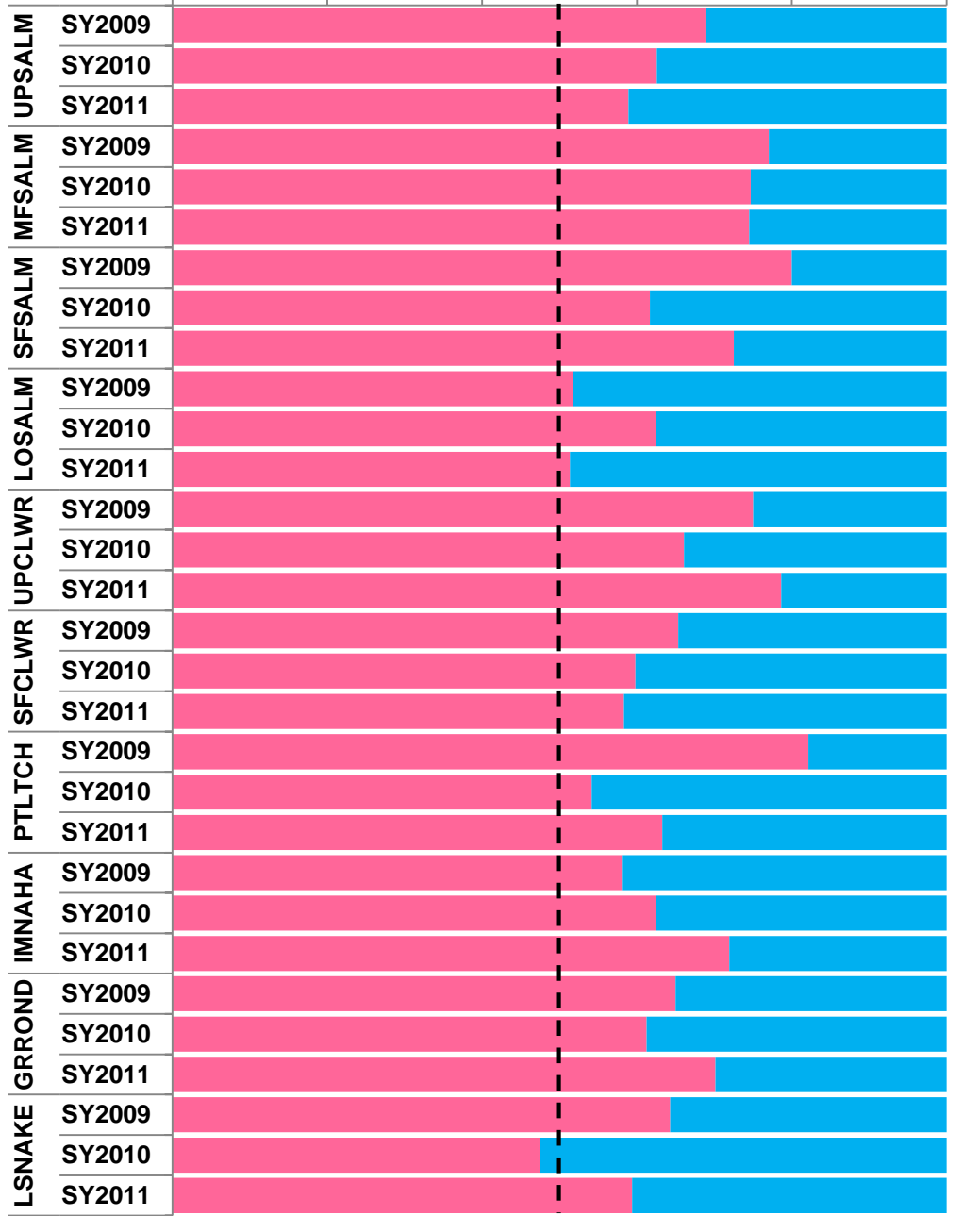
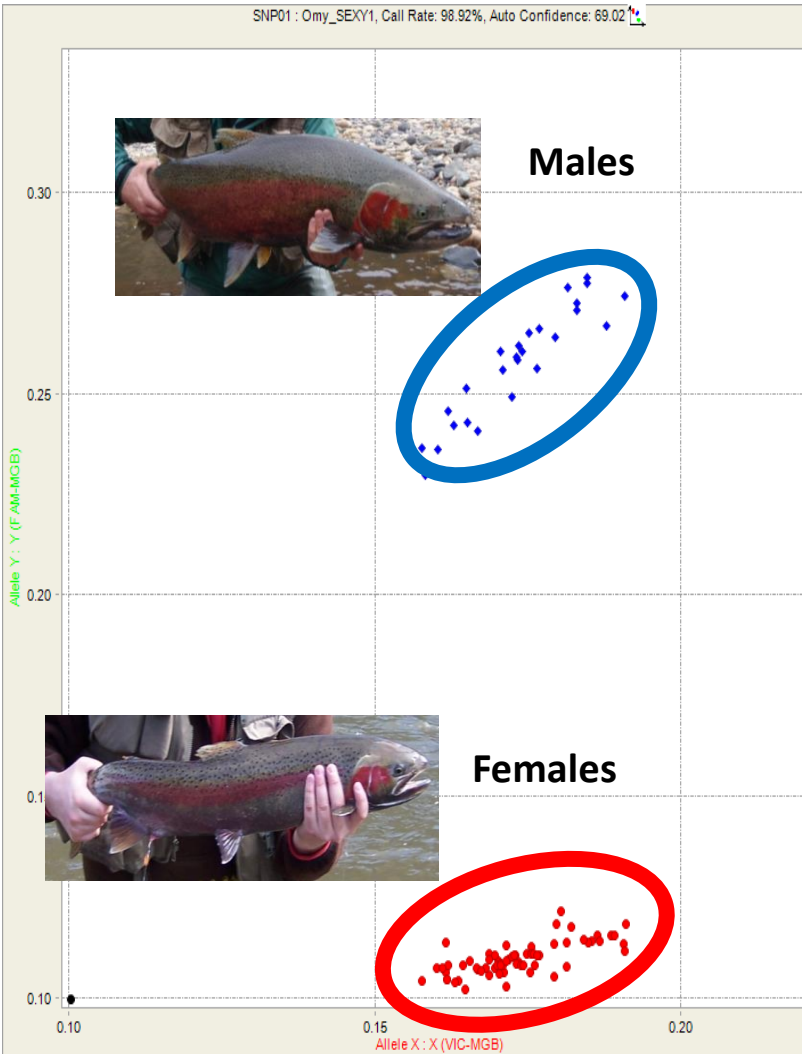
Upper Clearwater and S.F. Clearwater: early- to mid- October



# Sex ratios of Genetic Stocks

■ % Females ■ % Males

0% 20% 40% 60% 80% 100%



# When to use GSI?

When to use GSI:

- used primarily for wild fish
- there is a lot of differentiation among reference groups
- assign fish to its genetic stock

# What about PBT?

When to use PBT:

- used primarily for hatchery fish
- when the parents have been sampled/genotyped
- assign fish to individual parents

# What is Parentage Based Tagging?

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PBT uses similar techniques as those used in human parentage testing

# Conception of PBT

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## A Description of Full Parental Genotyping

Report Submitted to the Pacific Salmon Commission

Eric C. Anderson\*

John Carlos Garza\*

April 27, 2005

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DOI: 10.1534/genetics.105.048074

## The Power of Single-Nucleotide Polymorphisms for Large-Scale Parentage Inference

**Eric C. Anderson<sup>1</sup> and John Carlos Garza**

*Fisheries Ecology Division, Southwest Fisheries Science Center, Santa Cruz, California 95060*

Manuscript received July 11, 2005

Accepted for publication December 8, 2005



# Benefits of PBT

Provides same information as CWTs

- Run reconstruction (age, stock of returning adults)
- Stock composition of harvest

Tag recovery rates vastly improved

- Nearly 100% tagging rate of hatchery fish

Many issues associated with other methods eliminated

- No tag loss
- Non-lethally interrogated
- Passive mark (no handling of juveniles needed)
- No differential mortality

# Parental Based Tagging:

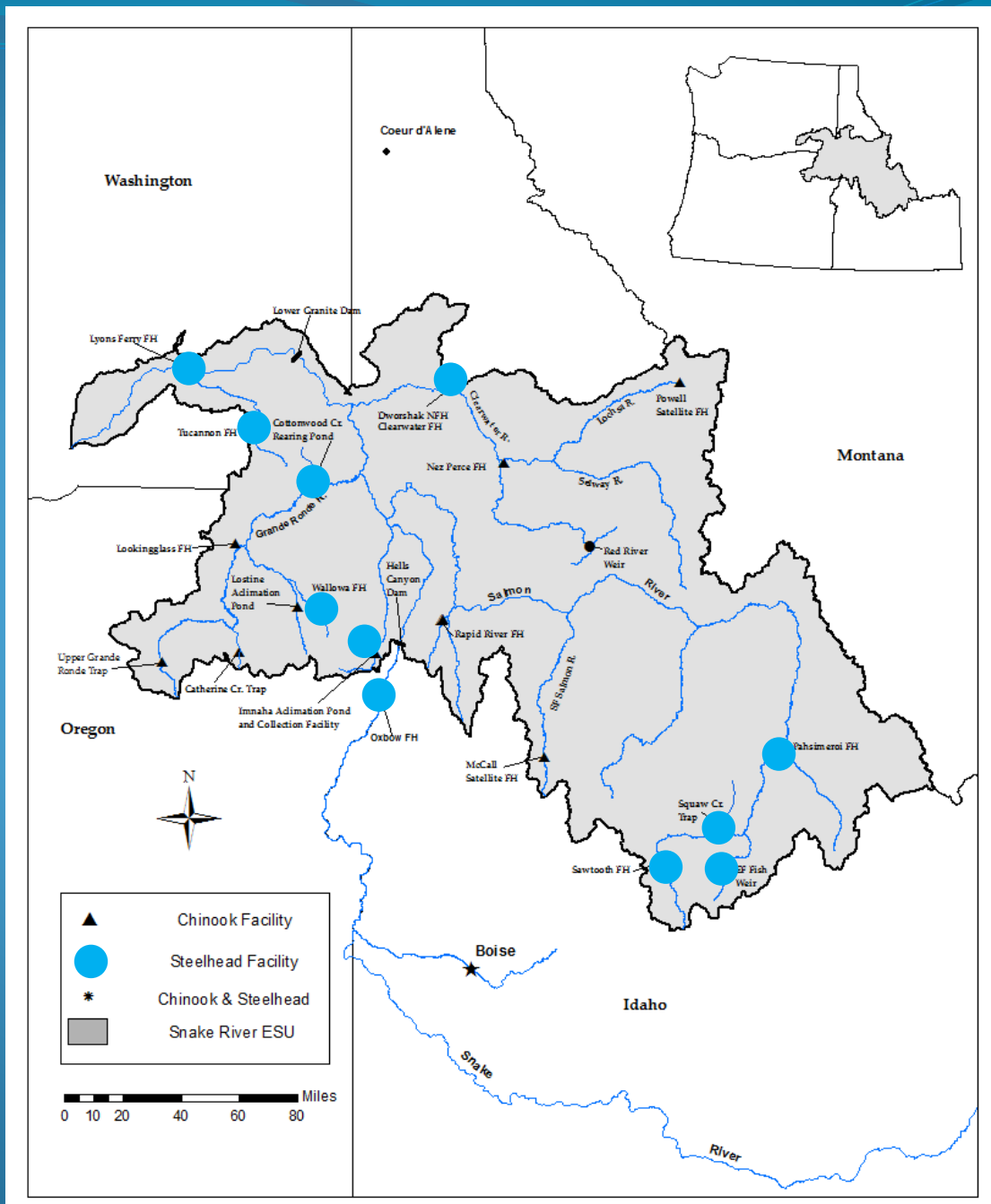
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PBT is a also two-step process:

1. **Generate parental baseline**
  - Genotype broodstock from contributing hatcheries

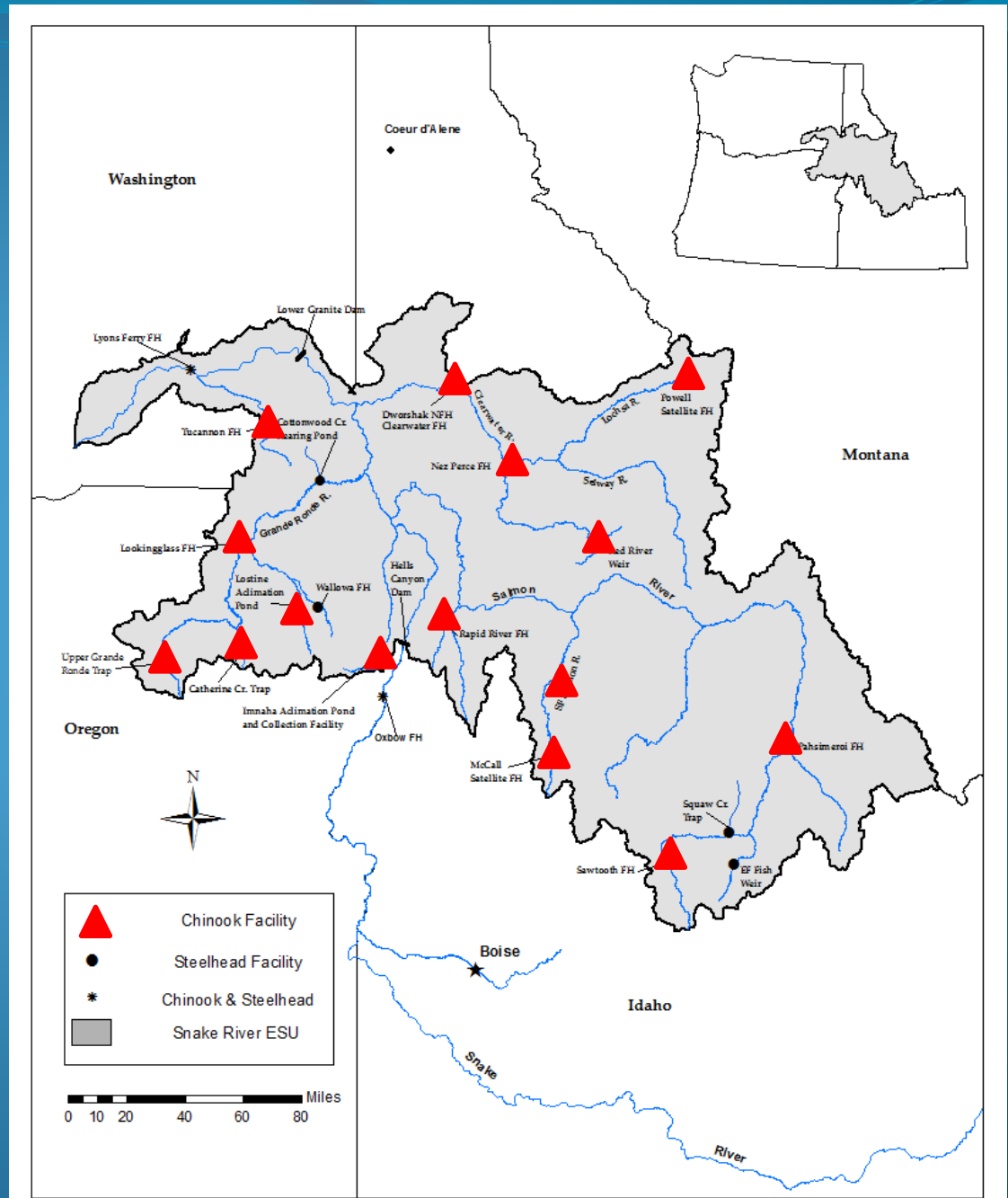
# Snake River Steelhead

- Majority sampled in 2008
- All broodstock sampled since 2009



# Snake River Chinook

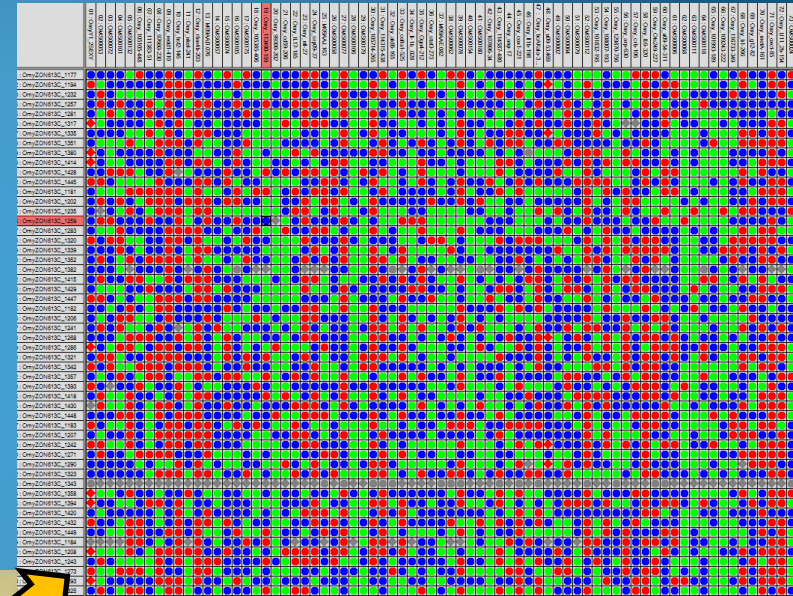
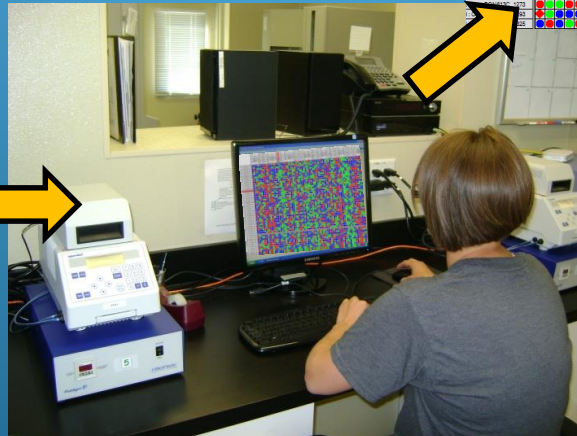
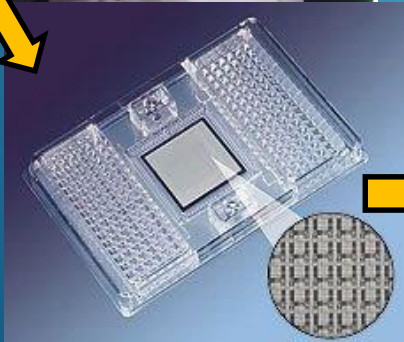
- All Spring/Summer Chinook broodstock sampled since 2008



# Building the Baseline:

Samples genotyped at 96 genetic markers

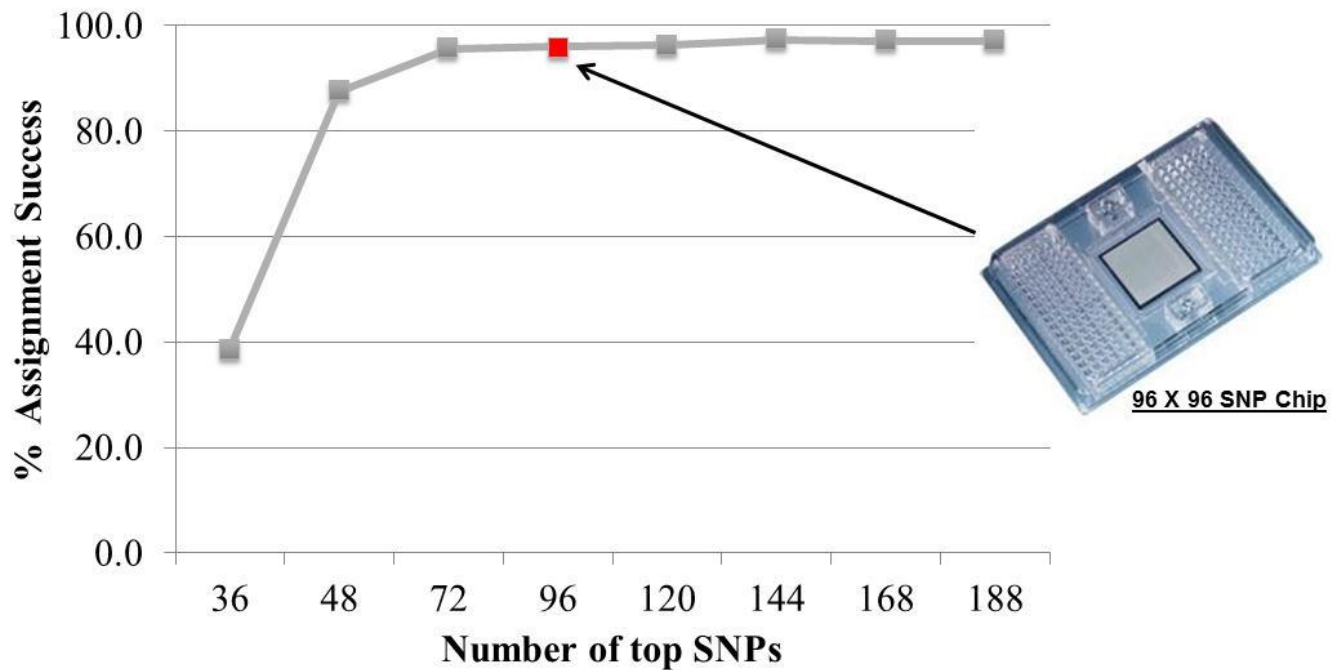
- Subset of the GSI loci



# SNP marker development:

Identified 96 SNPs that provide accurate parentage assignments.

Even when tens of thousands of possible parents are included!!!





# Steelhead

	Spawn Year				
	2008	2009	2010	2011	2012
Broodstock sampled	5,151	5,761	5,282	5,931	5,719
Genotyped	5,070	5,636	5,198	5,765	5,490
“Tagging” Rate of Offspring	96.9%	95.7%	96.9%	94.5%	92.2%
Smolts Produced *	~9.01 mil	~10.08 mil	~9.24 mil	~10.38 mil	~10.01 mil
Smolts “Tagged”	~8.74 mil	~9.65 mil	~8.96 mil	~9.81 mil	~9.2 mil

\* Assuming 3,500 smolts produced per broodstock pair

# How many steelhead are we tagging?

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- ~70% of outmigrating steelhead in the Columbia River are hatchery-origin fish
- 14.9 million hatchery steelhead released in the Columbia River basin each year
- **Of these, 9.1 million are Snake River origin (~61%)**



# Parentage Based Tagging:

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PBT is a also two-step process:

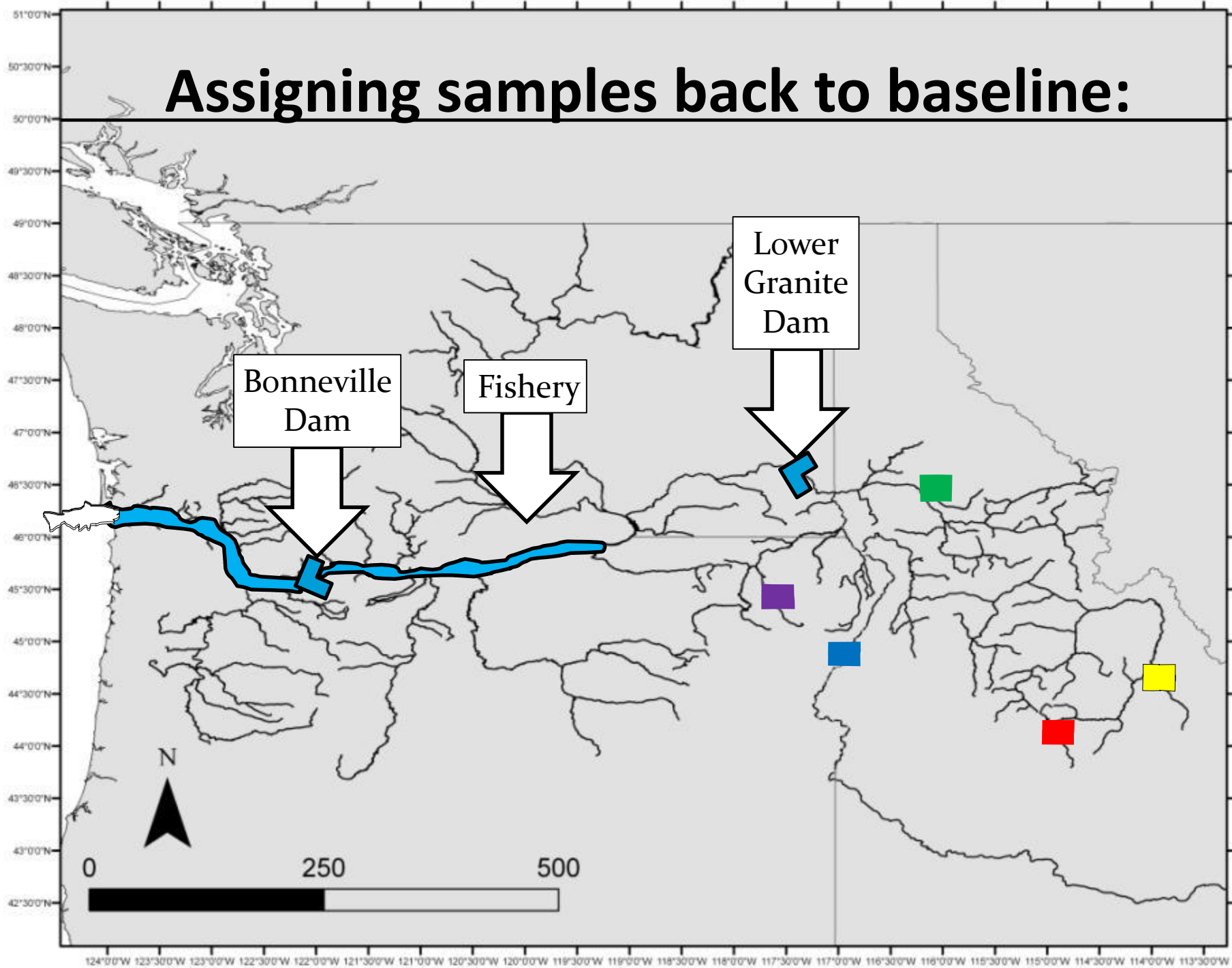
**1. Generate parental baseline**

- Genotype broodstock from contributing hatcheries

**2. Estimate composition of mixture**

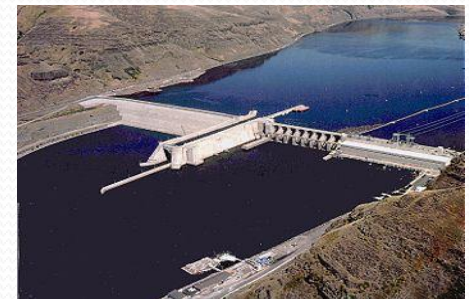
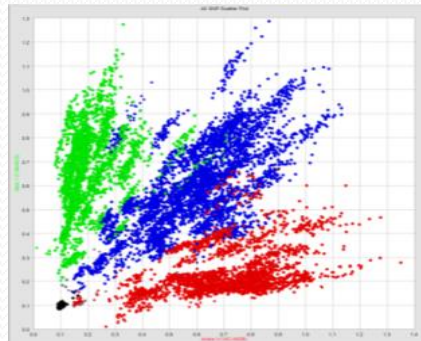
- Obtain genotype data from mixture samples to estimate contribution (e.g. fishery, juvenile, or escapement samples)

# Assigning samples back to baseline:



# Projects using PBT baseline

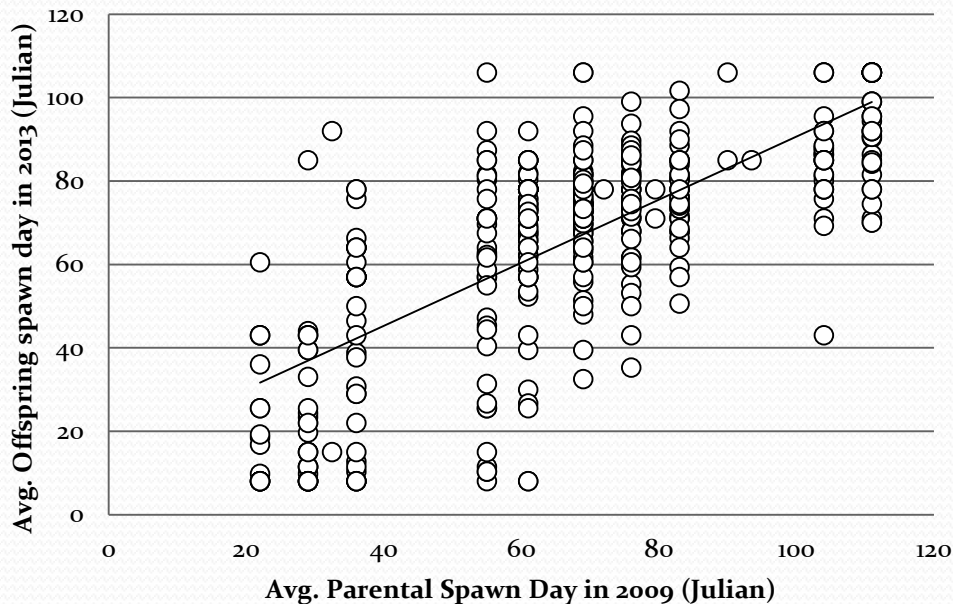
- Stock Composition of:
  - Columbia River Fisheries (Alan Byrne, IDFG)
  - Idaho Fisheries (Brian Leth, IDFG)
  - Escapement at Lower Granite Dam (Brian Leth, IDFG)
- Origin of Hatchery Kelts (Andrew Matala, CRITFC)
- Origin of Hatchery Strays (Matt Smith, USFWS)
- Origin of Bird-predated Smolts (David Kuligowski, NOAA)



# And, finally..multi-generational data

- Heritability of traits: SY2013 Assigned back to SY2009 (2-ocean)

**Heritability of Spawn Timing**



VERY heritable ( $h^2 = 0.76$ )

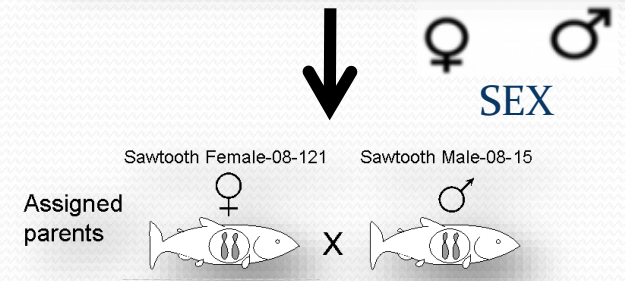


<http://www.inckr.com/photos/hatekay/4319654380/sizes/o>

# Ultimate PBT goal:

Where and when it was released

Identify parents



- ✓Diet
- ✓Disease
- ✓Rearing density
- ✓Temperature

Where it reared

Stock and age



Sawtooth Fish Hatchery

Where it incubated



This will require the development of similar types of databases that currently exist for CWTs and PIT tags!!!

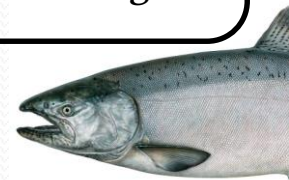


Photo Credit: Mademan National Fish Hatchery- USFWS

# Review:

## GSI (Genetic Stock Identification)

- Works well with highly differentiated populations
- Reference populations are sampled to create a baseline
- Used primarily to determine origin of wild fish

## PBT (Parentage Based Tagging)

- Uses parentage assignments to determine origin
- Broodstock are sampled annually to create a baseline
- Used primarily to determine origin of hatchery fish

# Questions?

