## Genetic Evaluation of Fall Chinook Salmon Carcasses from the White Salmon River, 2013-2021

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## Background

- ESA-listed tule fall Chinook salmon population in the White Salmon River
- Upriver bright (URB) Chinook salmon straying into White Salmon River
- Spawn timing
- Tule = Sept-Oct
- URB = late Oct-Nov



## Background

- URB production began at Little White Salmon National Fish Hatchery (LWS NFH) in 1982
- Production goals increased in 2009
- 4.4 million URB juveniles released annually 2012 to 2021 from LWS and Willard (WI) NFHs
- Past genetic studies have quantified hybridization with ESAlisted tule population



## Background: Previous Studies

- Mostly focused on outmigrating juveniles
- Smith \& Engle 2011
- $4.3 \%-15 \%=$ Tule $x$ URB hybrids in 2006-2008
- Smith et al. 2021
- $17 \%-32 \%$ fall run juveniles = hybrids in 2017-2019
- $8.4 \%$ of broodstock at LWS NFH = hybrids in 2015-2018



## Study Goals

- Evaluate the potential impact of hybrids used as broodstock at LWS and WI NFHs on the incidence of hatchery-origin strays.
- Estimate the proportion of hybrids among spawners for the URB and native tule fall Chinook populations in the White Salmon River.
- Use parentage-based tagging to determine the percent of carcasses that are misclassified as wild-origin spawners due to the non-detection of hatchery markings.
- Quantify proportion of misidentified fish used as broodstock at LWS and Spring Creek (SC) NFHs.


## Sampling: Carcasses

- 967 individuals
- Surveys by WDFW
- GTseq Panel
- 340 loci after filtering
- Sample size variable by year
- URB not targeted 2014-2017

| Year | Tule | URB |
| :---: | :---: | :---: |
| 2013 | 140 | 141 |
| 2014 | 190 | 1 |
| 2015 | 127 | - |
| 2016 | 23 | - |
| 2017 | 40 | - |
| 2018 | 13 | 70 |
| 2019 | 24 | 52 |
| 2020 | 24 | 31 |
| 2021 | 41 | 50 |
| Total | $\mathbf{6 2 2}$ | $\mathbf{3 4 5}$ |

## Sampling: Broodstock

Little White Salmon NFH

| Year | $\mathbf{N}$ |
| :---: | :---: |
| 2015 | 8,048 |
| 2016 | 7,313 |
| 2017 | 5,364 |
| 2018 | 1,730 |
| 2019 | 6,209 |
| 2020 | 4,310 |
| 2021 | 8,262 |

Spring Creek NFH

| Year | $\mathbf{N}$ |
| :---: | :---: |
| 2015 | 5,553 |
| 2016 | 4,651 |
| 2017 | 4,063 |
| 2018 | 6,252 |
| 2019 | 4,927 |
| 2020 | 5,450 |
| 2021 | 6,048 |

Genotyped by CRITFC - 257 GTseq loci

## Genetic Methods

- Identify hybrids in NewHybrids (carcasses) or Snapclust (broodstock)
- All sample years
- Hybrid classes:
- F1
- F2
- Tule backcross
- URB backcross
- Parental assignment for carcasses using SNPPIT
- Sample years 2018 to 2021
- Identify hatchery-origin spawners


## Parentage-based Tagging

- Genotype all hatchery broodstock

Wild

Hatchery

- Genotype returning fish (carcasses)
- Compare genotypes to identify hatcheryorigin individuals



## Results: Hybrid Proportion by Year (Carcasses)

- Lowest proportion of hybrids:
- 18.1\% in 2018
- Highest proportion of hybrids:
- 45.7\% in 2015
- Overall: 31.1\% per year



## Results: Hybrid Proportion by Year (Carcasses)

Tule


Upriver Bright


## Results: Ancestry Class by Collection Date



## Results: Ancestry of Hatchery Broodstock

8.7\% of broodstock at LWS NFH = hybrids


Ancestry Class

Tule

- F1

Tule Bx
URB Bx
1.8\% of broodstock at SC NFH = hybrids

## Results: Hatchery Parental Assignment

- 64 total hatchery-origin fish
- 25 marked (39.1\%)
- 39 unmarked (60.9\%)
- Hatchery markings
- Adipose clip
- Coded wire tag (CWT)
- 'Hatchery' or 'Wild' assignment
= current generation only

Genetic ID

|  |  | Hatchery <br> Assigned | Unassigned |
| :---: | :---: | :---: | :---: |
| Field ID | Hatchery Origin | 20 | 5 |
|  | Wild Origin | 39 | 241 |

## Results: Hatchery Parental Assignment for LWS NFH

| Year | Samples | \%Marked | \%Unmarked | \%Hatchery |
| :---: | :---: | :---: | :---: | :---: |
| $\mathbf{2 0 1 8}$ | 70 | $11.4 \%$ | $11.4 \%$ | $22.9 \%$ |
| $\mathbf{2 0 1 9}$ | 52 | $5.8 \%$ | $30.8 \%$ | $36.5 \%$ |
| $\mathbf{2 0 2 0}$ | 31 | $3.2 \%$ | $19.4 \%$ | $22.6 \%$ |
| $\mathbf{2 0 2 1}$ | 50 | $24.0 \%$ | $14.0 \%$ | $38.0 \%$ |
| Overall | 203 | $11.8 \%$ | $18.2 \%$ | $30.1 \%$ |

- Most hatchery strays were unmarked
- Implications for URB spawner estimates in the White Salmon River?


## Results: Ancestry of Hatchery-origin Carcasses

Genetic ID

|  | Tule | URB | F1 | F2 | Tule <br> Bx | URB <br> Bx | Total |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Tule | 1 | - | - | - | 1 | 1 | 3 |
|  | URB | - | 56 | 1 | - | - | 4 | 61 |
|  | Total | 1 | 56 | 1 | 0 | 1 | 5 | 64 |

- $10.9 \%$ of all returning hatchery fish were hybrids
- Seven total F1 hybrids detected 2018-2021; just one originated from a hatchery


## Results: Hatchery vs. Wild-origin Hybrids

| Run | Wild Origin |  |  | Hatchery Origin |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Samples | Hybrids | \%Hybrid | Samples | Hybrids | \%Hybrid |
| Tule | 99 | 42 | $42.4 \%$ | 3 | 2 | $66.7 \%$ |
| URB | 142 | 31 | $21.8 \%$ | 61 | 5 | $8.2 \%$ |

- More wild-origin hybrids than hatchery-origin
- Hatchery-origin hybrids not showing elevated stray rate
- URB Strays $=8.2 \%$ hybrids
- URB Broodstock $=8.4 \%$ hybrids (Smith et al. 2021)


## Conclusions

- Hatchery-origin hybrids are not straying to the White Salmon River at a greater rate than non-hybrids.
- More wild-origin hybrid spawners than hatchery-origin.
- Expected to yield continued reproduction of wild-origin hybrids.
- More hatchery fish are straying to the White Salmon River than previously detected.


## Acknowledgements

- CRITFC
- Shawn Narum
- Jon Hess
- Jeff Stephenson

- WDFW
- Elise Olk
- Kari Dammerman
- AFTC
- Jennifer Von Bargen
- Funding
- Army Corps of Engineers under John Day Mitigation


The findings and conclusions in this presentation are those of the authors and do not necessarily represent the views of the U.S. Fish and Wildlife Service.

## Questions?

- Scan QR code to access our report
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