Update on Genetic Monitoring throughout the Snake River Basin

Lance Hebdon and Matthew Campbell
Idaho Department of Fish and Game
71st Pacific States Marine Fisheries Commission Annual Meeting
August 21st, 2018

Eagle Fish Genetics Lab-2018

PSMFC staff = 13 full-time employees

IDFG = 2 full-time employees

Talk Outline

I. Background
- Why these projects were initiated
- What these genetic technologies are and how they work
- The major objectives achieved during proof-of-concept period
- Examples of current uses of Snake River genetic baselines

II. Major recent achievements of these genetic technologies in the Snake and Columbia River Basins and beyond
- Tracking of family units to release site
- Increased PBT sampling throughout the CRB
- Decreased genotyping costs/Increase in output
- SNPs under selection
  - Increased GSI precision
  - Identifying SNPs linked to specific traits

III. Future?

Why were these genetic projects initiated?

In 2008/2009 the Pacific Salmon Commission and the Independent Scientific Review Panel and Advisory Boards recommended large-scale evaluations of genetic technologies for salmon and steelhead management

Recommendations for Application of Genetic Stock Identification (GSI) Methods to Management of Ocean Salmon Fisheries.

Special Report of the GSI Steering Committee and the Pacific Salmon Commission's Committee on Scientific Cooperation.

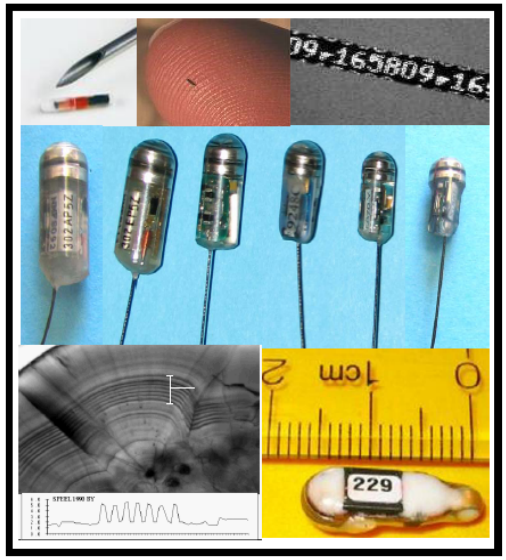
January 2008

PACIFIC SALMON COMMISSION

Pacific Salmon Commission Technical Report No. 23

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

Based on these recommendations and endorsements IDFG proposed two new projects to BPA for evaluating new genetic technologies in the Snake River Basin (awarded funding in July 2010):

home | about us | fish & wildlife | energy | news | reports, papers & videos

Fish & wildlife → Budgets → Fast Track BiOp Review → All proposals

Proposal 201003100: Snake River Chinook and Steelhead Parental Based Tagging

Jump to:

1. Administrative
2. Location
3. Species
4. Past accomplishments
5. Relationships
6. Objectives
7. Work elements
8. Budget
9. Future
10. Narrative

Reviews

home | about us | fish & wildlife | energy | news | reports, papers & videos

Fish & wildlife → Budgets → Fast Track BiOp Review → All proposals

Proposal 201002600: Chinook and Steelhead Genotyping for Genetic Stock Identification

Jump to:

1. Administrative
2. Location
3. Species
4. Past accomplishments
5. Relationships
6. Objectives
7. Work elements
8. Budget
9. Future
10. Narrative & other docs

Reviews

Collaborative projects between IDFG and CRITFC

IDFG Eagle Fish Genetics Lab
Eagle, ID

Collaborative Center for Applied Fish Science
Hagerman, ID

What these genetic technologies are and how they work

Parentage-based genetic tagging - PBT (Hatchery Fish)

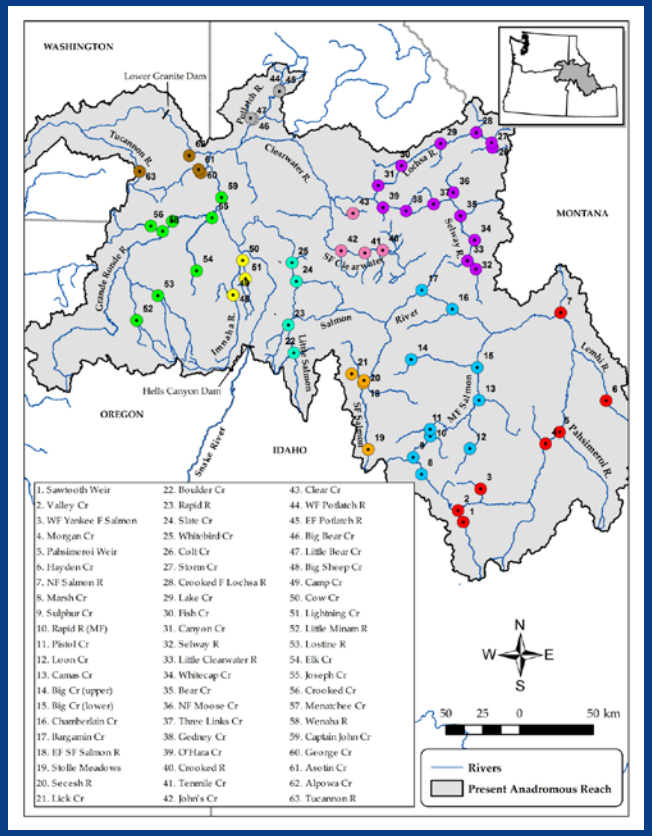
- Genetic-based fish tagging method that involves genotyping hatchery broodstock
- By genetically sampling the parents, all offspring are genetically "tagged"
- 'Tag' recovery is non-lethal, and possible at all life stages

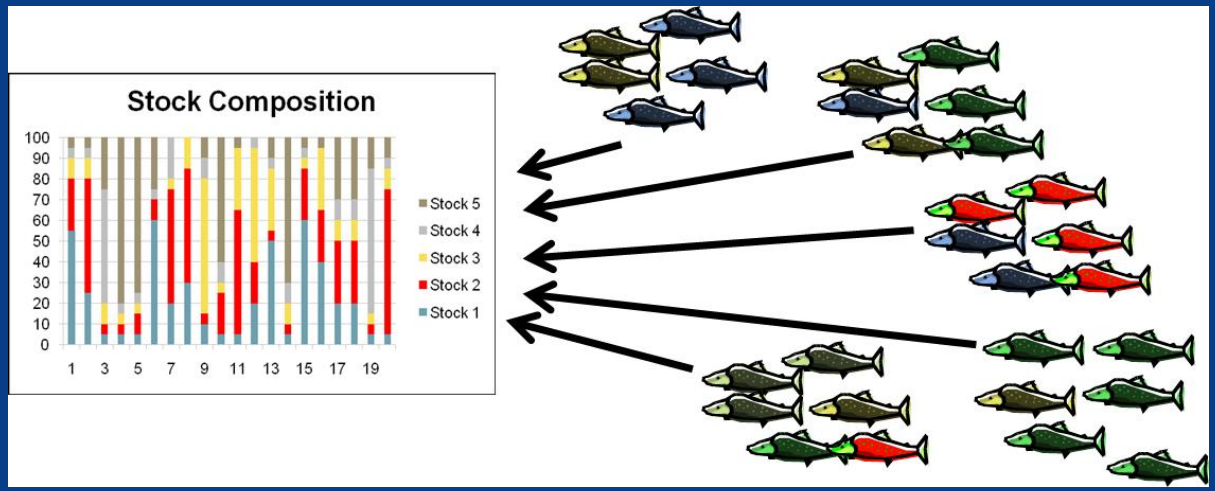
2 = 6,000!!!!

What these genetic technologies are and how they work

Genetic Stock Identification- GSI
(Wild fish)

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





Review of 2011 talk to PSMFC…

PBT achievements during proof-of-concept period:

What we demonstrated:

- PBT accurate and matched CWT assignments (Steele et al 2014)
- PBT/GSI genetic marker panels combined (efficient), multiple labs = same data
- High Snake River genetic tagging annually for each species (>95%) (2009-present)
  - ✓ ~9 million hatchery steelhead
  - ✓ ~14 million hatchery Chinook Salmon

It's all in the genes—including the tracking device

June 24, 2013, Canadian Science Publishing (NRC Research Press)

1046

NRC Research Press

ARTICLE

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

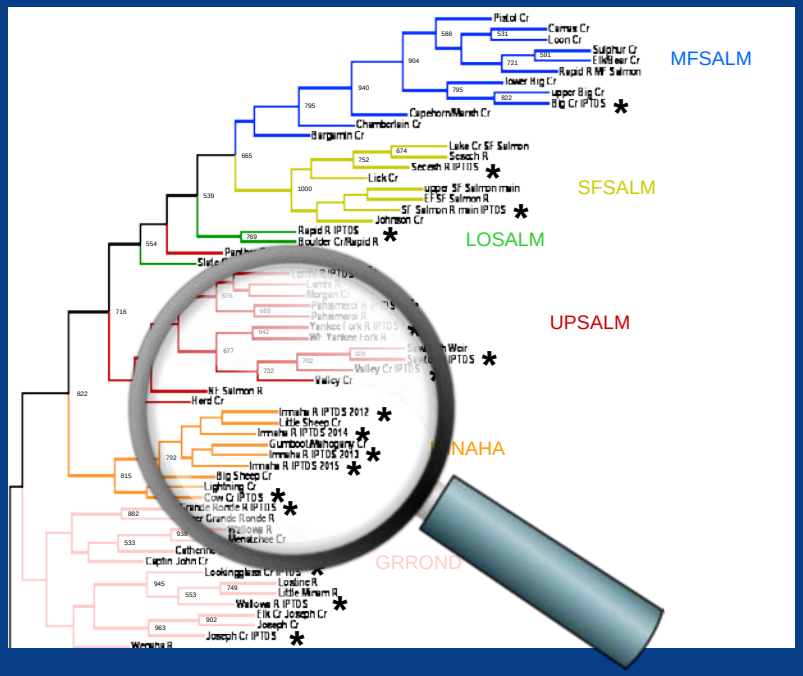
Craig A. Steele, Eric C. Anderson, Michael W. Ackerman, Maureen A. Hess, Nathan R. Campbell, Shawn R. Narum, and Matthew R. Campbell

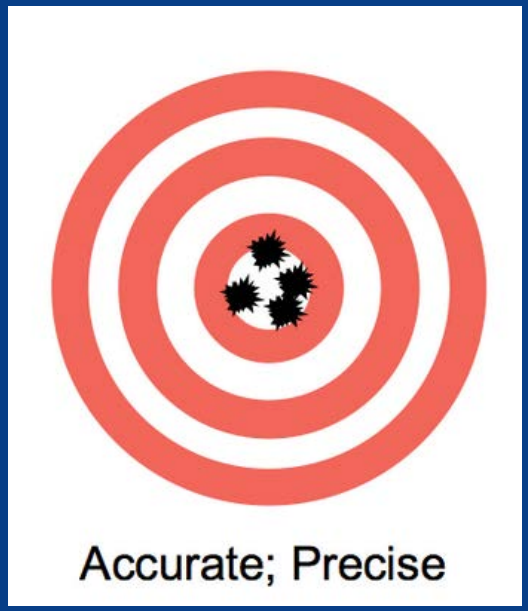
Abstract: Parentage-based tagging (PBT) is a promising alternative to traditional coded-wire tag (CWT) methodologies for monitoring and evaluating hatchery stocks. This approach involves the genotyping of hatchery broodstock and uses parentage assignments to identify the origin and brood year of their 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.

GSI achievements during proof-of-concept period:

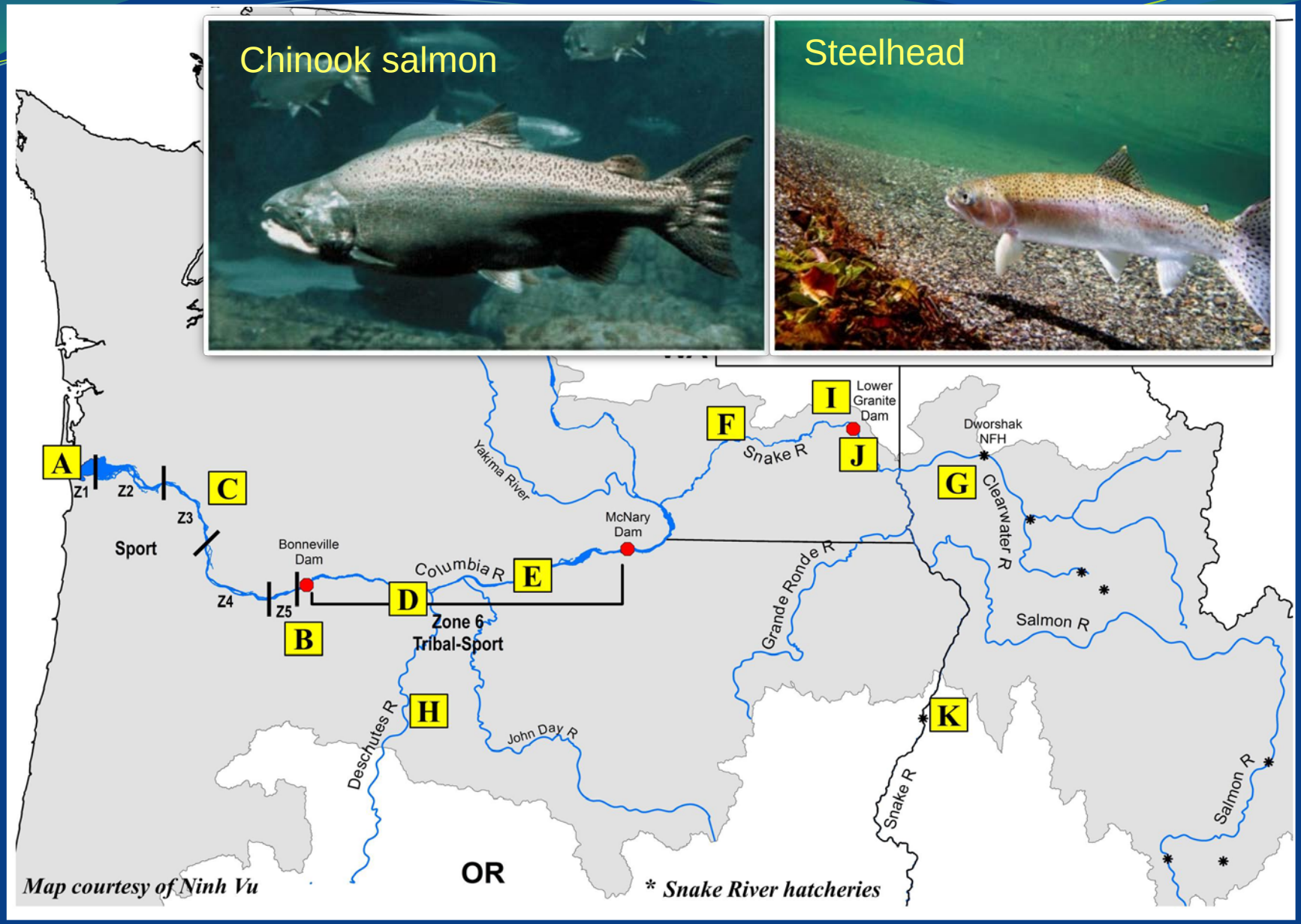
What we demonstrated:

- Can monitor these species at the ESU and MPG level
- Stock abundance estimates using GSI baselines exhibit low bias (Powell et al 2018) and high precision (Steinhorst et al 2016)





Examples of research and monitoring programs using Snake River steelhead and Chinook Salmon GSI/PBT baselines


Chinook salmon
Steelhead
A
Z1
Z2
C
Z3
Sport
Z4
Z5
B
Bonneville Dam
Columbia R
D
E
McNary Dam
Zone 6 Tribal-Sport
Yakima River
F
I
Lower Granite Dam
J
Snake R
Dworshak NFH
G
Clearwater R
Grande Ronde R
Salmon R
H
Deschutes R
John Day R
K
Snake R
Salmon R
OR
Map courtesy of Ninh Vu
* Snake River hatcheries

A Columbia River Estuary: Predation

NOAA is using these standardized genetic baselines to assess the genetic origin of salmon and steelhead eaten by sea lions and birds in the LCR

- ✓ Rub et al NOAA researchers concluded that *"about 68% of the fish tagged and sampled near Astoria were destined for the river and tributaries above Bonneville based on genetic testing"...*
- ✓ Kuligowski et al 2014-NOAA researchers concluded that *"PBT analysis suggests Snake River steelhead and Chinook Salmon are a larger proportion of the birds diets"...*

NOAA FISHERIES

Survival of adult spring/summer Chinook salmon through the estuary and lower Columbia River amid a rapidly changing predator population

A. Michelle Wargo Rub, Ben Sandford, Don Van Doornik, Matthew Nesbit, Samuel Rambo, Jesse Lamb, Louis Tullos, Gordon Axel, Brian Burke, Kinsey Frick, Mark Sorel, David Huff, & Rich Zabel
NOAA Fisheries Northwest Fisheries Science Center (NWFSC)

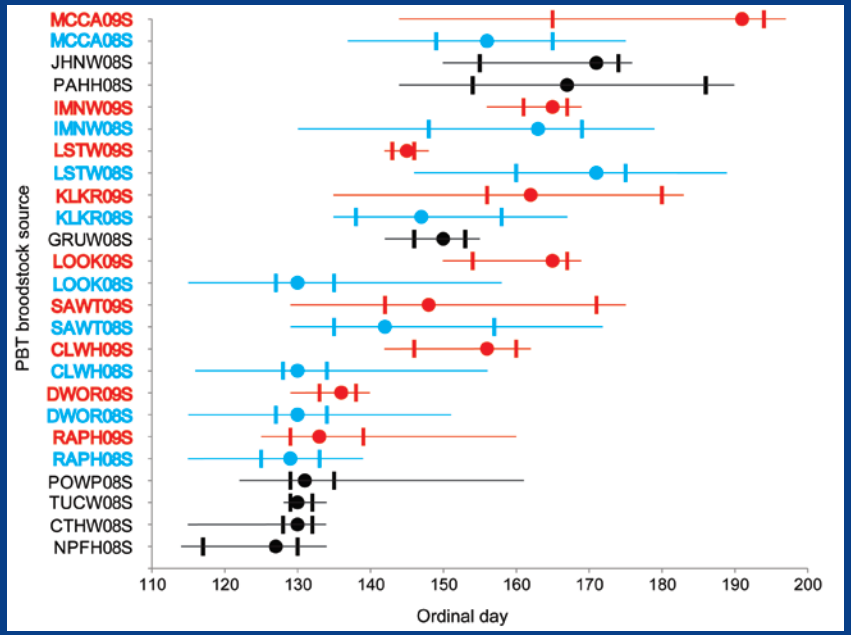
Genetic Analysis of Caspian Tern (*Hydroprogne caspia*) and Double Crested Cormorant (*Phalacrocorax auritus*) Salmonid depredation in the Columbia River Estuary 2006-2013

David Kuligowski[1], Laurie Weitkamp[1], Curtis Roegner[1], Daniel Roby[2], Ken Collis[3], Donald Lyons[4], Donald Van Doornik[1], Lauren Reinalda[4], Allen Evans[3] Tim Marcella[4], Peter Loschl[4], and David Teel[1].

B Bonneville Dam: Stock proportion, run-timing

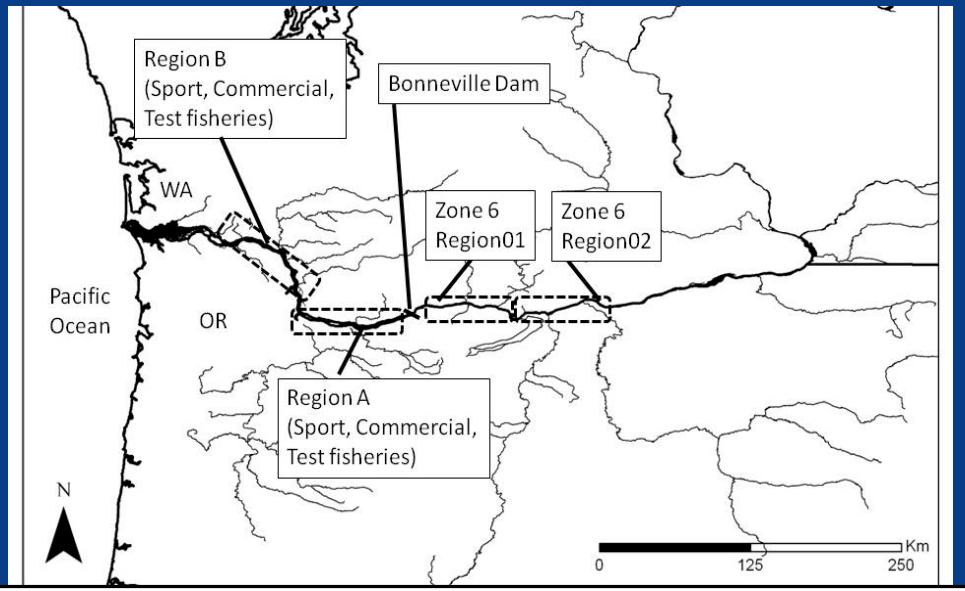
CRITFC estimates stock proportion of hatchery and wild Chinook Salmon and steelhead over Bonneville Dam

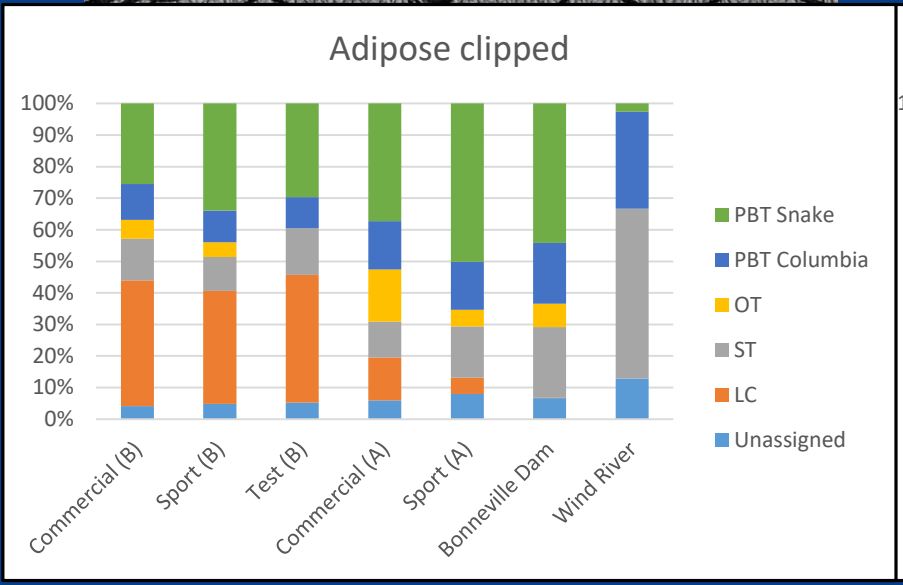
- ✓ 47% of ad-clipped adults assigned to Snake River hatcheries
- ✓ Chinook salmon jacks from 8 of 9 Snake River hatcheries show delayed run-timing compared to 4-year old fish

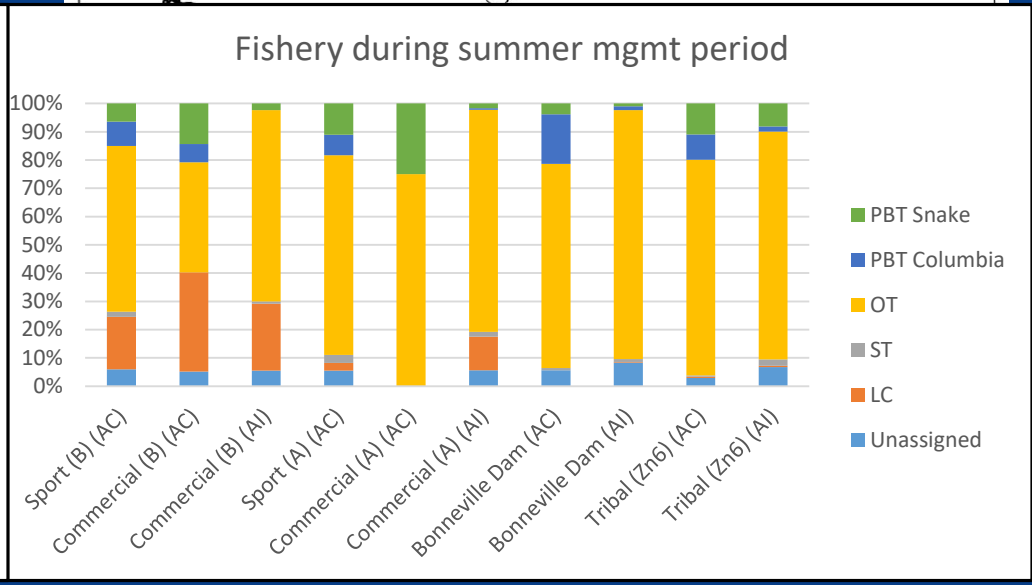


C - E

Mainstem Columbia River: CRITFC monitors Chinook Salmon harvest







C - G

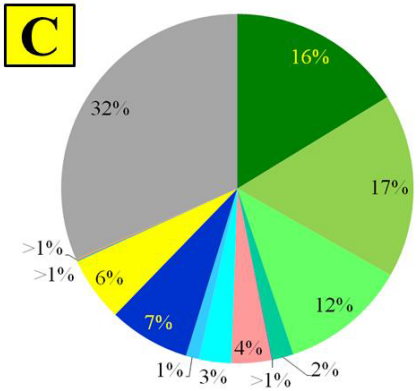
Columbia and Snake Rivers: IDFG (and others) monitors steelhead harvest

*Data courtesy of Alan Byrne Idaho Department of Fish and Game (*all data for SY2015 and considered preliminary)*

Objective: Estimate Snake River hatchery proportions within mixed stock fisheries

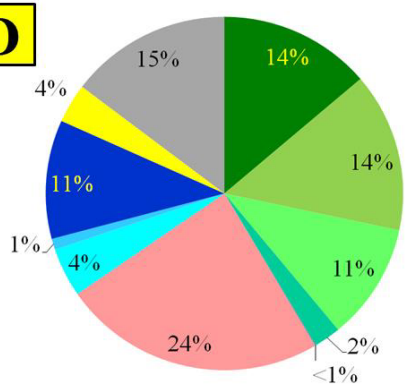
Results: Significant differences in stock composition observed within fisheries moving upstream in Columbia River

C



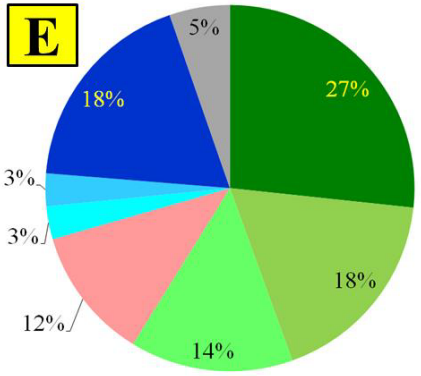
Sport Fishery – mouth to Bonneville Dam (N = 839)
15, 923 hatchery harvested*

D



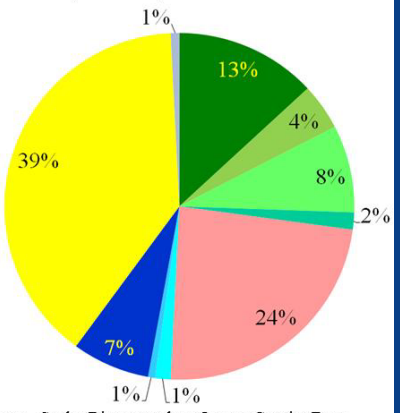
Tribal Zone 6 (N = 597)
9,718 hatchery harvested*

E



Sport Zone 6, Mouth of Deschutes
(N = 158)
N/A hatchery harvested

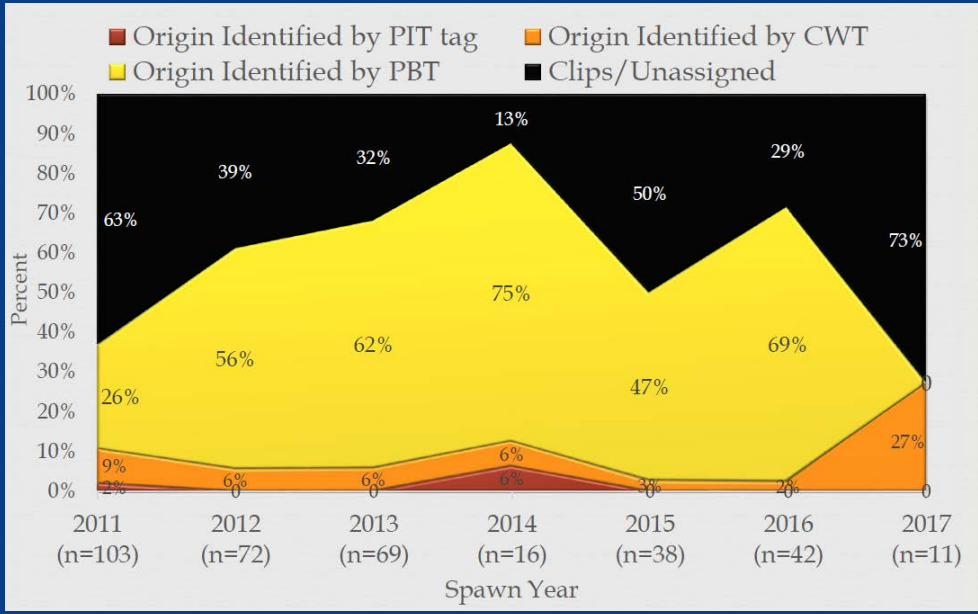
F



Sport Fishery – Snake River mouth to Lower Granite Dam
(N = 634)
7,160 hatchery harvested*

H Deschutes River: Straying and Reproductive Success

USFWS/ODFW/CRITFC used baseline to determine the origin of stray hatchery steelhead collected in mainstem Deschutes and tributaries (Bakeoven and Buck Hollow Creeks)



https://www.psmfc.org/steelhead/2018/FABER_SteelheadMgrs_Faber_primary.pdf

ODFW-Derrek Faber, Wayne Wilson, James Ruzycki, USFWS-Matt Smith

Hess et al 2016-

- **Assessed the origin of hatchery steelhead taking thermal refuge during migration**
- **Stock-specific migration time coincident with use of refuge during time of warm main-stem temperatures**

Migrating adult steelhead utilize a thermal refuge during summer periods with high water temperatures FREE

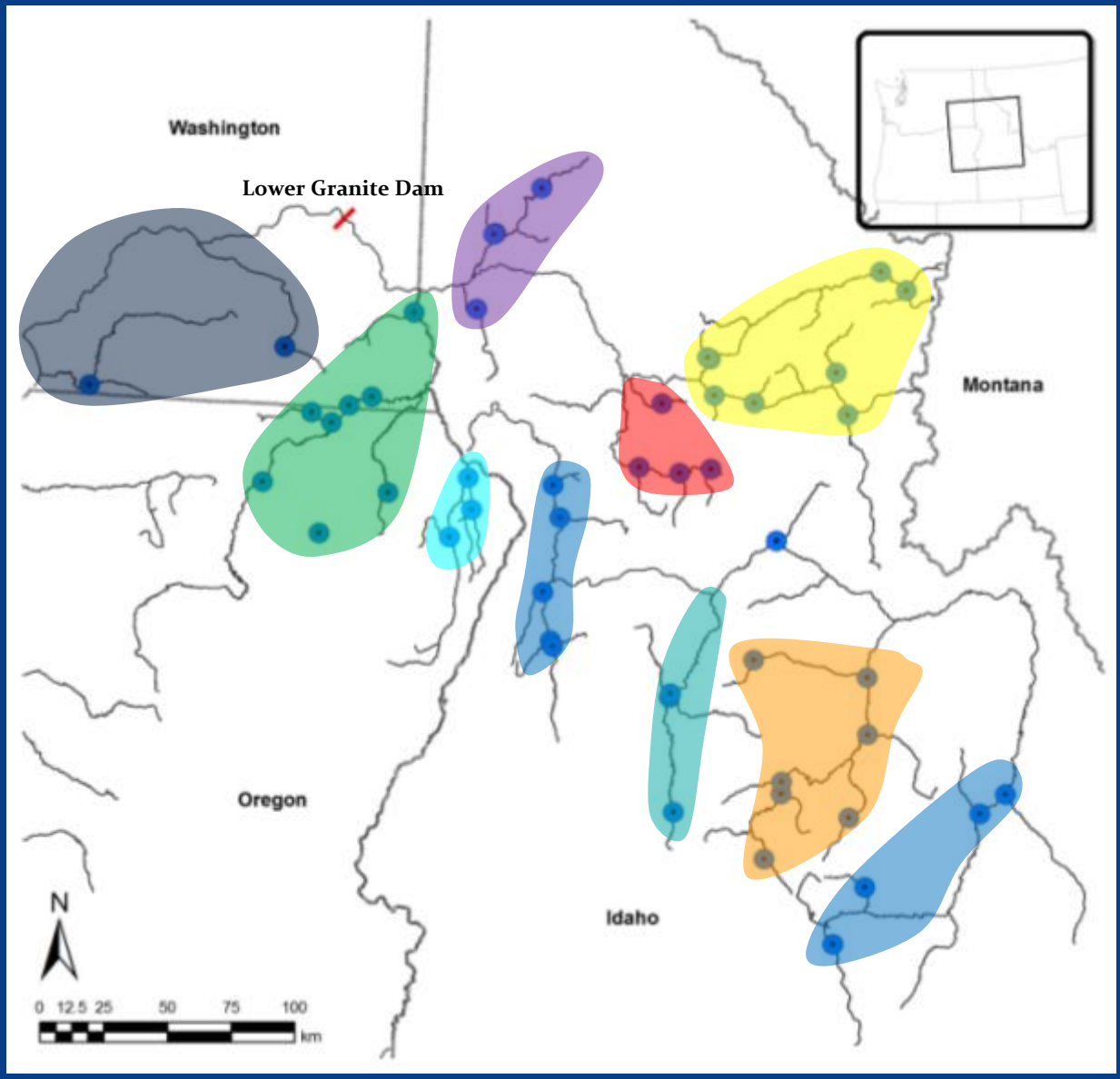
Maureen A. Hess ✉, Jon E. Hess, Andrew P. Matala, Rod A. French, Craig A. Steele, Jens C. Lovtang, Shawn R. Narum

ICES Journal of Marine Science, Volume 73, Issue 10, 1 November 2016, Pages 2616–2624, https://doi.org/10.1093/icesjms/fsw120

I Lower Granite Dam: Wild and hatchery abundance by 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

Some hatchery fish are unclipped/marked:

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

NOAA FISHERIES
National Oceanic and Atmospheric Administration

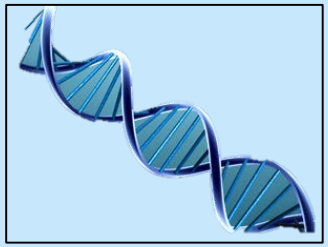
NOAA Requires accurate estimates of wild abundance!!!!!

Wild versus Hatchery Determination

LGR Trap
"wild fish"

Adult Trapping Facility

Hatchery
PBT Match?



NO

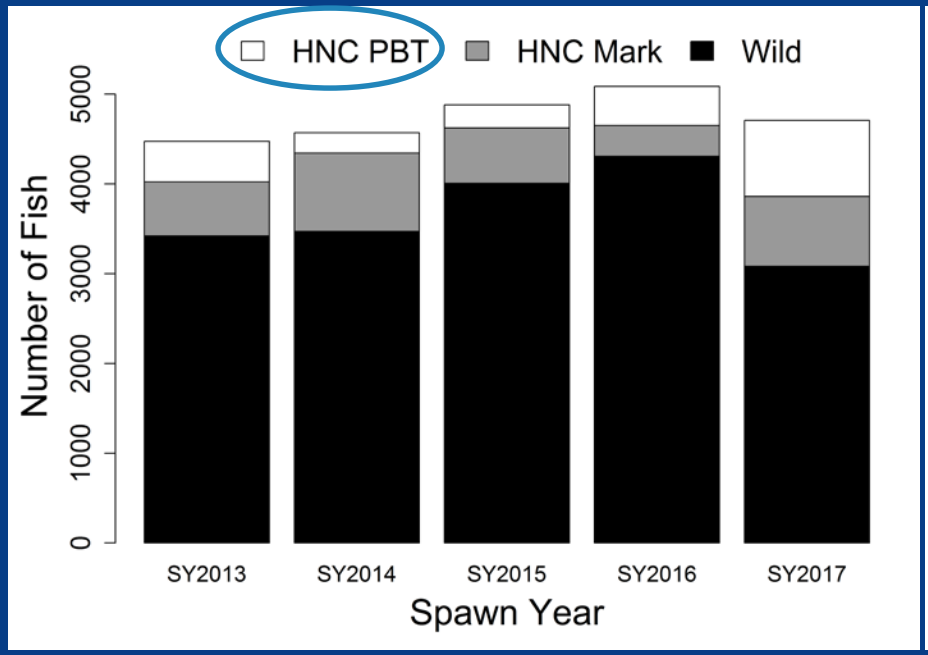
YES

WILD

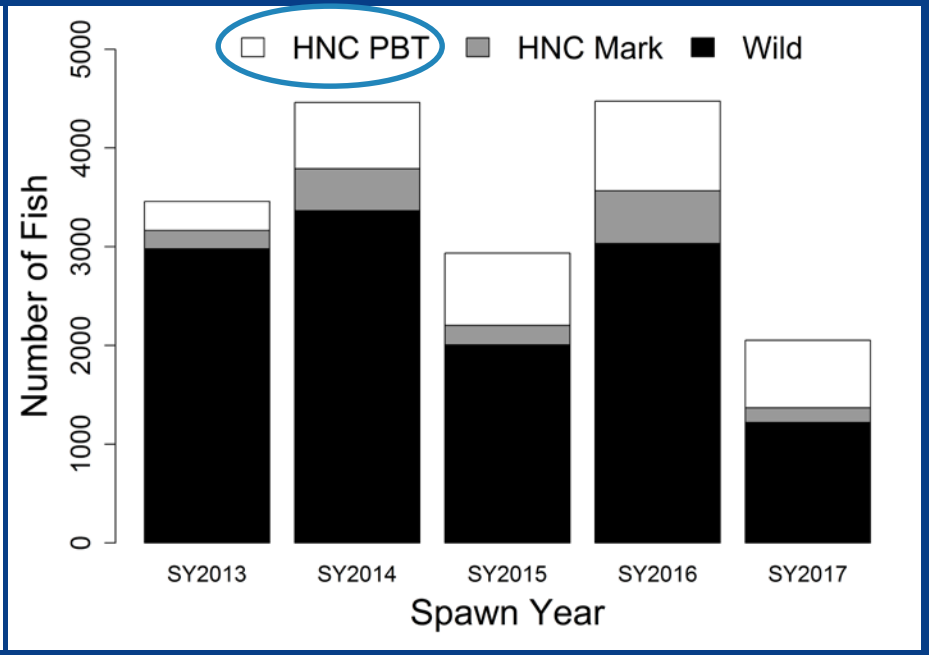
unmarked hatchery

Removing unclipped hatchery fish critical!

PBT makes the difference!!!!!!



Steelhead

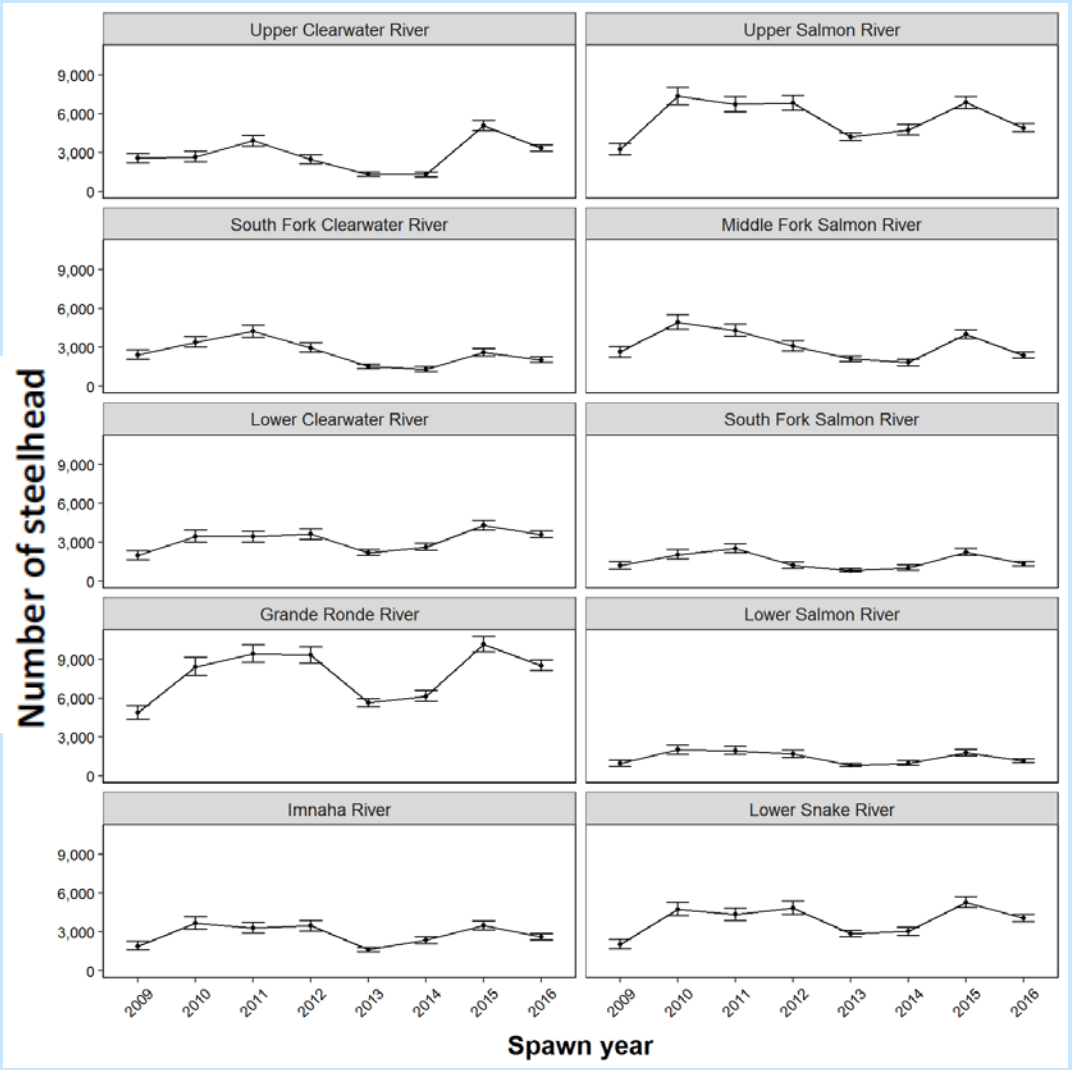


Chinook Salmon

Species	Without PBT	With PBT	Difference	%
Steelhead	19,592	15,576	4,016	20.4%
Chinook	9,049	5,793	3,256	35.9%

Only now can we get accurate estimates of wild abundance back to the Snake River!!!

Wild Escapement - Genetic Stock



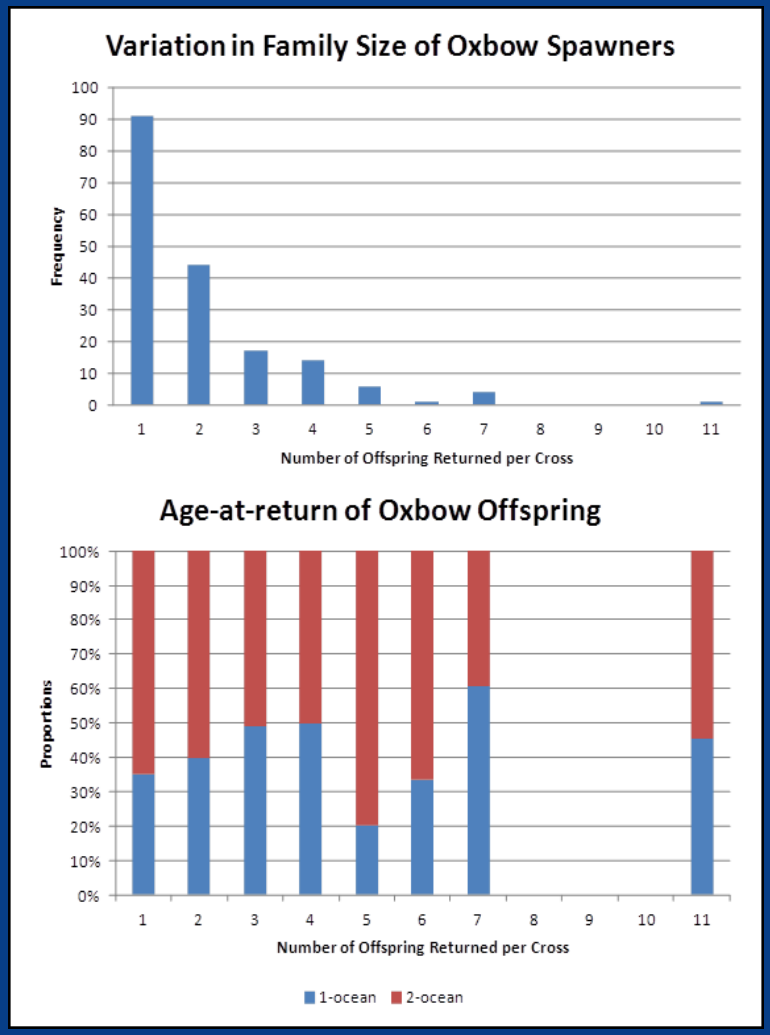
Steelhead

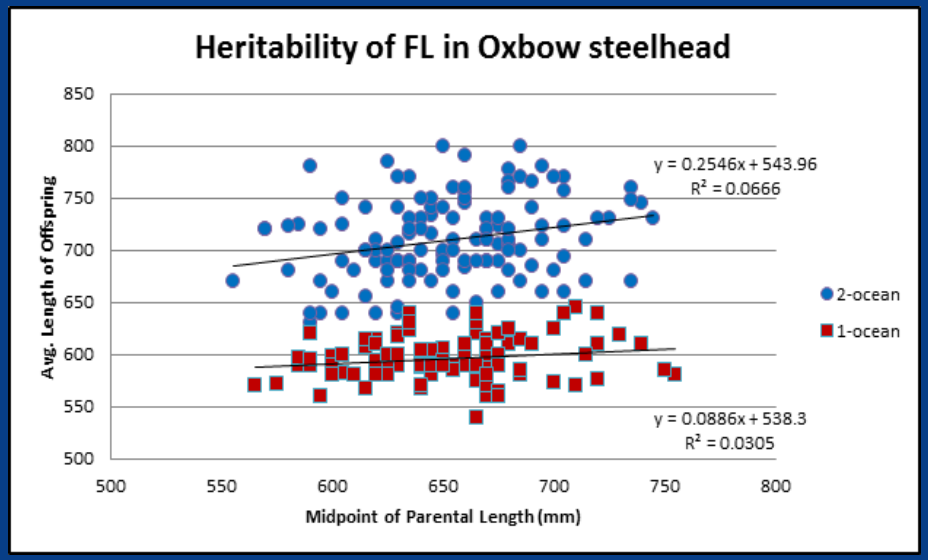
- Annual estimates of wild abundance needed to determine recovery status are now available annually!!!!
- Same estimates available for Snake River Chinook ESU
- Available by age, sex, etc.

Escapement above Lower Granite Dam of STHD by stock from spawn years 2009 to 2016

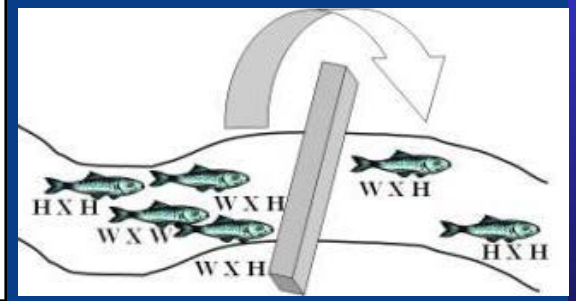
K Meanwhile.....Back at the hatchery

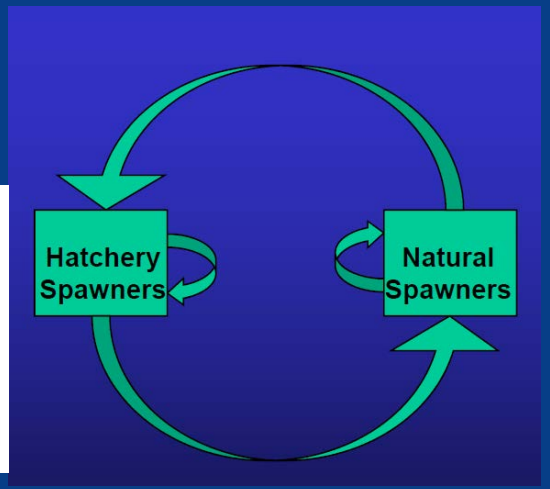
Since all broodstock are sampled and genotyped each year, PBT also allows precise estimates of broodstock effective population size of, inter-hatchery stray rates, and demographic characteristics of individual broodstocks and release groups. Combined with sampling of wild fish above weirs allows monitoring of integrated/segregated management goals.

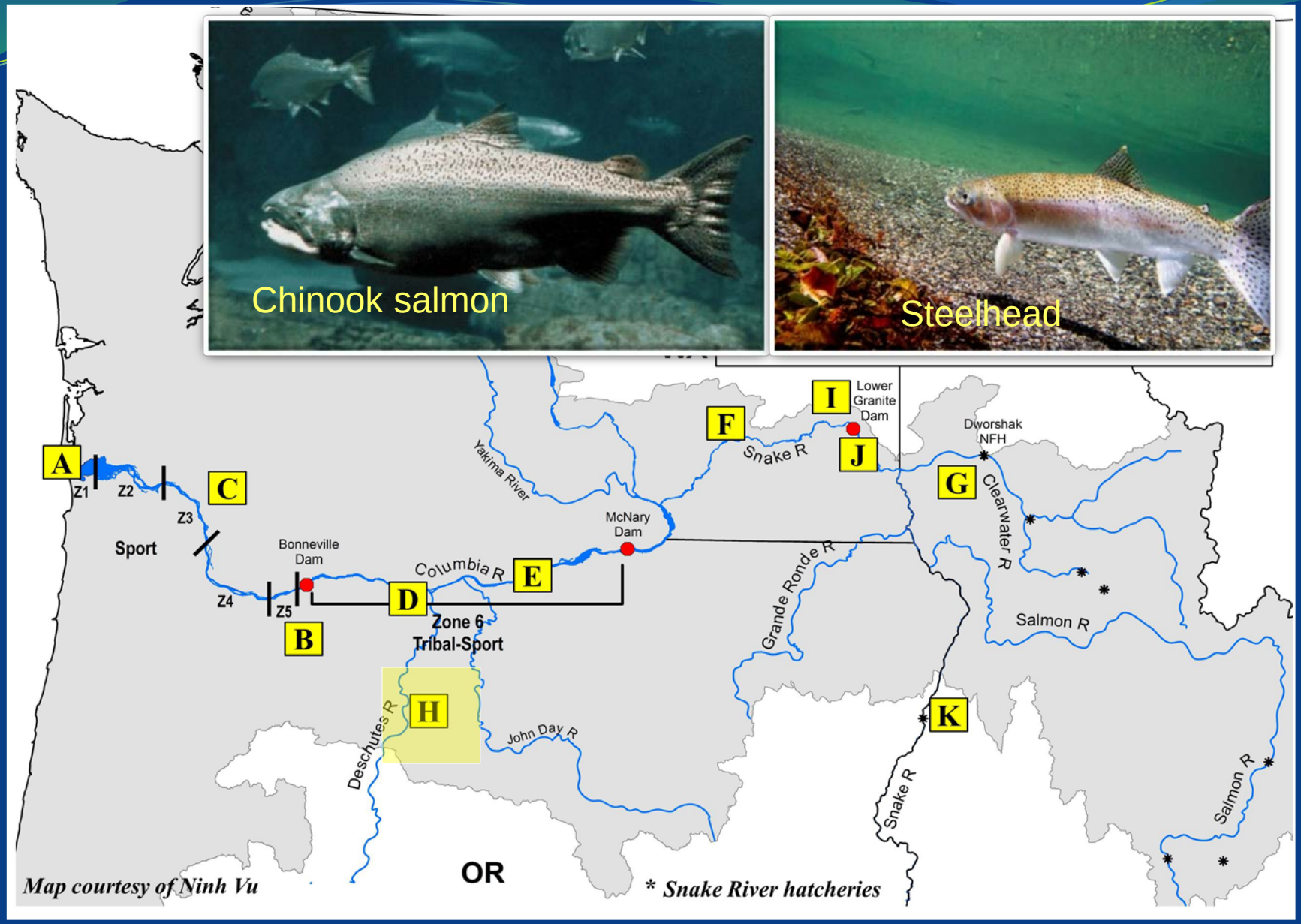




Integrated/Segregated






Chinook salmon
Steelhead
A
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Bonneville Dam
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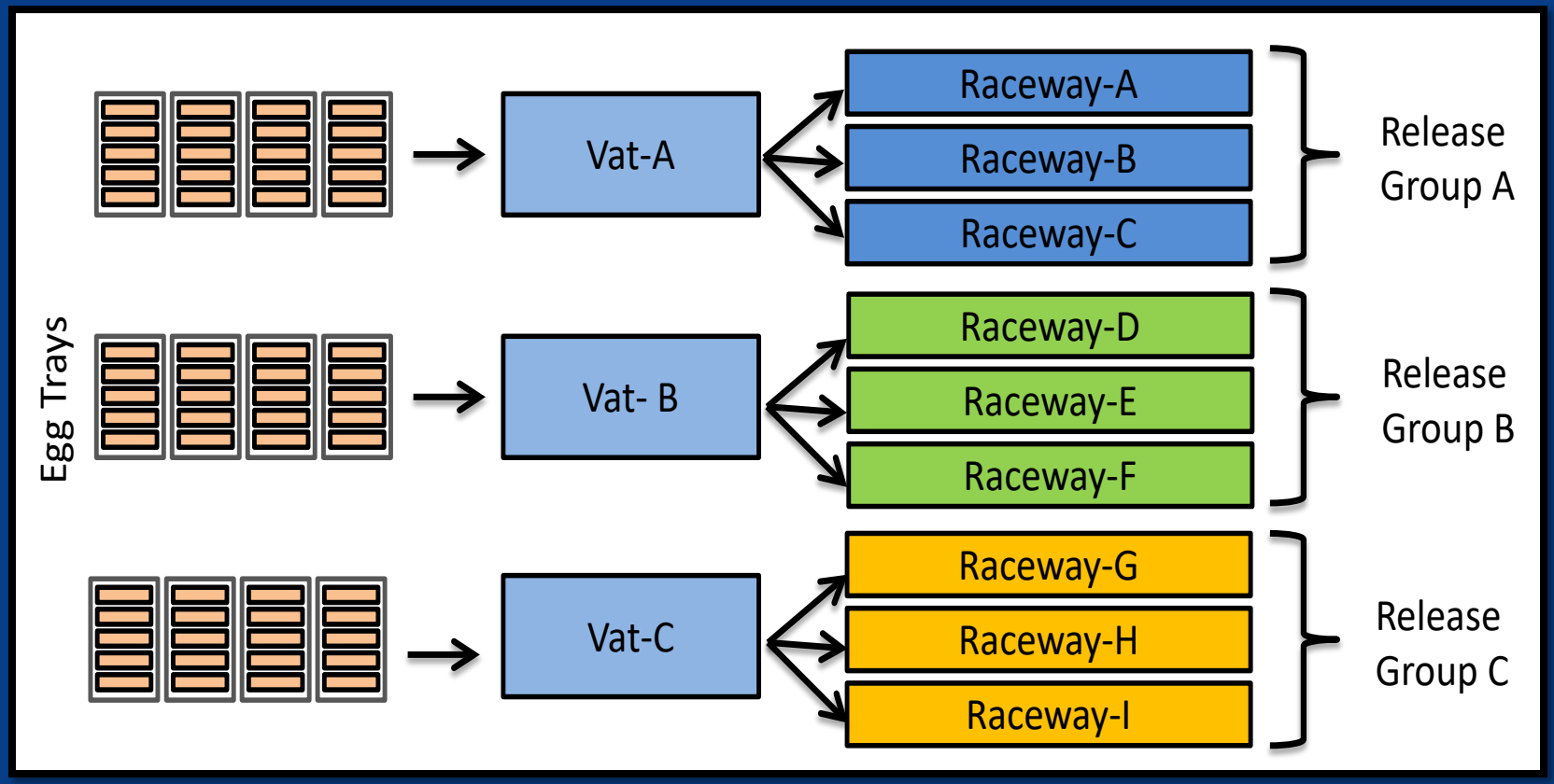
F
I
Lower Granite Dam
Snake R
J
Dworshak NFH
G
Clearwater R
Grande Ronde R
Salmon R
K
Snake R
Salmon R
OR
Map courtesy of Ninh Vu
* Snake River hatcheries

Major achievements in PBT/GSI in the Snake and Columbia River Basins and beyond.....

(since last presentation to PSMFC)

Achievements:

- Hatchery and management staff at IDFG developed protocols and procedures for tracking families from spawn to release
- High PBT tagging rates have been realized at the hatchery stock, rearing stock, and release site levels



Huge thanks to Carl Stiefel for his vision and leadership for developing family tracking protocols for LSRCP hatcheries!!!!!

PBT tagging rates at the hatchery stock level:

Hatchery Stock	Total Unique Families Genotyped	Total Females Genotyped	Total Females Spawned	Total Males Genotyped	Total Males Spawned	Number of smolts Released	Number of PBT tagged smolts tracked to release group	PBT tagging Rate
Dworshak	646	667	670	491	500	2,953,935	2,848,122	0.964
EFSR Natural	11	11	12	13	13	59,209	54,275	0.917
Osbow	100	103	103	100	102	578,380	561,534	0.971
Pahsimeroi	355	355	357	357	357	1,740,352	1,730,602	0.994
Sawtooth	285	286	286	285	286	1,381,958	1,377,126	0.997
Upper Salmon B-run	69	69	69	62	62	258,674	258,674	1.000
S.F. Clearwater	205	214	214	125	131	931,522	892,346	0.958
Pahsimeroi-Egg Box	137	143	144	138	144	N/A	N/A	0.951
Total/Average	1808	1848	1855	1571	1595	7,904,031	7,722,679	0.969

Average: 96.9%

PBT tagging rates at the rearing stock level:

Hatchery Stock	Rearing Stock	Total Unique Families Genotyped	Total Females Genotyped	Total Females Spawned	Total Males Genotyped	Total Males Spawned	Number of smolts Released	Number of PBT tagged smolts tracked to release group	PBT tagging Rate
Dworshak	Clearwater	130	141	142	105	111	587,719	538,053	0.915
S.F. Clearwater	Clearwater	69	69	69	62	62	258,674	258,674	1.000
Dworshak	Dworshak	470	479	481	345	347	2,228,021	2,177,068	0.977
EFSR Natural	Hagerman	11	11	12	13	13	59,209	54,275	0.917
Sawtooth	Hagerman	285	286	286	285	286	1,381,958	1,377,126	0.997
Dworshak	Magic	46	47	47	41	42	138,195	135,255	0.979
Pahsimeroi	Magic	93	93	93	93	93	480,493	480,493	1.000
Upper Salmon	Magic	205	214	214	125	131	931,522	892,346	0.958
Oxbow	Niagara	100	103	103	100	102	578,380	561,534	0.971
Pahsimeroi	Niagara	262	262	264	262	264	1,259,859	1,250,315	0.992
Pahsimeroi	SBT Egg Box	137	143	144	138	144	N/A	N/A	0.951
Total/Average		1808	1848	1855	1569	1595	7,904,031	7,725,138	0.969

Average: 96.9%

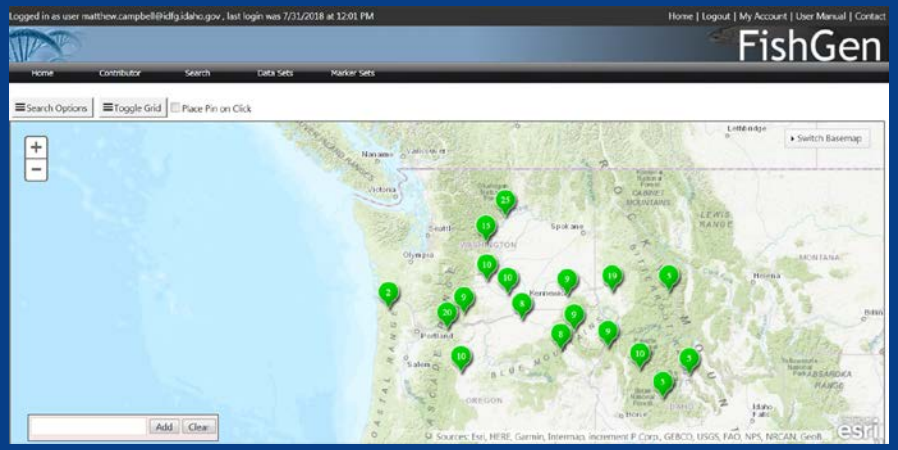
PBT tagging rates at the release group level:

Hatchery Stock	Rearing Stock	Release Site	Mark/Tag	Total Unique Families Genotyped	Total Females Genotyped	Total Females Spawned	Total Males Genotyped	Total Males Spawned	Number of smolts Released	Number of PBT tagged smolts tracked to release group	PBT tagging Rate
DWOR	Meadow Cr.	2013	AD	44	48	48	44	48	159,547	146,251	0.917
DWOR	Meadow Cr.	2013	Adint	27	28	29	28	29	69,403	64,617	0.931
DWOR	Newsome	2013	Adint	34	35	35	34	35	134,353	130,514	0.971
DWOR	Red House	2013	AD	44	50	50	35	39	224,416	197,486	0.880
SFCLW	Meadow Cr.	2013	AD	31	31	31	31	31	107,394	107,394	1.000
SFCLW	Meadow Cr.	2013	Adint	47	47	47	40	40	151,280	151,280	1.000
DWOR	Clear Creek	2013	AD	102	107	109	90	92	360,430	134,555	0.373
DWOR	Dworshak	2013	AD	305	313	314	202	203	1,201,895	918,867	0.765
DWOR	Lolo	2013	Adint	63	63	63	58	58	247,629	247,629	1.000
DWOR	Red House	2013	AD	127	127	127	94	94	418,067	284,500	0.681
EFNAT	East Fork	2013	Adint	11	11	12	13	13	59,209	54,275	0.917
SAW	McNabb Pt	2013	AD	31	32	32	31	32	118,874	115,159	0.969
SAW	Sawtooth	2013	AD	254	254	254	254	254	1,263,084	1,263,084	1.000
DWOR	Pahsimeroi	2013	Adint	46	47	47	41	42	138,195	135,255	0.979
PAH	Colston	2013	AD	16	16	16	16	16	93,986	93,986	1.000
PAH	Little Salmon	2013	AD	41	41	41	41	41	198,548	198,548	1.000
PAH	Red Rock	2013	AD	16	16	16	16	16	94,415	94,415	1.000
PAH	Shoup	2013	AD	20	20	20	20	20	93,544	93,544	1.000
USAL	Little Salmon	2013	AD	79	82	82	52	54	237,997	229,290	0.963
USAL	Squaw Creek	2013	AD	38	39	39	26	27	186,763	181,974	0.974
USAL	YFK 3rd Bridge	2013	AD	57	60	60	34	36	241,504	225,762	0.935
USAL	YFK Ponds	2013	ADint	75	80	80	55	59	265,258	210,296	0.793
OX	Hells Canyon	2013	AD	100	103	103	100	102	578,380	561,534	0.971
PAH	Hells Canyon	2013	AD	8	8	8	8	8	N/A	N/A	1.000
PAH	Little Salmon	2013	AD	102	102	104	104	104	441,206	384,012	0.870
PAH	Pahsimeroi	2013	AD	152	152	153	162	162	818,653	767,869	0.938
PAH	Egg-Box	2013	ADint	137	143	144	138	144	N/A	N/A	0.951
				2007	2055	2064	1767	1799	7,904,032	6,992,098	0.918

Average: 91.8%

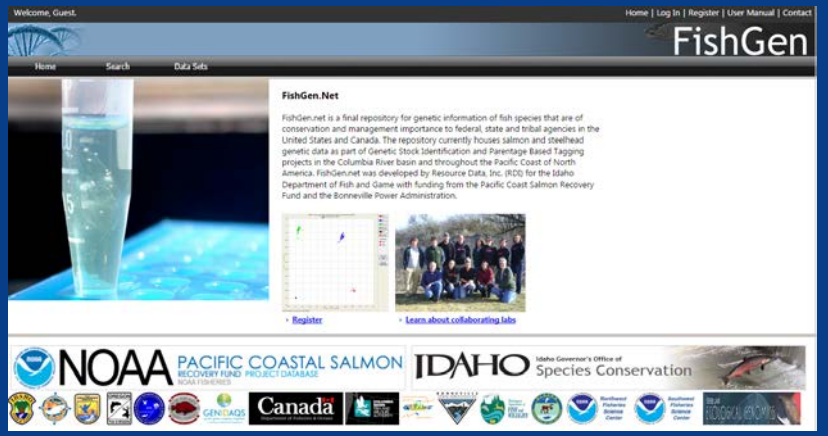
Achievements:

- FishGen



All PBT/GSI baselines available on FishGen

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



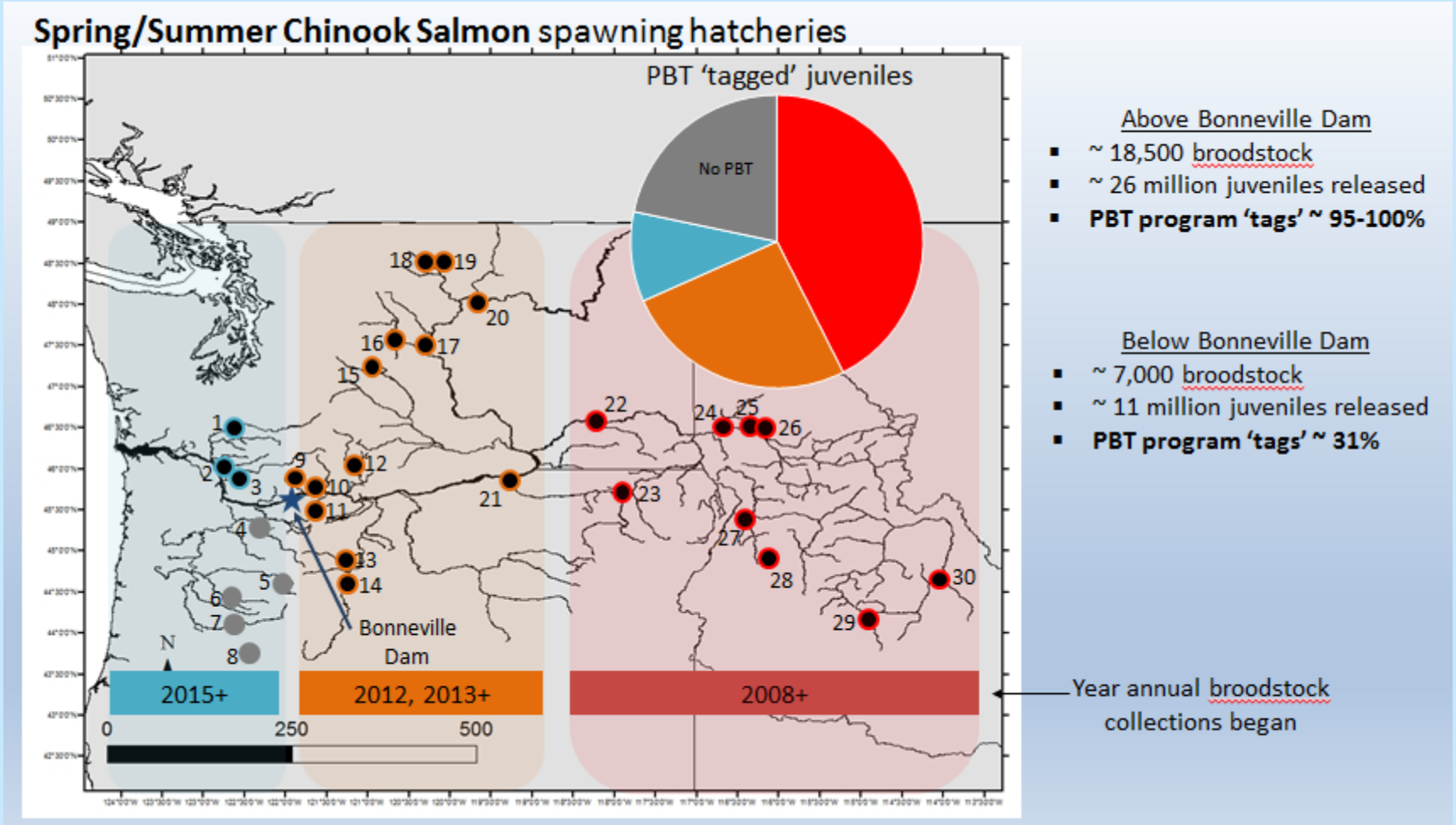
Achievements:

PBT expansion throughout the Columbia River Basin

Dr. Shawn Narum and Maureen Hess

Columbia Inter-Tribal Fish Commission

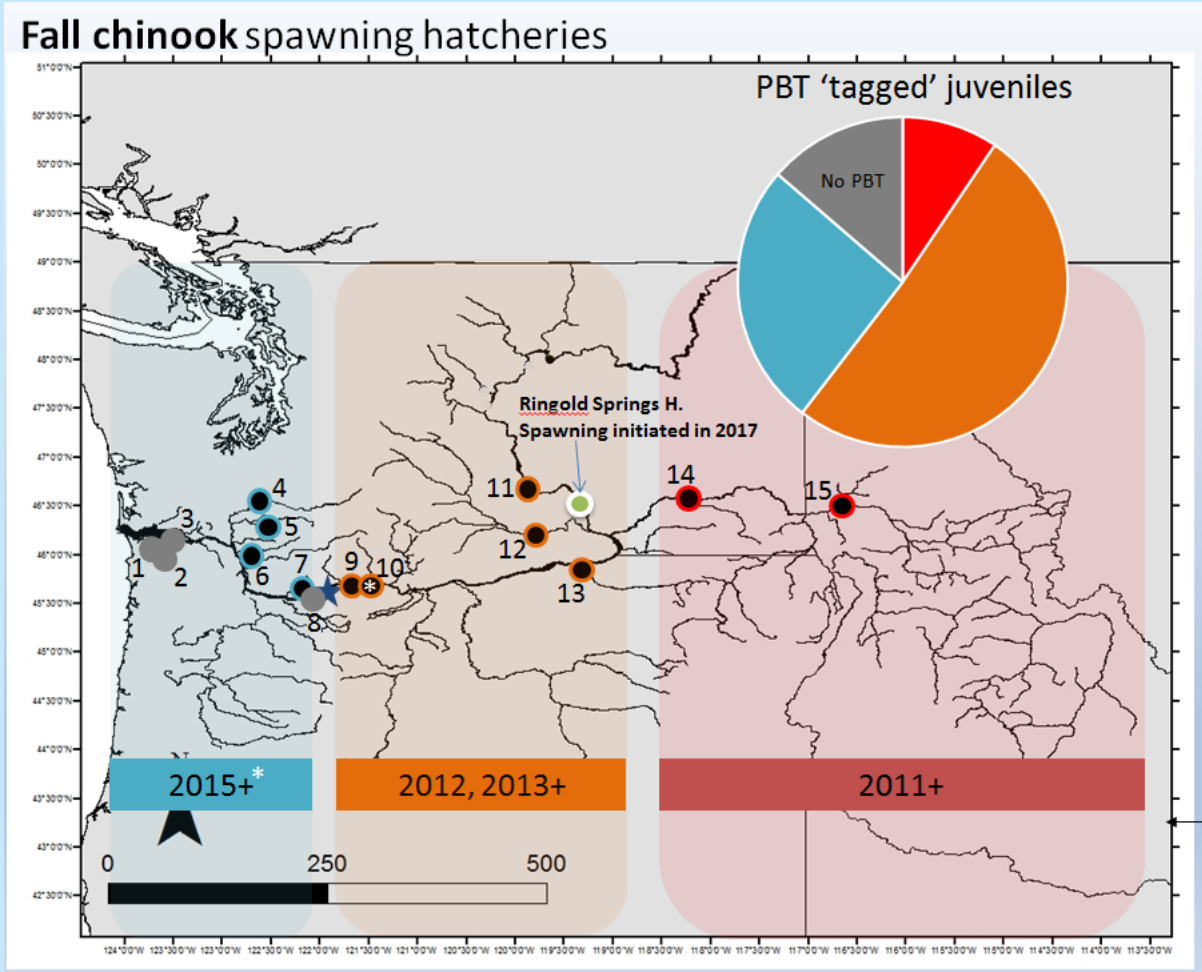
PBT expansion in the Columbia River Basin



Star = Bonneville Dam, Gray = broodstock NOT sampled

% released smolts tagged – estimated from Fish Passage Center, migration year 2015

PBT expansion in the Columbia River Basin



Above Bonneville Dam

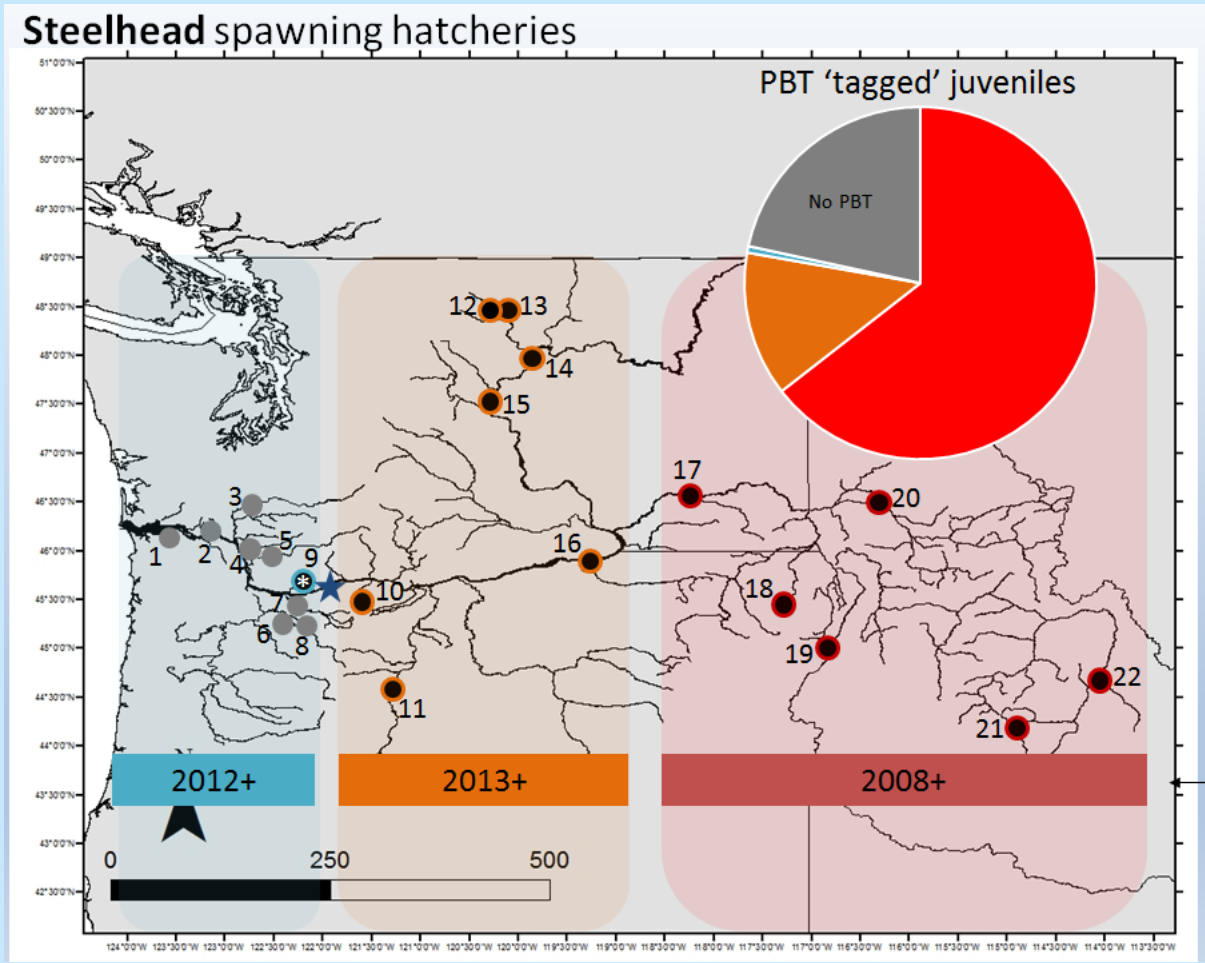
- ~ 21,000 broodstock
- ~ 41 million juveniles released
- **PBT program 'tags' ~ 95-100%**

Below Bonneville Dam

- ~ 14,000 broodstock
- ~ 28 million juveniles released
- **PBT program 'tags' ~ 65%**

Year annual broodstock collections began

PBT expansion in the Columbia River Basin



Above Bonneville Dam

- ~ 7,000 broodstock
- ~ 12 million juveniles released
- **PBT program 'tags' ~ 95-100%**

Below Bonneville Dam

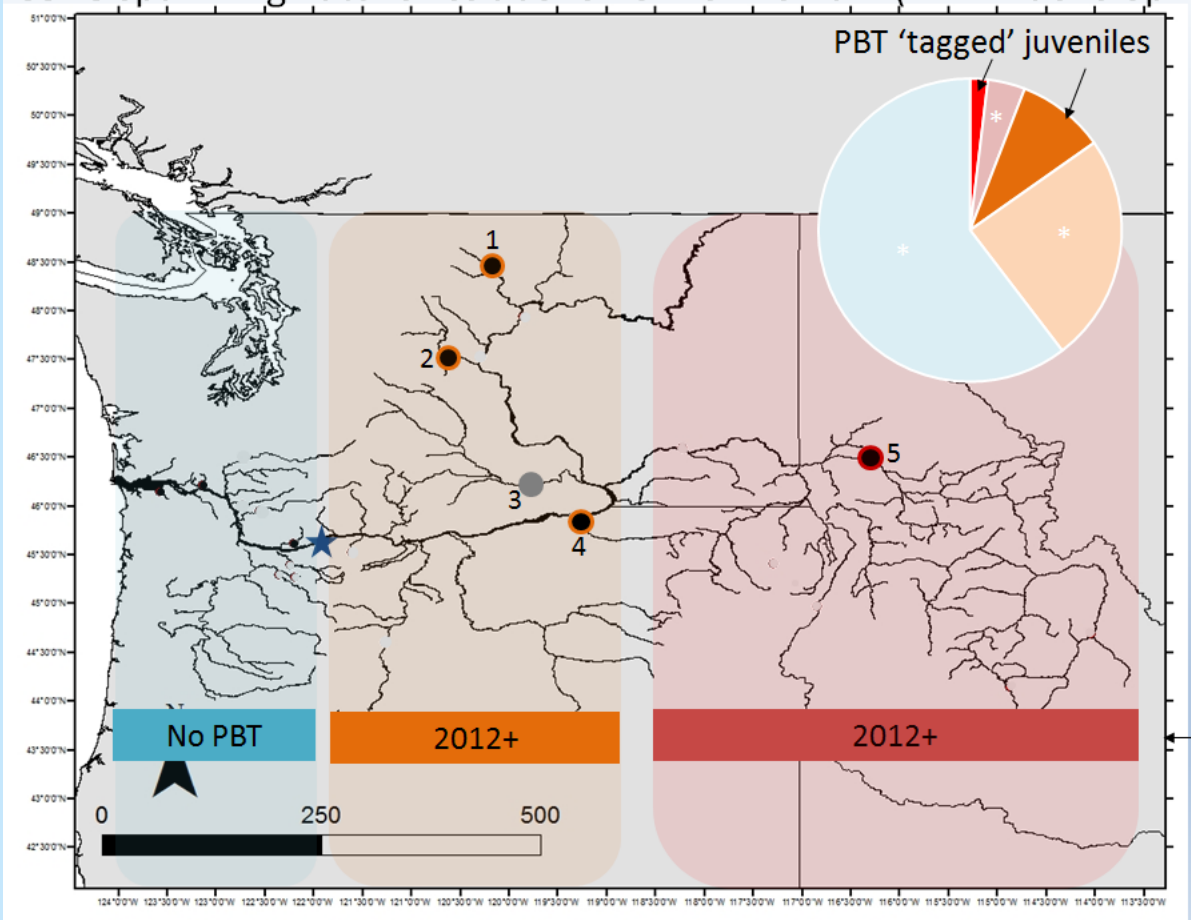
- ~ 3,000 broodstock
- ~ 3 million juveniles released
- **PBT program 'tags' 0%**

Year annual broodstock collections began

* Skamania release above Bonneville

PBT expansion in the Columbia River Basin

Coho spawning hatcheries above Bonneville Dam (PBT in development)



Above Bonneville Dam
- ~ 8 million juveniles released
- **PBT program 'tags' ~ 28%**

Below Bonneville Dam
- ~ 12 million juveniles released
- **PBT program 'tags' 0%**

Year annual broodstock collections began

* Juveniles from Lower Columbia programs (no PBT)

Achievements:

New genetic platforms and techniques have greatly increased power and throughput while decreasing costs

MOLECULAR ECOLOGY RESOURCES
Molecular Ecology Resources (2014) doi: 10.1111/1755-0998.12357

Genotyping-in-Thousands by sequencing (GT-seq): A cost effective SNP genotyping method based on custom amplicon sequencing

NATHAN R. CAMPBELL STEPHANIE A. HARMON and SHAWN R. NARUM
Columbia River Inter-Tribal Fish Commission, 3059F National Fish Hatchery Road, Hagerman, ID 83332,USA

Abstract

Genotyping-in-Thousands by sequencing (GT-seq) is a method that uses next-generation sequencing of multiplexed PCR products to generate genotypes from relatively small panels (50–500) of targeted single-nucleotide polymorphisms (SNPs) for thousands of individuals in a single Illumina HiSeq lane. This method uses only unlabelled oligos and PCR master mix in two thermal cycling steps for amplification of targeted SNP loci. During this process, sequencing adapters and dual barcode sequence tags are incorporated into the amplicons enabling thousands of individuals to be pooled into a single sequencing library. Post sequencing, reads from individual samples are split into individual files using their unique combination of barcode sequences. Genotyping is performed with a simple perl script which counts amplicon-specific sequences for each allele, and allele ratios are used to determine the genotypes. We demonstrate this technique by genotyping 2068 individual steelhead trout (*Oncorhynchus mykiss*) samples with a set of 192 SNP markers in a single library sequenced in a single Illumina HiSeq lane. Genotype data were 99.9% concordant to previously collected TaqMan™ genotypes at the same 192 loci, but call rates were slightly lower with GT-seq (96.4%) relative to Taqman (99.0%). Of the 192 SNPs, 187 were genotyped in ≥90% of the individual samples and only 3 SNPs were genotyped in <70% of samples. This study demonstrates amplicon sequencing with GT-seq greatly reduces the cost of genotyping hundreds of targeted SNPs relative to existing methods by utilizing a simple library preparation method and massive efficiency of scale.

Keywords: amplicon sequencing, genotyping by sequencing, GT-seq, next-generation sequencing, SNP

Received 16 July 2014; revision received 24 November 2014; accepted 26 November 2014

Introduction

Single-nucleotide polymorphism (SNP) markers are used for a variety of research applications in the fields of ecological, conservation and agricultural genetics. This includes population genomics, genomewide association studies (GWAS), parentage analysis, and population identification (Narum *et al*. 2013). Relatively new genotyping techniques using next-generation sequencing (NGS) platforms now make it possible to both identify and genotype thousands to millions of SNPs directly from sequencing data. Methods such as restriction-site-associated DNA sequencing (RAD-seq; Baird *et al*. 2008), RNA sequencing and whole-genome shotgun can all be used for genotyping (Davey *et al*. 2011). The cost per genotype collected using these NGS methods is low due to the large number of SNP genotypes that can be generated. Despite the ever decreasing costs of NGS, these genotyping-by-sequencing (GBS) methods remain less cost effective than alternative 5′ exonuclease methods for applications that require only a few hundred SNP markers.

Historically, SNP markers were first identified through sequencing and then selected SNPs were subsequently converted into allele detection assays such as the 5′ exonuclease assay [examples include TaqMan™ (Life Technologies), KASPar (KBiosciences) and SNP type (Fluidigm)] for genotyping (Seeb *et al*. 2011). High-quality genotypes could then be produced for large numbers of individuals from DNA extracts of varying quality and quantity using such PCR-based genotyping methods (e.g. Campbell & Narum 2008). All 5′ exonuclease methods require a unique reaction for each combination of DNA sample and assay (locus-specific primers mixed with allele-specific fluorescent probes) to produce each SNP genotype. Therefore, the cost per SNP genotype is relatively high compared to high-density array genotyping (examples: Affymetrix SNP arrays, Illumina genotyping arrays). However, when the number of SNP loci to

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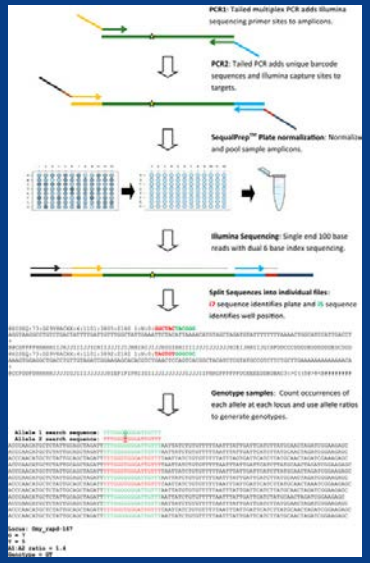
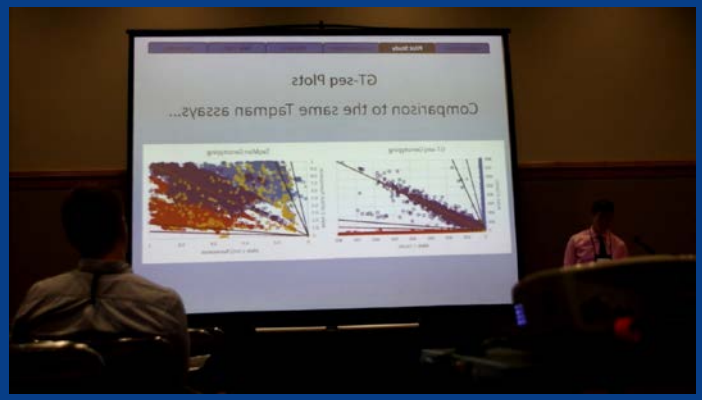
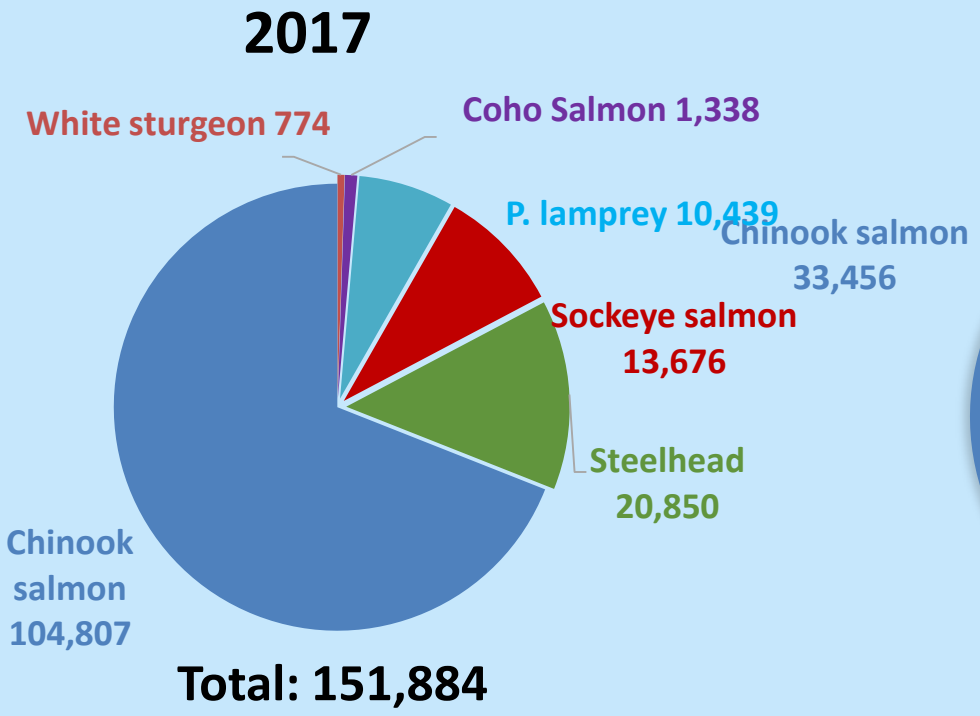




CRITFC!

Achievements:

High Genotyping Capacity



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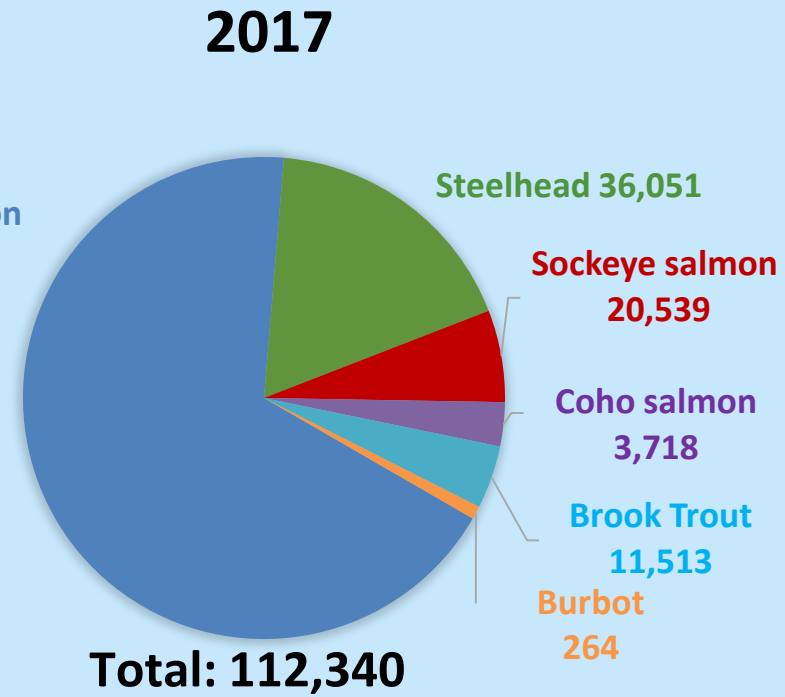
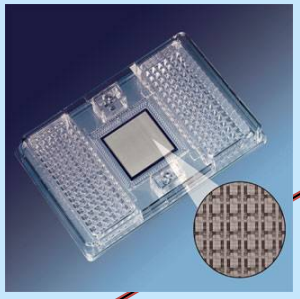


IDFG

Improved Cost Efficiency

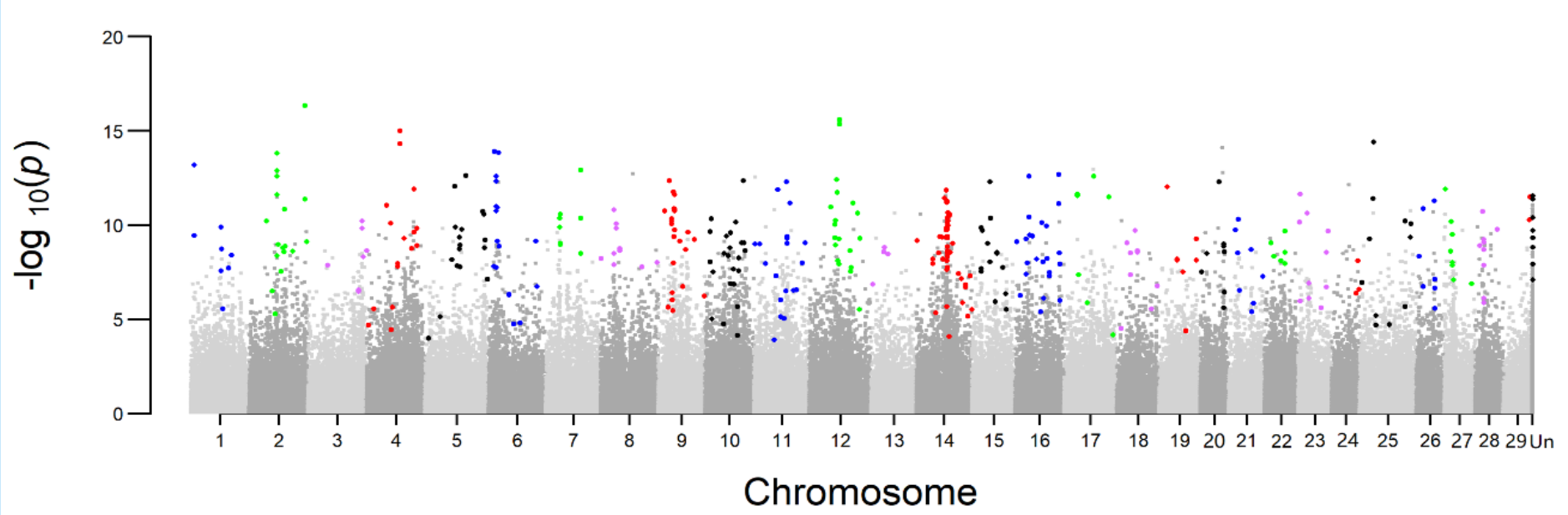
GT-seq – Genotyping-in-thousands by sequencing



Campbell and Narum 2015, Mol. Ecol. Res

- **Powerful scans across the genome allows the identification of highly informative snps (often linked to traits under selection).**

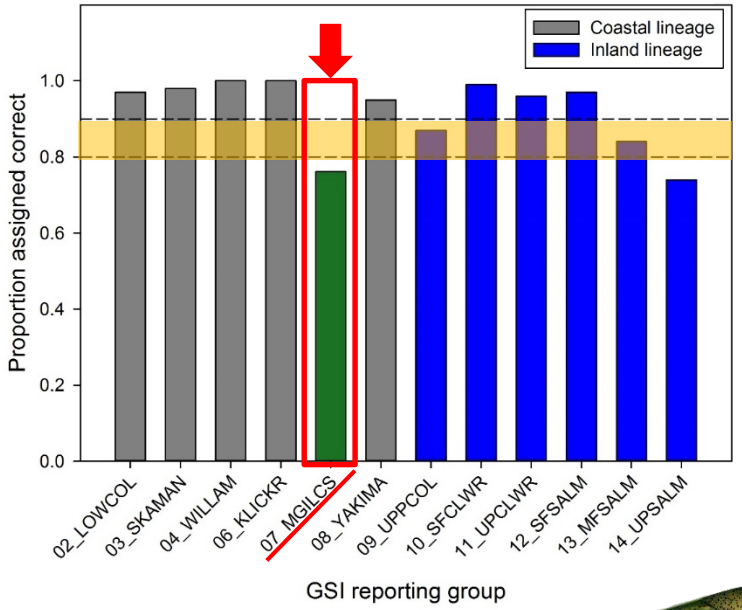
Allows identification of more powerful markers for GSI



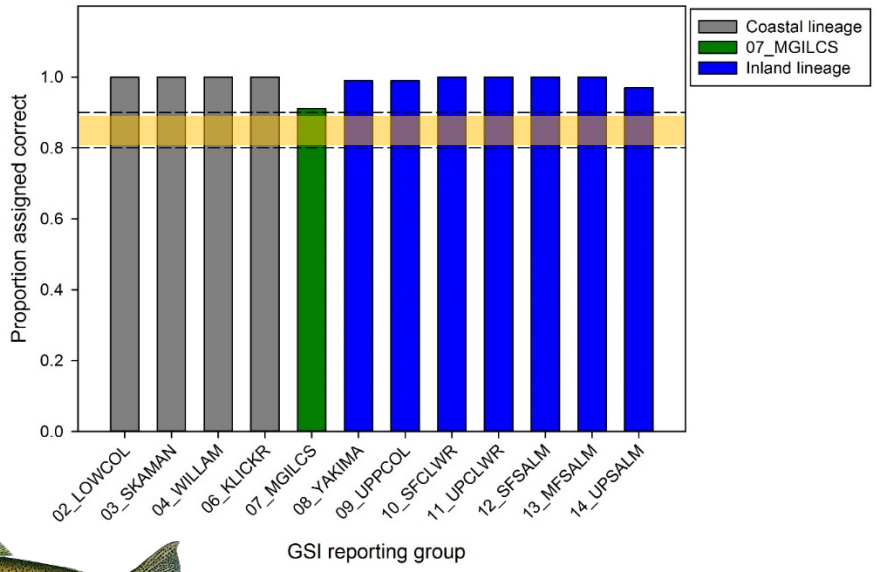
Chen et al. Narum (2018)

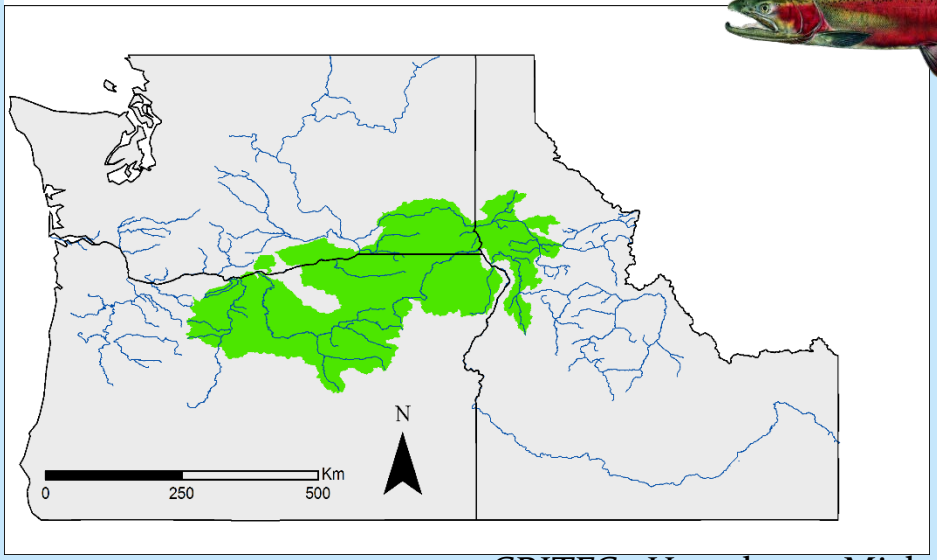
Accuracy of Steelhead GSI

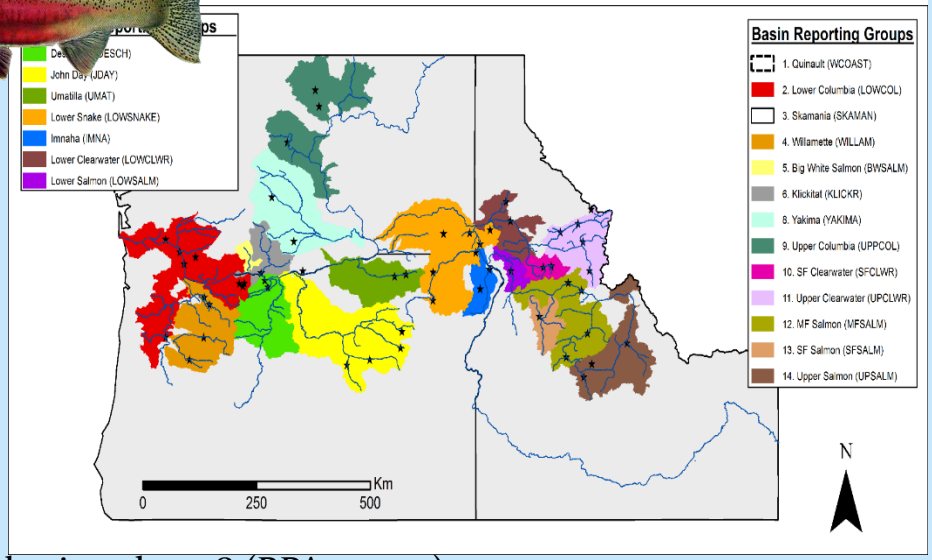
Difficult stocks to resolve



Additional outliers improve accuracy







CRITFC: Hasselman, Micheletti et al. 2018 (BPA report)

PBT programs are not limited to the Columbia River Basin:

California

PBT developed by Carlos Garza & Eric Anderson NOAA

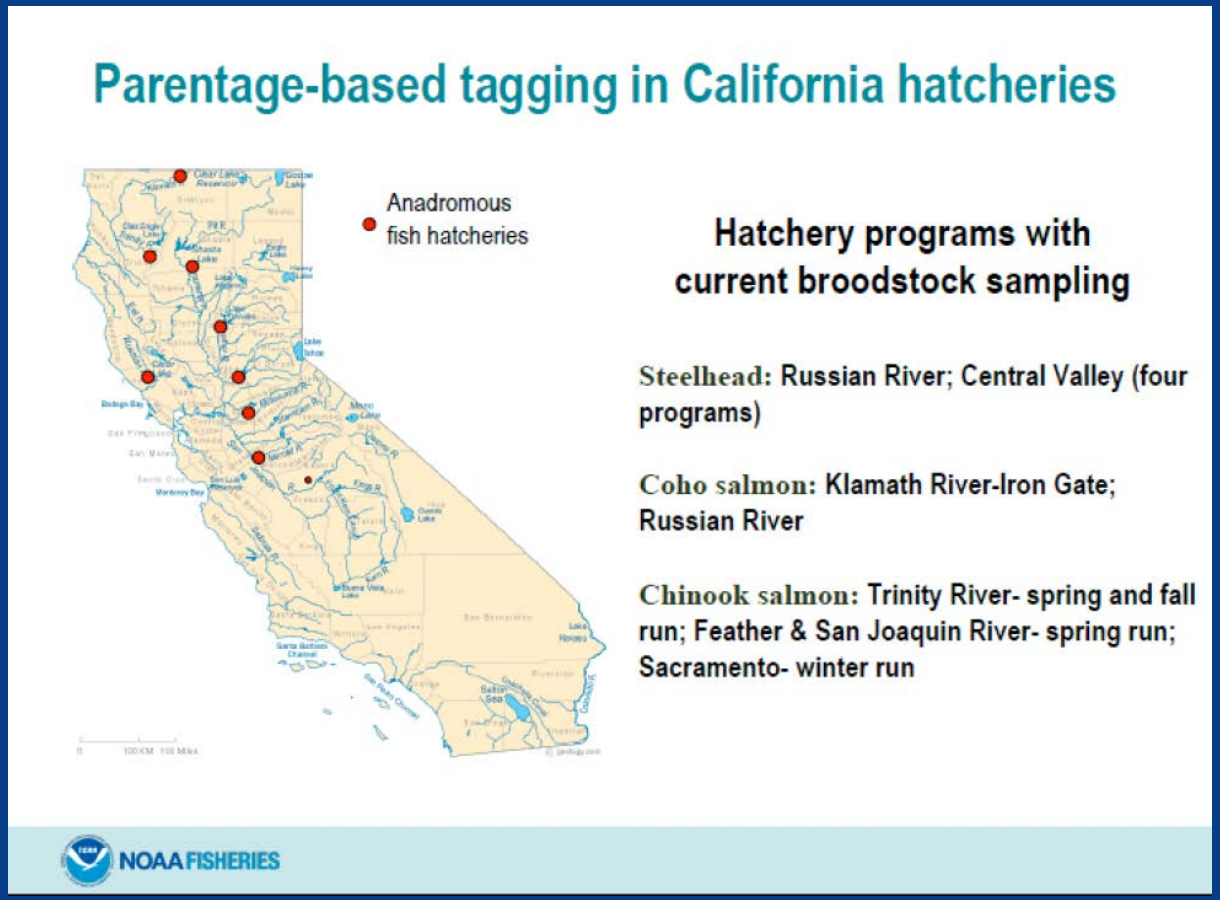
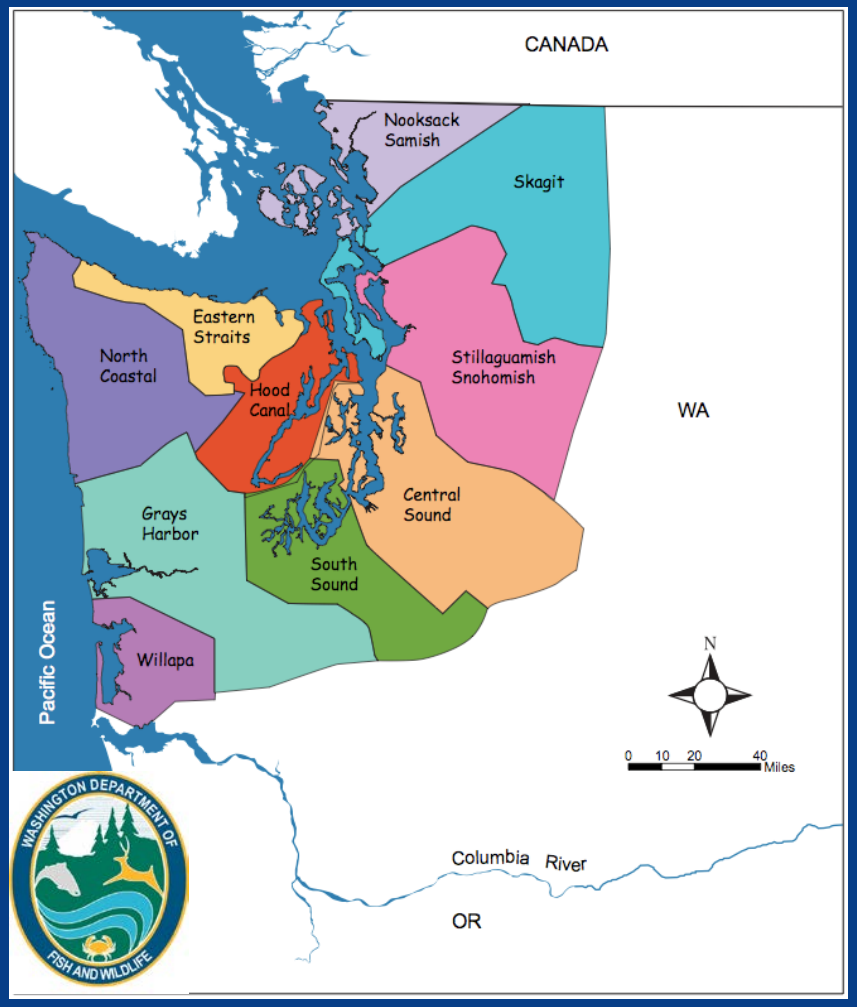


Image taken from slide prepared by Carlos Garza. Full presentation available: https://swfsc.noaa.gov/uploadedFiles/Events/Meetings/Fish_2015/8_1_Garza.pdf

PBT programs are not limited to the Columbia River Basin:

Washington Coast-WDFW



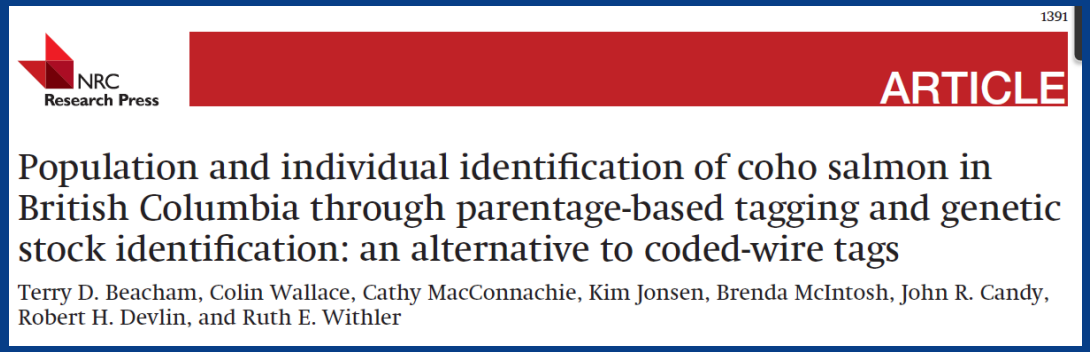
- WDFW sampling started in 2013
- 14 hatcheries
- Samples collected, but not analyzed yet

PBT programs are not limited to the Columbia River Basin:

British Columbia-DFO

Chinook Salmon:
- Sampling started in 2014
- 390 SNP loci
- 10 hatcheries

Coho Salmon:
- Sampling started in 2012
- All hatchery populations sampled in 2014 and 2015
- ~20,000 samples
- 490 SNP loci


1391

NRC Research Press

ARTICLE

Population and individual identification of coho salmon in British Columbia through parentage-based tagging and genetic stock identification: an alternative to coded-wire tags

Terry D. Beacham, Colin Wallace, Cathy MacConnachie, Kim Jonsen, Brenda McIntosh, John R. Candy, Robert H. Devlin, and Ruth E. Withler

- ✓ The overall accuracy of assignment for 1,939 coho salmon to the correct population was 100%, and to correct brood year within population was also 100%.
- ✓ With 23 regions defined by the coded-wire tag (CWT) program, mean regional assignment accuracy of individuals via GSI was 98.4% over all 23 regions.
- ✓ **Demonstrated that a PBT–GSI system of identification could provide an alternative to CWT program for assessment and management of Canadian-origin coho salmon.**

Other Recommendations:

Pacific Salmon Commission Chinook Technical Committee 2015:

- A reassessment of the relative costs and merits of the PBT-based or hybrid PBT/CWT systems should be undertaken again in five years or possibly sooner if technological changes or significant reductions in cost warrant it. http://www.psmfc.org/wp-content/uploads/2015/08/CSC-Complete-PBT-Review.11August2015.pdf

Northwest Power and Conservation Council Tagging Forum

- Funding should continue for developing and evaluating GSI and PBT throughout the basin and be re-evaluated in 5-10 years. https://www.nwcouncil.org/sites/default/files/Fish-Tagging-Forum-Council-Decision-letter-August-2013-4-.pdf

Other Recommendations:

Senate Appropriations Committee 2015:

The Committee supports **continued research and testing of genetic stock identification [GSI] management techniques** in the Pacific salmon fishery to meet the dual purpose of protecting weak and the Endangered Species Act listed stocks, while allowing for sustainable commercial and recreational access to healthy stocks in the wild. **NMFS shall continue to support GSI research, including the collection, analysis, and testing of methods that rely on genetics-based data to identify and track the location of federally protected stocks in the wild.**

PSMFC Resolution- 2012

- ..Supports further efforts to fund necessary work to make these data available for salmon management, as long as such funds done' come at the expense of current federal fisheries research and management.

Other Recommendations:

Technical Report number 23, Vancouver British Columbia Pacific Salmon Commission 2008

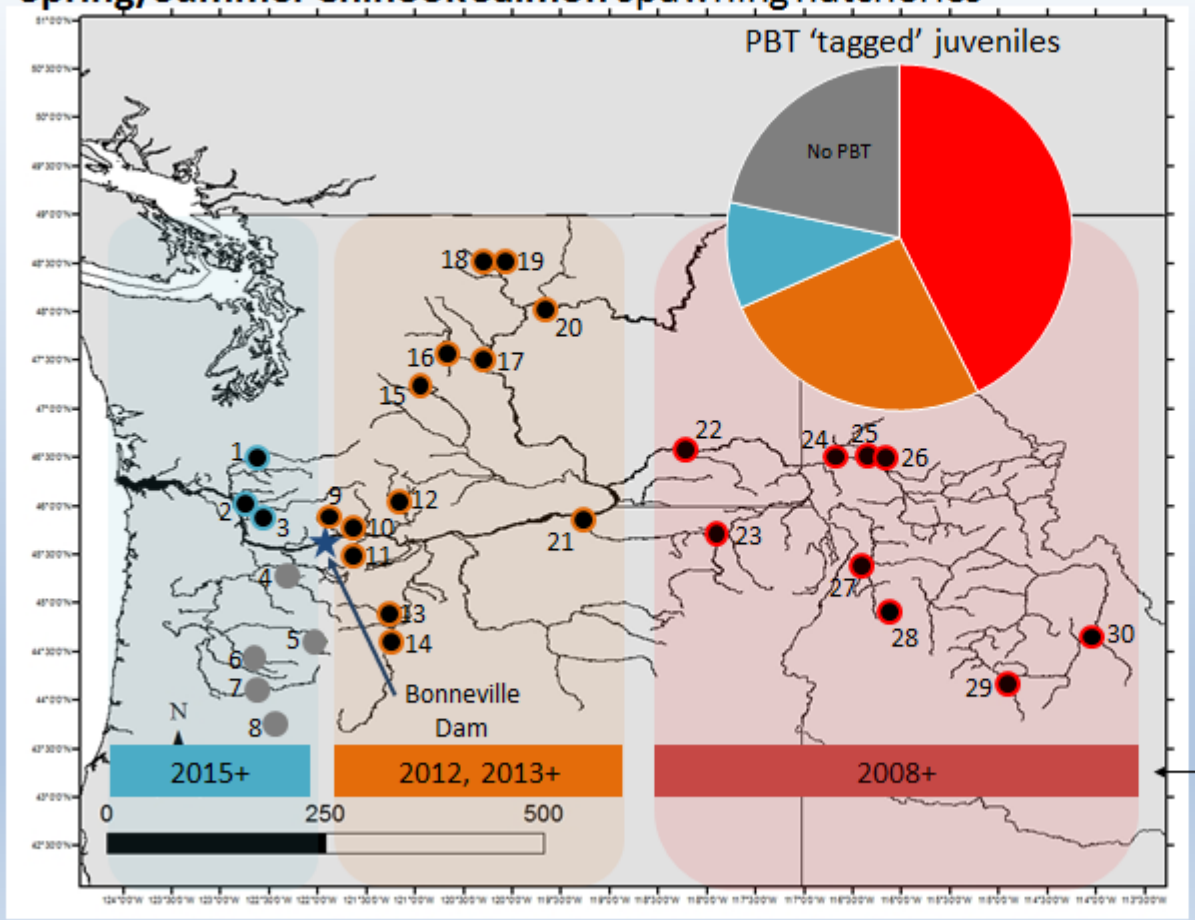
For various historical, logistical, and financial reasons, the U.S. West Coast fishery harvest management community has generally resisted genetic methods

Future:

- **Genetic Technology works- management and ancillary benefits**
- **IDFG and CRITFC committed to using this technology throughout the Columbia/Snake Rivers**

- **Broader Adoption?**
- **Expansion relies on funding, design and development of database system similar to RMIS/CWT data**
  - ✓ **Coast-wide sampling system and design**
  - ✓ **Databases for data compilation, validation, managing releases, recoveries, and dissemination of data and reports**
  - ✓ **Staff and committees to oversee program**

Spring/Summer Chinook Salmon spawning hatcheries



Above Bonneville Dam

- ~ 18,500 broodstock
- ~ 26 million juveniles released
- **PBT program 'tags' ~ 95-100%**

Below Bonneville Dam

- ~ 7,000 broodstock
- ~ 11 million juveniles released
- **PBT program 'tags' ~ 31%**

Year annual broodstock collections began