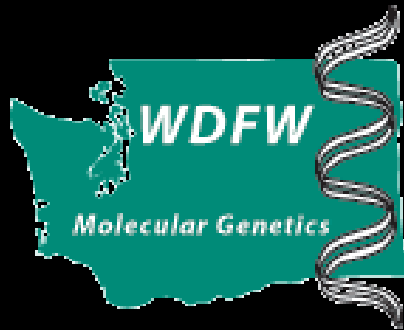


# Genetic stock identification of Chinook salmon in the Yakima River basin and population-of-origin assignments for Chinook smolts collected at Chandler trap

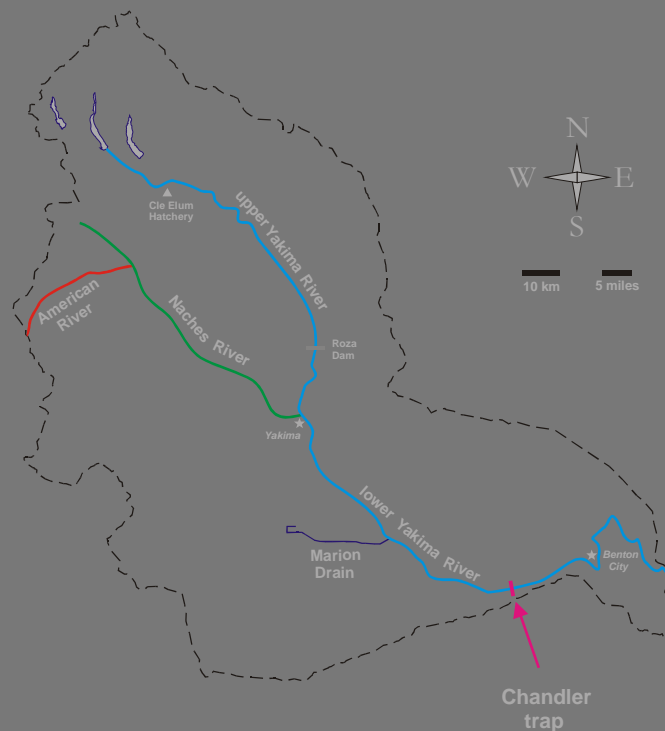
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# Introduction and Background

- Joint project between WDFW (WA Dept. of Fish and Wildlife) and YN (Yakama Nation); microsatellite analyses from 2000 - 2007
- Three spring stocks - American R., Naches R., upper Yakima R.
- Two fall stocks - Marion Drain and lower Yakima R.



# Introduction and Background

- The counts of smolts outmigrating at Chandler Trap are used to determine total passage of smolts at Prosser Dam
- Count and Passage data for smolts provided by Yakama Nation staff (Dave Lind)
- Genetic samples were taken by Yakama Nation staff (Mark Johnston) from the Chinook smolts that go through the diversion channel and are counted
- WDFW MGL calculate a proportional number of smolts to analyze

# Introduction and Background

- A microsatellite DNA baseline was developed using samples from each of the five representative populations
- A statistical evaluation of the baseline collections was conducted to determine the relationship of those five populations
- A population-of-origin analysis was conducted using five time strata to determine stock composition of smolts outmigrating past Chandler Trap
- Stock abundance can then be evaluated using the percentages from the population-of-origin analysis

## Collections

- **Baseline** – Twenty-one collections (collected between 1989 and 2007) were sampled from spawning areas representing each of the five populations (there were no new baseline collections added in 2008)
- **Marion Drain** – Samples were collected in 2007 to determine if Chinook in Marion Drain are genetically distinct to the lower Yakima R. or if they are now indistinguishable from the lower Yakima R.
- **Known-origin** – Samples were collected from the Naches R. and upper Yakima R. in 2006 & 2007 to determine the ability of the baseline to assign individuals to the correct population-of-origin
- **Unknown-origin smolts** – Smolt samples were collected at Chandler trap from January – July, 2007 for genetic analysis (proportional of the total number of smolts outmigrating)

# Baseline Collections

Collection Source	Collection Code	N =	Collection Source	Collection Code	N =
American R. SP	89AG	80	Marion Drain F	89BX	100
	91DQ	102		92FQ	92
	93DO	18		93DY	8
	03EH	100		05LU	65
		<u>300</u>		07HP	<u>27</u>
				292	
Naches R. SP	89AC	76	low Yakima R. F	90DF	109
	89AI	26		93DW	82
	93DQ	50		98FB	61
	93DR	32			<u>61</u>
				252	
Lit Naches R. SP	04BI	42			
	04EM	56			
		<u>282</u>			
up Yakima R. SP	92DN	24			
	97DA	123			
	03GO	99			
		<u>246</u>			

# Laboratory Methods

- DNA was extracted from fin tissue
- PCR amplification was performed using 11 microsatellite loci
- Amplified products were run through an ABI-3730 DNA-Analyzer
- Electropherograms were scored using GENEMAPPER software v.3.7



# Analyses of the baseline collections in 2007

- Tests of population structure and variation - genotypic differentiation,  $F_{ST}$ , linkage disequilibrium,  $F_{IS}$ , and allelic richness.
- Jackknife Analysis - Analysis to remove each individual in the baseline collections and assign it back to the most likely population-of-origin. This procedure tests each baseline collection to determine how well individuals will assign to that population based on the allele frequency differences that exist among populations.
- Neighbor-joining tree - Cavalli-Sforza and Edwards chord distance



# Analysis of the Marion Drain collections

- Baselines used for analysis –

Baseline for analysis of Marion Drain included the 1989 collection from Marion Drain and the 1990 collection from the lower Yakima River

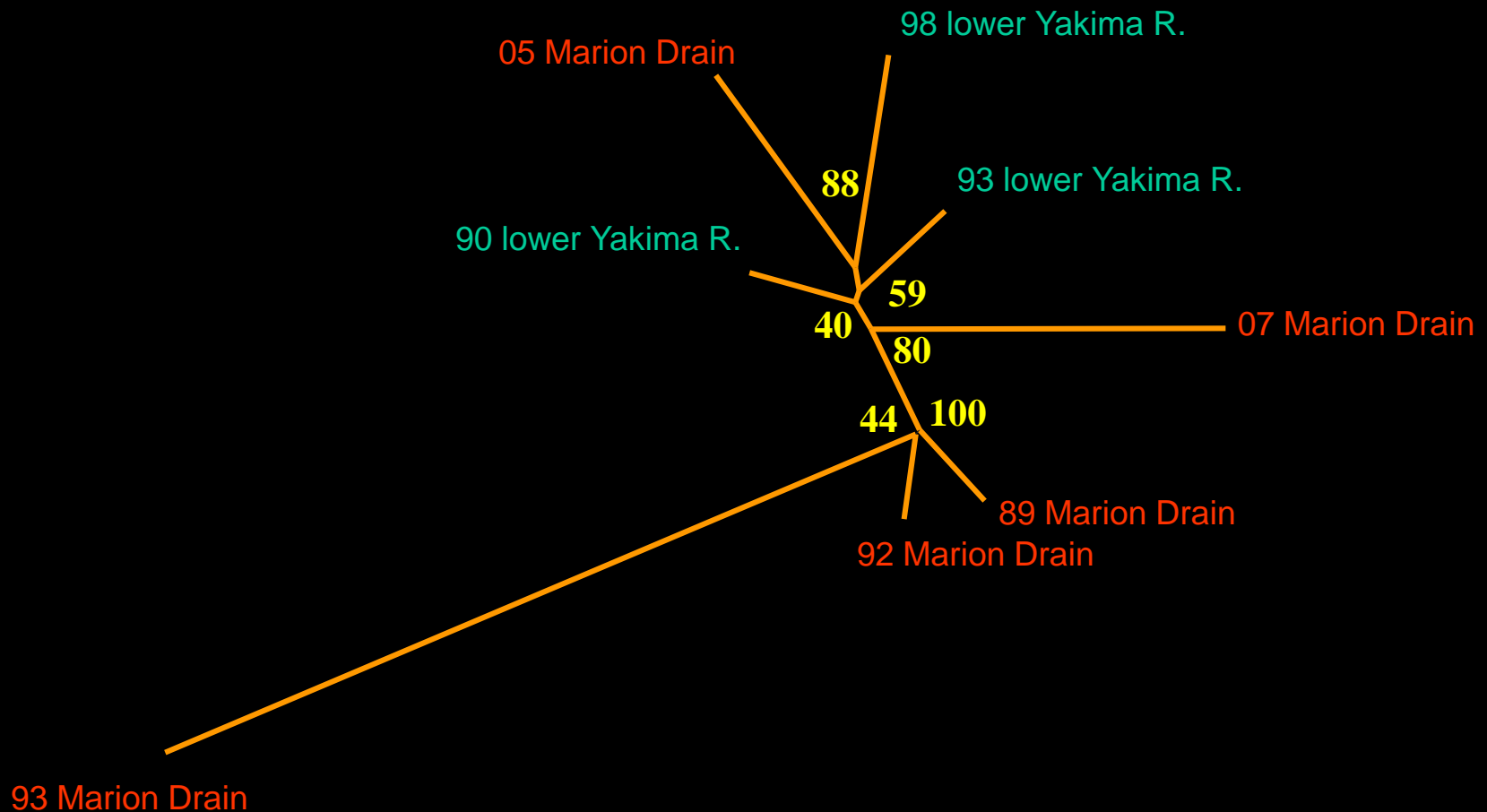
- Mixture analysis –

Analysis to assign a population-of-origin to individual of unknown-origin. Allele frequency of unknown individual is compared with all populations in the baseline to determine the population with the most similar allele frequency. A likelihood ratio is calculated for each individual that is assigned a population. The higher the ratio the more likely the individual is from that assigned population.

# Population-of-origin Assignments – Marion Drain

	1992 n = 72	1993 n = 6	2005 n = 29	2007 n = 15
Marion Drain	55 (76.4%)	6 (100.0%)	3 (10.3%)	6 (40.0%)
lower Yakima R.	17 (23.6%)	0 ( 0.0%)	26 (89.7%)	9 (60.0%)

Neighbor-joining tree using Cavalli-Sforza and Edwards (1967) chord distance. Bootstrap values are shown for clusters separating the collections from Marion Drain and the lower Yakima River



# Analysis of the known-origin collections

- Baselines used for analysis –

Baseline for the analysis of the known-origin collections included 19 collections (without the 2005 and 2007 Marion Drain collections)

- Mixture analysis –

Analysis to assign a population-of-origin to individual of unknown-origin. Allele frequency of unknown individual is compared with all populations in the baseline to determine the population with the most similar allele frequency. A likelihood ratio is calculated for each individual that is assigned a population. The higher the ratio the more likely the individual is from that assigned population.

# Population-of-origin Assignments – Known-origin

2006 & 2007  
n = 25 Total

Naches R.

14 assigned at > 90% posterior probability  
All 14 assigned to Naches R.

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2007  
n = 35 Total

upper Yakima R.

32 assigned at > 90% posterior probability  
All 32 assigned to upper Yakima R.

## Proportionalization of unknown-origin smolts

- 159,252 – Total Estimated Chinook smolt Passage past Prosser
- 17,965 – Total count (including hatchery and wild Chinook)
- 2,361 – Genetic samples taken
  - 40 – January (samples taken on 5 days)
  - 87 – March (samples taken on 10 days)
  - 843 – April
  - 1,025 – May
  - 366 – June/July

(1.48% of estimated passage; 13.14% of Total Count)
- 1,500 – Genetic Samples Analyzed

# Proportionalization of unknown-origin smolts

**Date of smolt outmigration**

**Estimated smolt passage for each date**

**Total number of genetic samples collected for each date**

**Percentage of estimated smolt passage for each date**

**Percentage of passage X Total Number of Genetic Samples Collected**

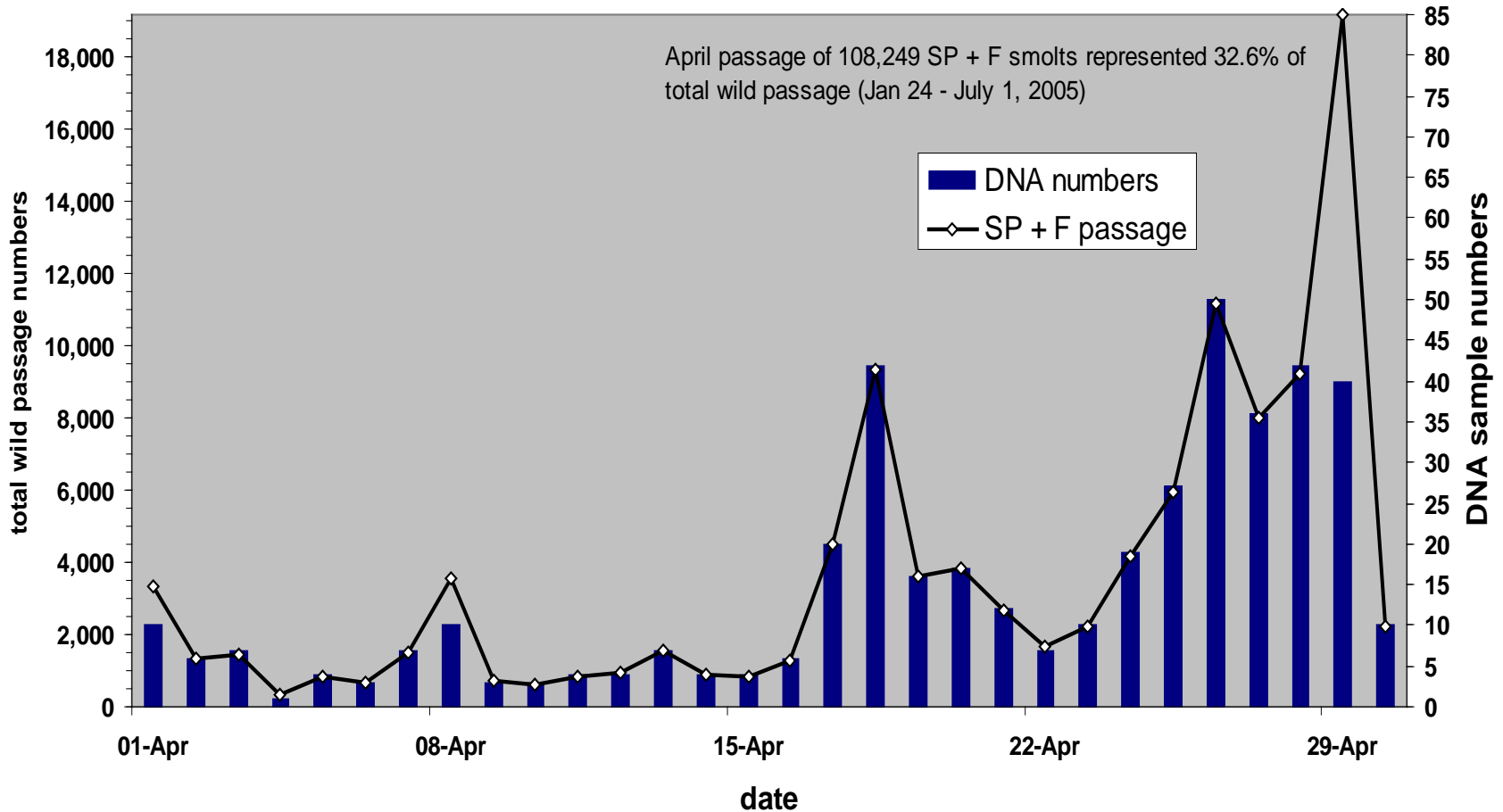
**Total number of genetic samples collected X Total number of samples to be Analyzed  
Percentage of passage X Total Number of Genetic Samples Collected**

**In the end**

**The number of samples to be analyzed per day up to a total of 1,500 samples**

# Proportional Subsampling of Smolts for the April Stratum

April 2005 stratum (N = 431 analyzed; 1,005 sampled)





# Analysis of the unknown-origin smolt collections

- Baseline used for analysis –

Baseline for the analysis of the smolt collections included 19 collections (without the 2005 and 2007 Marion Drain collections)

- Mixture analysis –

Analysis to assign a population-of-origin to individual of unknown-origin. Allele frequency of unknown individual is compared with all populations in the baseline to determine the population with the most similar allele frequency. A likelihood ratio is calculated for each individual that is assigned a population. The higher the ratio the more likely the individual is from that assigned population.

# Population-of-origin Assignments – Smolts 2007

	American SP	Naches SP	up Yak R. SP	Marion Drain F	low Yak R. F
January	9.1%	18.2%	72.7%	0.0%	0.0%
March	14.5%	32.3%	53.2%	0.0%	0.0%
April	6.8%	24.7%	68.4%	0.0%	0.2%
May	13.5%	24.0%	43.1%	0.7%	18.7%
June – July	0.6%	0.6%	10.3%	0.6%	87.9%

# Population-of-origin Assignments – Smolts 2004 - 2007

		American SP SP	Naches SP SP	up Yak SP SP	Marion Drain F Drain F	low Yak R. F
2004	Jan - Feb	5.2%	31.6%	62.8%	0.0%	0.4%
	March	3.9%	25.0%	71.0%	0.0%	0.0%
	April	18.9%	38.0%	43.1%	0.0%	0.0%
	May	19.5%	19.6%	16.9%	9.2%	34.8%
	June – July	3.6%	2.5%	5.7%	10.9%	77.3%
2005	Jan - Feb	20.2%	33.9%	46.0%	0.0%	0.0%
	March	20.2%	1.9%	77.9%	0.0%	0.0%
	April	23.6%	28.6%	28.5%	7.5%	11.9%
	May	3.4%	2.6%	4.7%	22.8%	66.4%
	June – July	0.0%	3.5%	22.0%	12.7%	61.8%
2006	Jan - Feb	5.3%	39.7%	54.4%	0.0%	0.6%
	March	0.0%	22.3%	77.7%	0.0%	0.0%
	April	4.6%	34.5%	60.9%	0.0%	0.0%
	May	3.3%	37.0%	54.1%	0.1%	5.5%
	June – July	0.0%	1.3%	9.0%	15.7%	74.1%
2007	January*	9.1%	18.2%	72.7%	0.0%	0.0%
	March*	14.5%	32.3%	53.2%	0.0%	0.0%
	April	6.8%	24.7%	68.4%	0.0%	0.2%
	May	13.5%	24.0%	43.1%	0.7%	18.7%
	June – July	0.6%	0.6%	10.3%	0.6%	87.9%

## Conclusions

- The five populations are genetically differentiated. The American and Naches Rivers are the least differentiated. The spring and fall are very different.
- Marion Drain is mixed with lower Yakima River and Marion Drain Chinook; however there are still some samples that are assigning to Marion Drain with high probability
- Mixture analysis of unknown-origin smolts collected at Chandler Trap revealed that the upper Yakima River spring smolts was the most abundant spring population and lower Yakima fall smolts were the most abundant fall population.

## Acknowledgements

- BPA funds for the YKFP and WA state general funds supported this work effort
- Mark Johnston (YN), Yakama Nation Chandler trap crew and WDFW staff for collecting samples
- David Lind (YN) for Chandler Trap Chinook count and passage data
- Jim Shaklee and Ken Warheit (WDFW) for the proportional sampling design