# DNA-Based Pedigree Assignments of Chinook Salmon from the Yakima River

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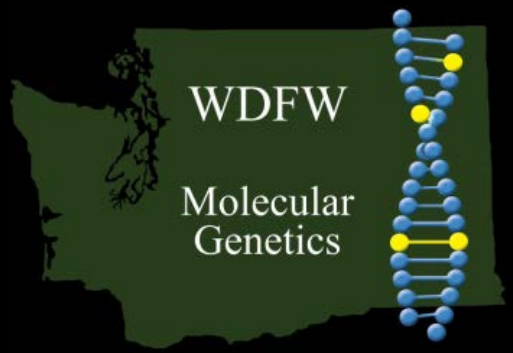


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# Background

- Joint project between WA Department of Fish and Wildlife (WDFW) and Yakama Nation (YN)
- Project objective is to assess the relative fitness of natural-origin Chinook with different percentages of hatchery ancestry in natural environment of the upper Yakima River
- Collection of hatchery-origin adult males and females, jacks, and precocious male Chinook at Roza Dam 2003 – 2006; hatchery- and natural-origin Chinook 2007 - present
- Genetic analysis using microsatellite DNA loci follows the same methodology used for the analysis of Chinook in the Cle Elum spawning channel

# Laboratory Methods

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

# Cherril setting up DNA extraction

# Laboratory Methods

- DNA was extracted from fin tissue
- PCR amplification was performed using microsatellite loci
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# Cheryl setting up PCR reaction

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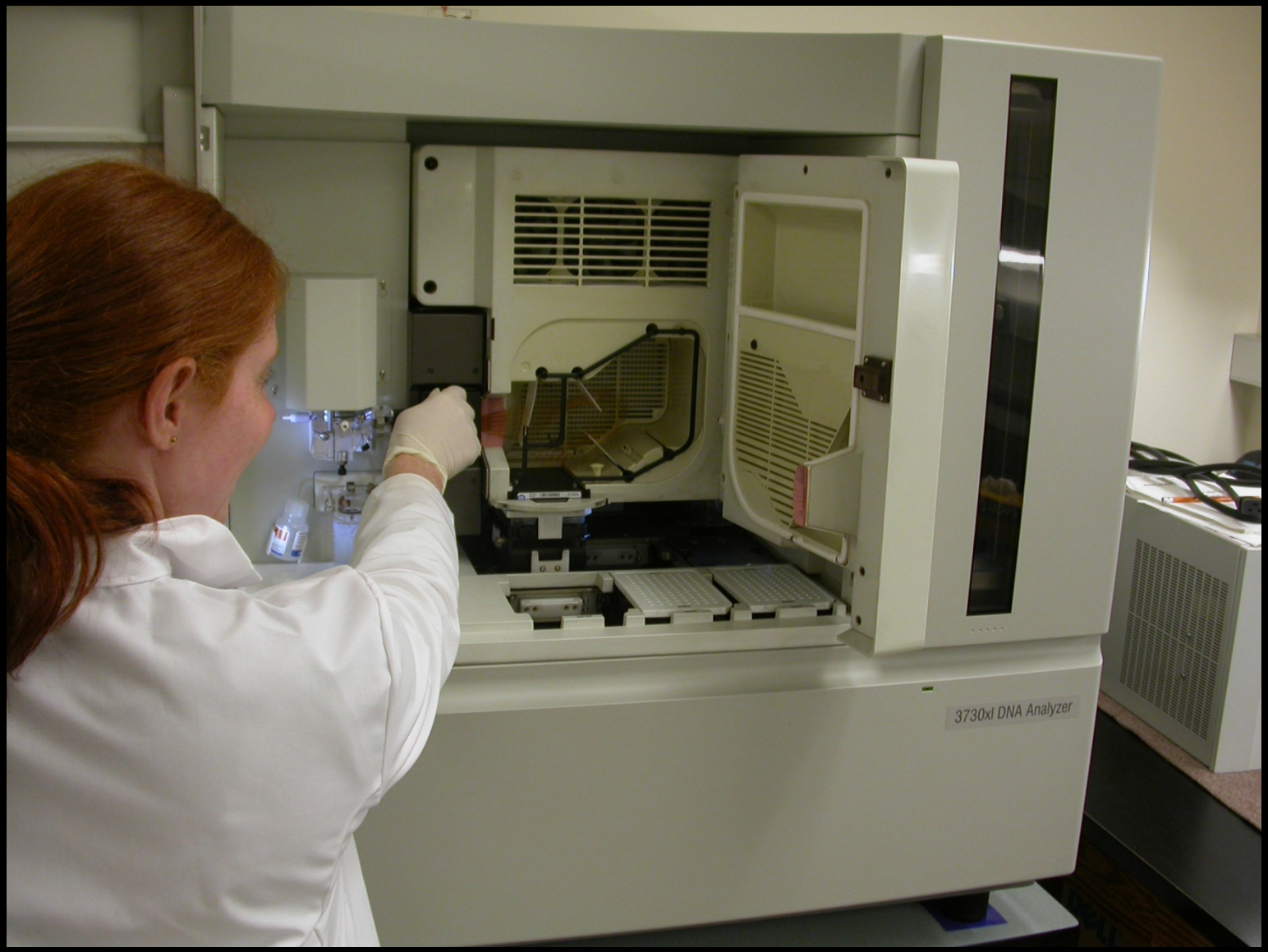
# Jennifer loading the ABI-3730

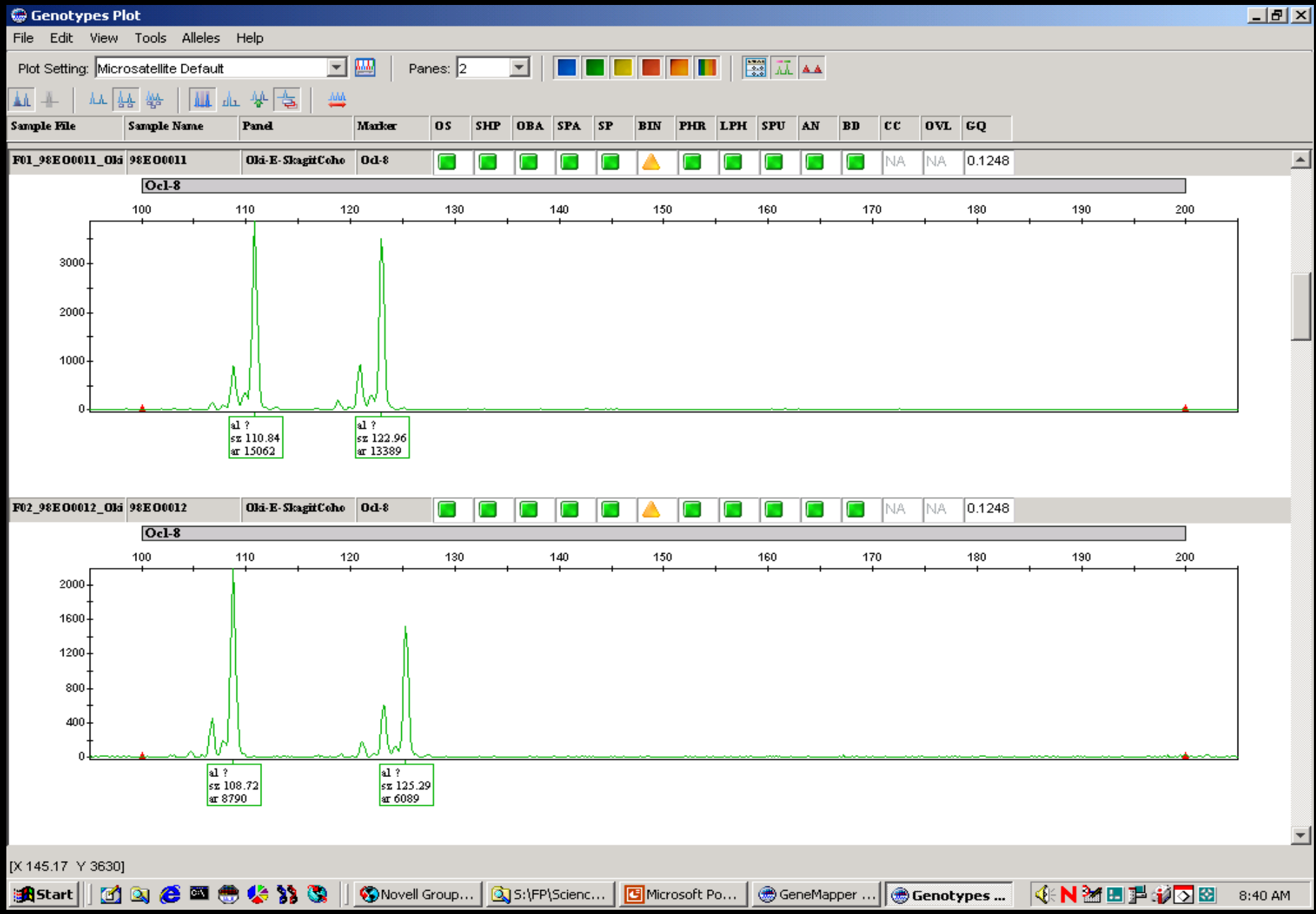


# Laboratory Methods

- DNA was extracted from fin tissue
- PCR amplification was performed using microsatellite loci
- Amplified products were run through an ABI-3730 Genetic Analyzer
- Electropherograms were scored using GENEMAPPER software v.3.7 (38,436 individual electropherograms)
- Data was binned using GAPS allele naming

# Jennifer Scoring an Electropherogram

# Electropherogram – Ocl-8



# Laboratory Methods

- DNA was extracted from fin tissue
- PCR amplification was performed using microsatellite loci
- Amplified products were run through an ABI-3730 Genetic Analyzer
- Electropherograms were scored using GENEMAPPER software v.3.0
- Data was binned using GAPS allele naming

# Locus Data

| Locus | N Alleles | N parents Genotyped | $H_o$ | $H_e$ | Excl (1) | Excl (2) |
|---|---|---|---|---|---|---|
| Ogo-2 | 11 | 2,186 | 0.825 | 0.821 | 0.475 | 0.648 |
| Ogo-4 | 11 | 2,188 | 0.801 | 0.806 | 0.456 | 0.632 |
| Oki-100 | 26 | 2,117 | 0.919 | 0.904 | 0.682 | 0.811 |
| Omm-1080 | 44 | 2,162 | 0.937 | 0.961 | 0.852 | 0.920 |
| Ots-201b | 29 | 2,118 | 0.915 | 0.904 | 0.679 | 0.809 |
| Ots-208b | 29 | 2,115 | 0.930 | 0.941 | 0.787 | 0.880 |
| Ots-211 | 28 | 2,123 | 0.930 | 0.931 | 0.757 | 0.861 |
| Ots-212 | 24 | 2,182 | 0.887 | 0.887 | 0.631 | 0.774 |
| Ots-213 | 29 | 2,185 | 0.921 | 0.936 | 0.769 | 0.869 |
| Ots-3M | 9 | 2,185 | 0.652 | 0.651 | 0.254 | 0.435 |
| Ots-9 | 6 | 2,186 | 0.678 | 0.656 | 0.237 | 0.400 |
| Ots-G474 | 13 | 2,190 | 0.362 | 0.367 | 0.072 | 0.211 |
| Ssa-197 | 25 | 2,180 | 0.902 | 0.906 | 0.683 | 0.812 |
| Ssa-408 | 27 | 2,160 | 0.728 | 0.916 | 0.709 | 0.830 |

Excl (1) = Exclusionary ability of the locus when neither parent is known
Excl (2) = Exclusionary ability of the locus when one parent is known

# Evaluation of Parentage Assignments

- Maximum likelihood parentage assignments performed with the program CERVUS 3.0

- Assignments for offspring were calculated for the two most likely male and female parent pair. The parent pair assignment with two mismatches or less was accepted

- Individuals that did not assign to a parent pair were then analyzed for a female parent only and male parent only (assignments with two or less mismatches were accepted)

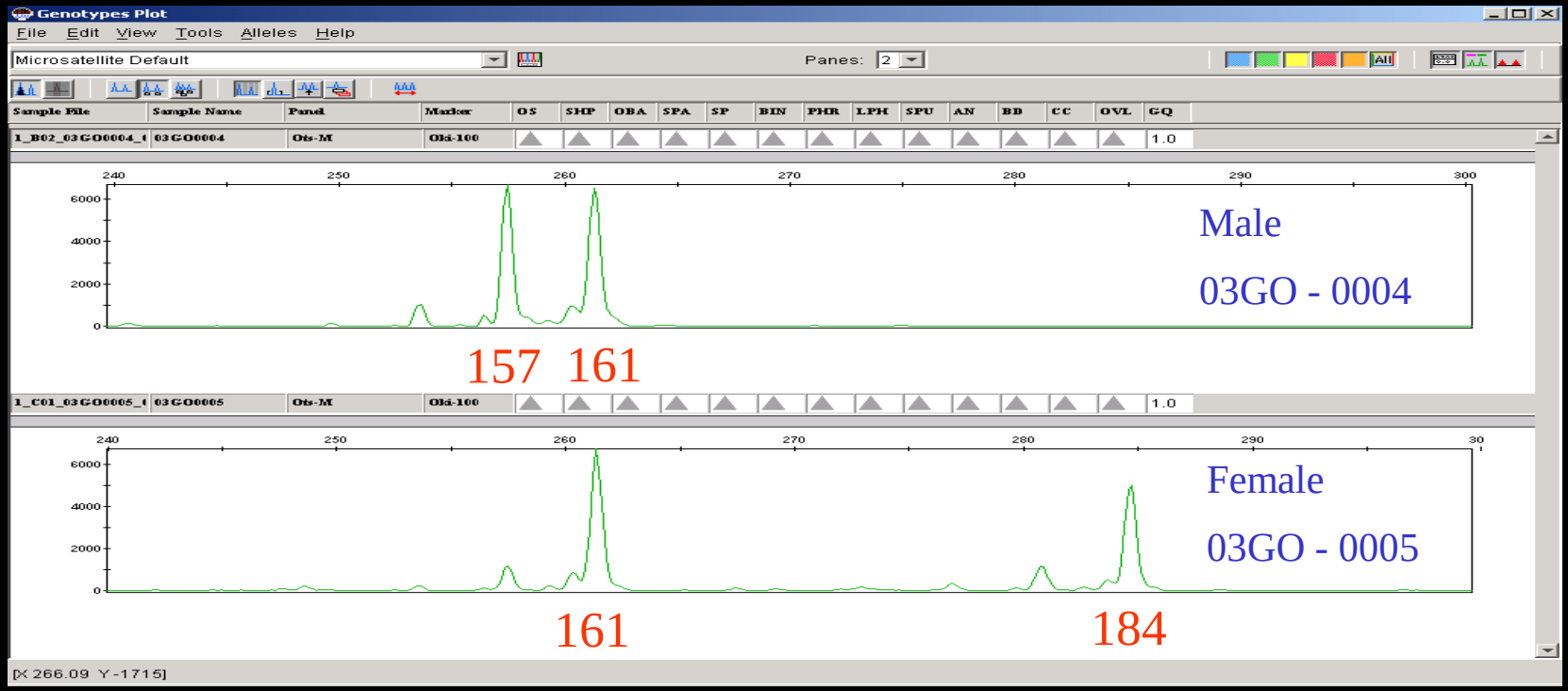
- Maximum likelihood analysis was then conducted using the program MYKISS

- An additional 22 individuals were assigned to a parent pair

# Causes of Mismatching

- Germ-line mutation – a parent passes a changed allele to their offspring (sequence or allele changes during replication)
- PCR error (or process error) – error introduced by poor amplification from lower quality DNA extracts
- Genotyping error – inadvertent human error and computer software error in scoring due to multiple peaks being selected

# Electropherogram – Oki-100




# Mismatching

| | Oki-100 | Ots-3M | Ots-213 |
|---|---|---|---|
| Female – 1 | 100/100 | 100/100 | 100/100 |
| Female – 2 | 200/200 | 200/200 | 200/200 |
| Male –1 | 120/120 | 120/120 | 120/120 |
| Male – 2 | 240/240 | 240/240 | 240/240 |
| Offspring – 1 | 100/120 | 100/120 | 100/120 |
| Offspring – 2 | 200/240 | 200/240 | 200/240 |
| Offspring – 3 | 100/120 | 100/120 | 100/240 |

## Expected proportion - Hatchery- and Natural-origin Chinook

- 2,284 – Hatchery-origin Chinook count at Roza Dam
- 1,558 / 1,147 – Natural-origin Chinook count at Roza Dam
  (411 – Natural-origin Chinook brood)
- 2,284/3,431 = 0.6657 – P ; 1,147/3,431 = 0.3343 – Q

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- 44.3% Hatchery-origin (H X H) – $P^2$
- 44.5% Hatchery & Natural-origin (H X N & N X H) – 2PQ
- 11.2% Natural-origin (N X N) - $Q^2$

## Observed returns -
## Hatchery- and Natural-origin Chinook

- 161 / 569 offspring were assigned parental pair

  Hatchery X Hatchery (28.3%)

- 230 / 569 offspring were assigned a mother only

  Hatchery X Natural (40.4%)

- 62 / 569 offspring were assigned a father only

  Natural X Hatchery (10.9%)

- 116 / 569 offspring did not assign a male or female

  Natural X Natural (20.4%)

# Comparison of Expected and Observed Percentages of Hatchery and Natural-Origin Chinook

| | Expected | Observed |
|---|---|---|
| H X H | 45.0% | 28.3% |
| H X N & N X H | 44.0% | 51.3% |
| N X N | 11.0% | 20.4% |

## Conclusions

- Preliminary data
- The number of observed natural-origin Chinook exceeds the expected amount while hatchery-origin is lower than expected
- More female only assignments than male assignments of hatchery-origin

## Future Work

- Analysis of 1999 brood to determine an error rate for calculating N X N offspring in the 2007 collection
- Analysis of remaining 2007 four year Chinook
- Analysis of 2004 adults and 2008 offspring
- Analysis of 2011 and 2012 returns

# Acknowledgements


- BPA funds for the YKFP supported this work effort
- Mark Johnston and crew from the Yakama Nation at Roza Dam for collecting samples
- Jennifer Von Bargen for all laboratory analysis