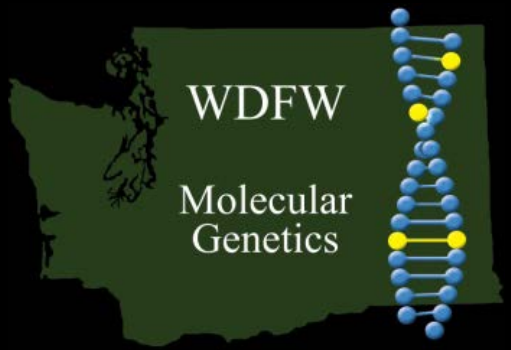
DNA-Based Pedigree Analysis of Chinook Salmon from the Yakima River

Todd W. Kassler, Scott M. Blankenship, Kenneth I. Warheit, and Craig A. Busack

Washington Department of Fish and Wildlife



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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 reproductive success of Chinook in the upper Yakima River
- Collection of hatchery-origin adult males and females, jacks, and precocious male Chinook occurred at Roza Dam from 2003 – 2006
- Collection of both hatchery- and natural-origin Chinook has occurred from 2007 - present
- Genetic analysis using microsatellite DNA loci is used to determine parentage. Methodology used for the analysis is the same as we have used for 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

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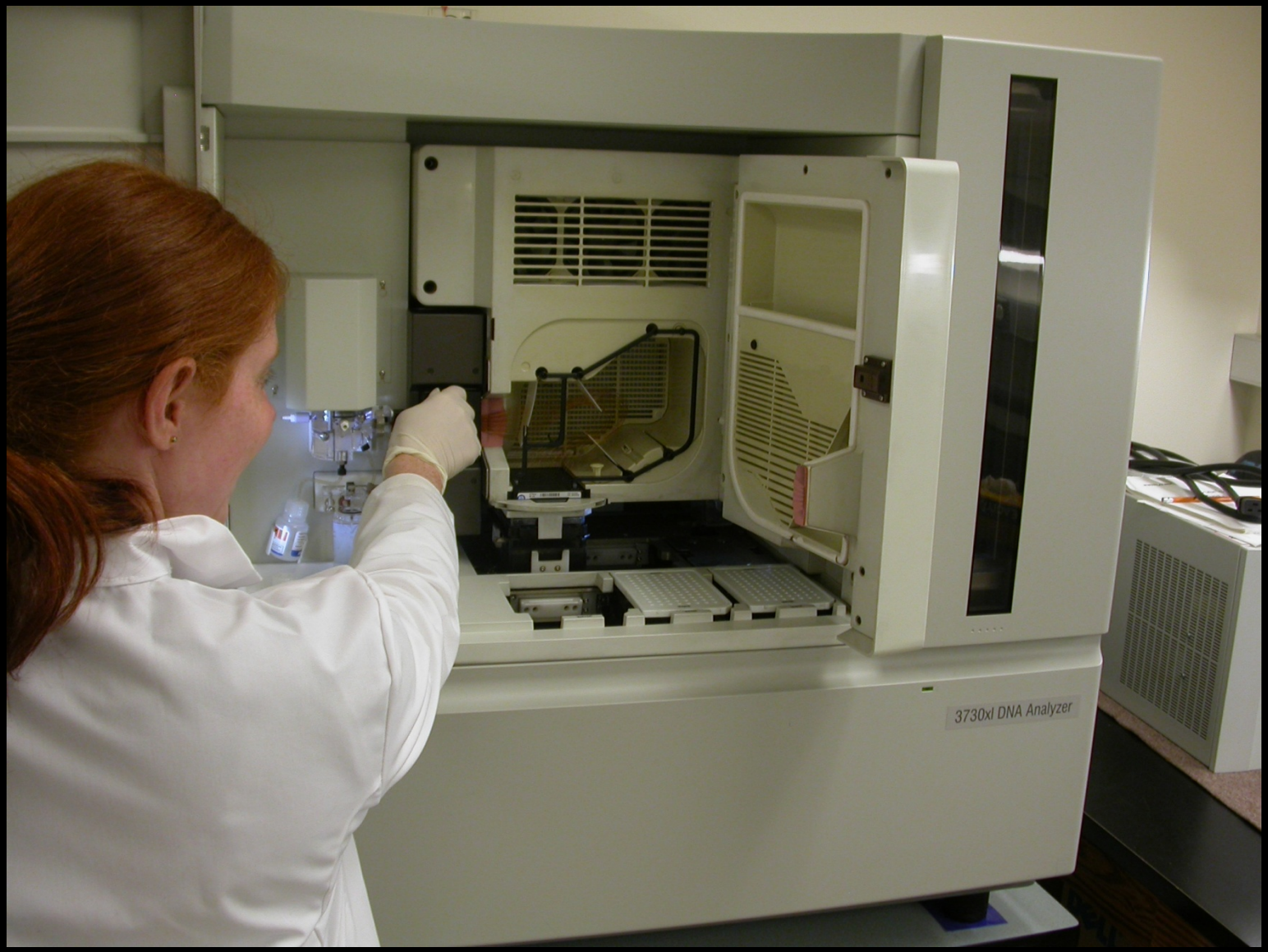
Jennifer loading the ABI-3730



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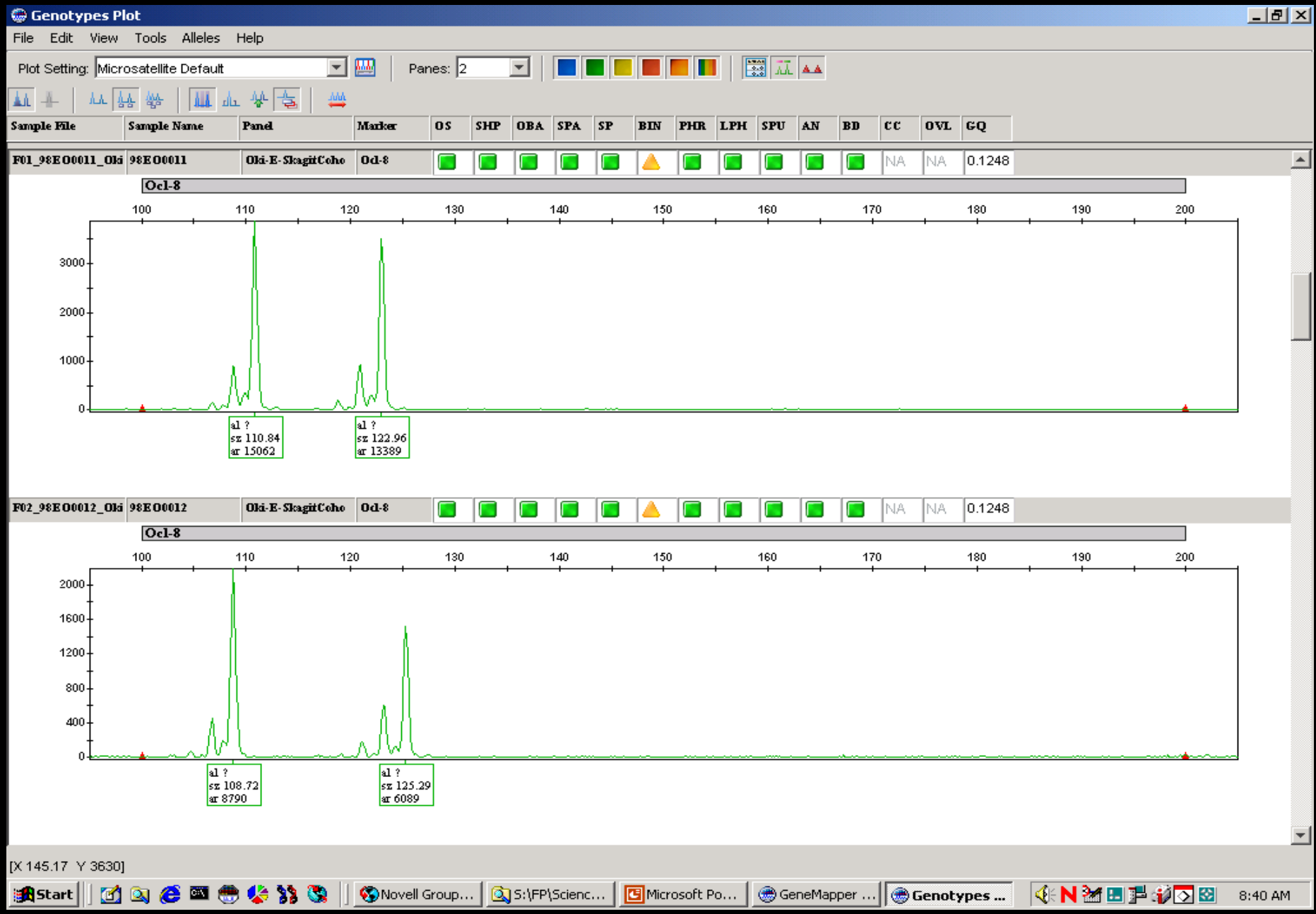
- Data was binned using GAPS allele naming

Jennifer Scoring an Electropherogram

Electropherogram – Ocl-8



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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

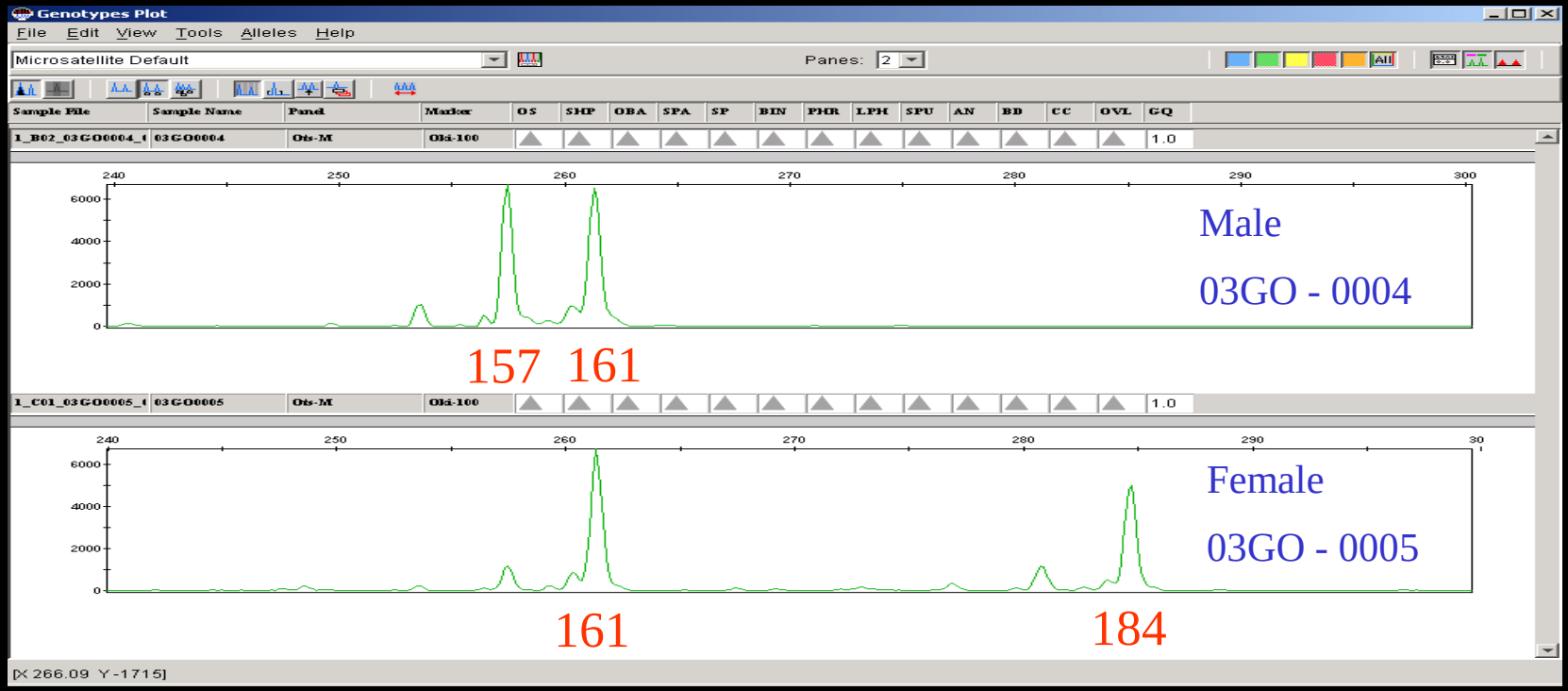
- Assignments for offspring were calculated for the most likely male and female parent pair. The parent pair assignment with two mismatches or less was accepted

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

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 in 2007 return

- 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

- 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

- **229 / 1,153 offspring were assigned parental pair**

  Hatchery X Hatchery (19.9%)

- **443 / 1,153 offspring were assigned a mother only**

  Hatchery X Natural (38.4%)

- **163 / 1,153 offspring were assigned a father only**

  Natural X Hatchery (14.1%)

- **318 / 1,153 offspring did not assign a mother or father**

  Natural X Natural (27.6%)

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

	Expected	Observed
H X H	45.0%	19.9%
H X N & N X H	44.0%	52.5%
N X N	11.0%	27.6%

Conclusions

- Preliminary data –
  - Still need to calculate assignment errors (probability of assigning incorrect parent)
  - Estimate significance of the assignments
- The number of observed natural-origin Chinook is higher than expected
- The number of observed hatchery-origin Chinook is lower than expected
- More hatchery-origin females assigned as a parent than hatchery-origin males

Future Work

- Statistical analysis of 1999 and 2000 brood to determine an error rate for calculating N X N offspring in the 2007 and 2008 collections
- Analysis of 2004 adults (completed this year)
- Analysis of 2008 offspring (scheduled for this upcoming year)
- Analysis of third generation (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