DNA-Based Stock-of-Origin Assignments of Chinook Salmon Smolts Outmigrating Past Chandler Trap (Yakima River) in 2005

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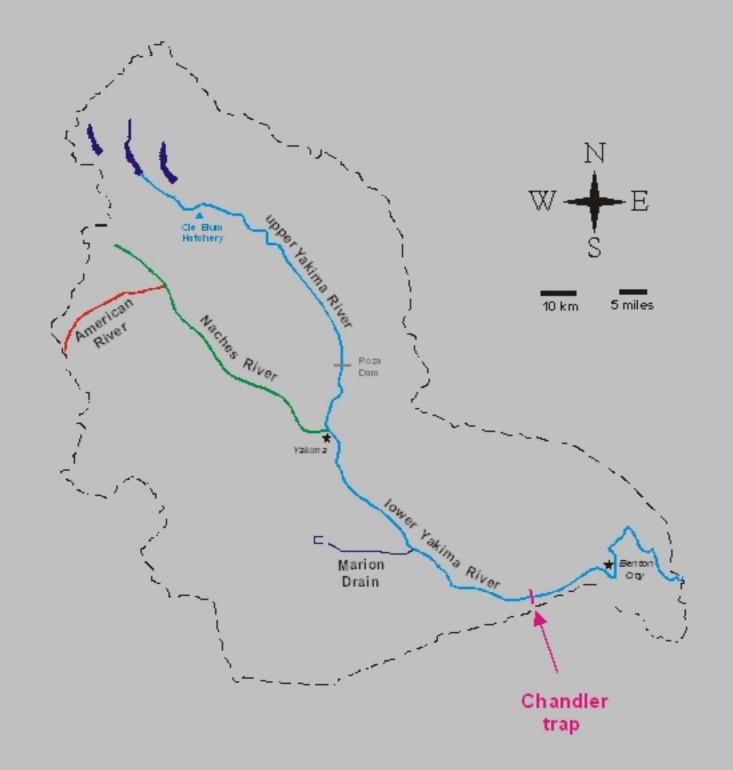




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Background

- Joint project between WDFW (WA Dept. of Fish and Wildlife) and YN (Yakama Nation)
- Five major stocks groups in Yakima River Basin that pass Chandler Trap – American R. SP, Naches R. SP, upper Yakima R. SP, Marion Drain F, and lower Yakima R. F
- A microsatellite DNA baseline was developed using samples from each of the five representative stocks
- Mixture analysis provided a means to calculate stock composition estimates of individual smolts outmigrating past Chandler Trap
- Five time strata were evaluated for stock composition to determine abundance of each stock over time



Collections

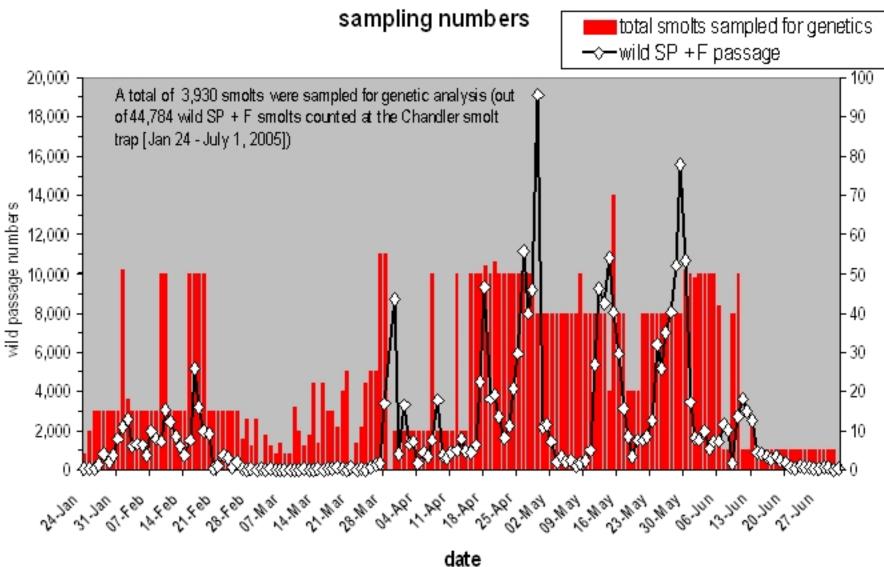
- Baseline Collections Eighteen collections (collected between 1989 and 2005) were sampled from spawning areas for each of five stocks
- Known-origin smolts Smolt samples were collected from known locations to test the genetic baseline for ability to assign smolts to the correct stock-of-origin
- Unknown-origin smolts Smolt samples were collected at Chandler trap from January – July for genetic analysis (proportional of the total number of smolts outmigrating)
- Unknown-origin smolts for pathology analysis Smolt samples were collected at Chandler Trap to monitor disease levels of different stocks

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
		200		05LU	65
					265
Naches R. SP	89AC	76			
	89AI	26	low Yakima R. F	90DF	109
	93DQ	50		93DW	82
	93DR	32			191
Lit Naches R. SP	04BI	42			
	04EM	56			
		282			
un Vakima B. SB	OSDN	24			
up Yakima R. SP		24			
	97DA	123			
	03GO	99			
		246			

Outmigration past Chandler Trap

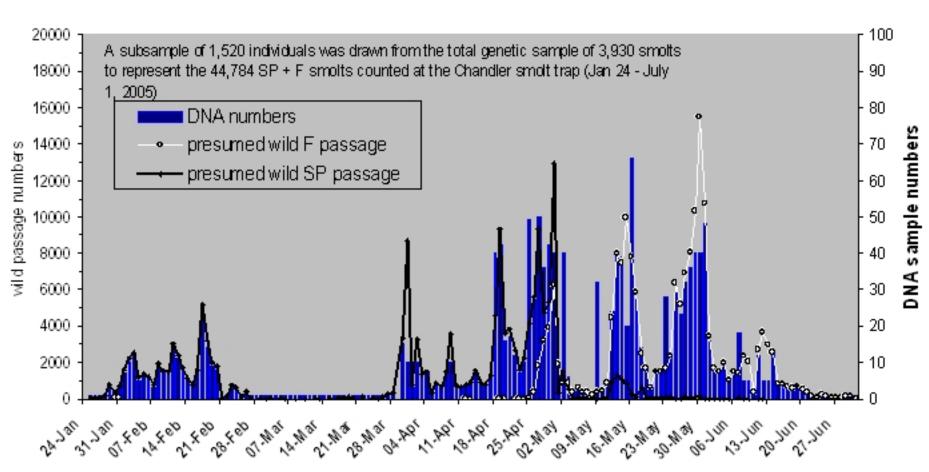
Jan - July 2005 Chandler smolt estimated wild passage & total genetic



DNA sample numbers

Proportional Subsampling of smolts collected for genetic analysis

Jan - July 2005 Chandler smolt estimated wild passage and proportional DNA sub-sampling numbers



Laboratory Methods

- DNA was extracted from fin tissue
- PCR amplification was performed using 11 microsatellite loci
- Amplified products were run through an ABI-3730 Genetic
 Analyzer
- Electropherograms were scored using Genemapper software v.3.0
- Data was exported and binned using Microsatellite Binner v.1.h
 (available from S.F. Young, WDFW)

Jennifer setting up DNA extraction



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Jennifer setting up thermalcycler



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Judy loading the ABI-3730



Electropherogram - Omm-1080



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Analyses

■ Jacknife Analysis of the Baseline - Analysis to remove each individual in the baseline collections and assign it back to the most likely stock-of-origin. This procedure tests each baseline collection to determine how well individuals will assign to that stock based on the allele frequency differences that exist among stocks.

• Mixture analysis – Analysis to assign a stock-of-origin to individual of Unknown-origin. Multilocus genotype of an unknown individual is compared with all stocks in the baseline to determine the stock with the most similar allele frequency. A likelihood ratio is calculated for each individual that is assigned a stock. The higher the ratio the more likely the individual is from that assigned stock.

Results – Jacknife Baseline

	American R. SP	Naches R. SP	up Yak R. SP	Marion Drain F	Iow Yak R. F
American SP	92.5%	5.5%	0.0%	0.0%	0.0%
Naches R. SP	13.5%	71.3%	13.1%	0.0%	0.0%
up Yak R. SP	0.8%	9.3%	89.0%	0.0%	0.0%
Marion 34.3% F	1.2%	1.2%	0.0%	60.7%	
low Yak R. 70.7% F	0.0%	1.0%	0.0%	28.3%	

Results – known-origin smolts

2004

N = 150 (2 individuals did not assign)

9 individuals mis-assigned

139/148 = 93.9%

2005

N = 100 (2 individuals did not assign)

3 individuals mis-assigned (up Yakima R. SP as Naches R. SP)

95/98 = 96.9%

Results – unknown-origin smolts

le man	January-				
June- 2004 July	February		March	April	May
N total	264	166	415	515	140
N unassigned	0	2	1	2	8
American R. SP	4.9%	3.1%	20.8%	21.0%	2.9%
Naches R. SP	31.1%	24.4%	35.5%	19.2%	2.9%
upper Yakima R. SP	63.6%	72.5%	43.7%	15.5%	5.9%
Marion Drain F	0.0%	0.0%	0.0%	1.9%	15.5%
lower Yakima R. F	0.4%	0.0%	0.0%	42.4%	72.8%
2005					
N total	201	56	431	522	110
N unassigned	4	3	12	7	0
American R SP	20.3%	18.9%	22.9%	3.5%	0.0%
Naches R. SP	35.0%	3.8%	30.1%	2.7%	2.7%
upper Yakima R. SP	44.7%	77.4%	27.2%	4.7%	24.6%

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upper Yakima R. SP	44.7%	77.4%	27.2%	4.7%	24.6%
Marion Drain F	0.0%	0.0%	6.0%	11.7%	2.7%
lower Yakima R. F	0.0%	0.0%	13.8%	77.5%	70.0%

Results – unknown-origin smolts for pathology analysis

	2004	2005
N total	200	200
N unassigned	3	4
American R. SP	36.0	% 36.7%
Naches R. SP	35.5%	23.5%
upper Yakima R. SP	27.5%	31.1%
Marion Drain F	0.5%	5.1%
lower Yakima R. F	0.5%	3.6%

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Conclusions

- Analysis of the known-origin smolts revealed over 93% of the smolts were correctly identified to stock-of-origin in 2004 and over 96% in 2005
- Analysis of unknown-origin smolts collected at Chandler trap revealed that the Upper Yakima River spring smolts were the most abundant spring stock and lower Yakima fall smolts were the most abundant fall stock in both 2004 and 2005

However, there was variation in the smolt abundance from the different stocks during the individual time strata

 Analysis of the unknown-origin smolts collected for pathology revealed a range in abundance from 23 to 37% for the three spring stocks

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