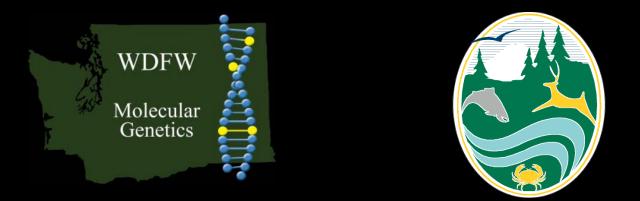
DNA-Based Pedigree Analysis of Chinook Salmon from the Yakima River

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Yakima Basin Science and Management Conference June 15-16, 2011

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

Laboratory Methods









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



161

2000

1000

04EX - 0118

184

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

Chinook Adults 2003 and 2004 -

2003

- 2,201 Hatchery-origin Chinook collected and analyzed (includes 368 jacks and 39 precocial males)
- 0 Natural-origin Chinook collected and analyzed
- 1,151 Hatchery-origin adult Chinook counted at Roza Dam
- <u>1,133</u> Hatchery-origin jacks Chinook counted at Roza Dam 2,284
- 784 Natural-origin adults Chinook counted at Roza Dam
- 774 Natural-origin jacks Chinook counted at Roza Dam

2004

- 2,542 / 2,160 Hatchery-origin Chinook collected / analyzed (includes 20 jacks and 7 precocial males) 382 samples left to analyze
- 0 Natural-origin Chinook collected and analyzed
- 2,985 Hatchery-origin adult Chinook counted at Roza Dam
- 216 Hatchery-origin jacks Chinook counted at Roza Dam 3,201
- 7,093 Natural-origin adults Chinook counted at Roza Dam
- 711 Natural-origin jacks Chinook counted at Roza Dam

Expected proportion -

Hatchery- and Natural-origin Chinook counts 2003

- 2,284 Hatchery-origin Chinook counted at Roza
- 1,558 / 1,086 Natural-origin Chinook counted at Roza (472 – Natural-origin Chinook brood)
- 2,284 / 3,370 = 0.6777 P ; 1,086 / 3,370 = 0.3223 Q
- 45.9% Hatchery-origin (H X H) P²
- 43.7% Hatchery & Natural-origin (H X N & N X H) 2PQ
- 10.4% Natural-origin (N X N) Q²

Expected proportion -

Hatchery- and Natural-origin Chinook counts in 2004

- 3,201 Hatchery-origin Chinook count at Roza Dam
- 7,804 / 7,322 Natural-origin Chinook count at Roza Dam (482 – Natural-origin Chinook brood)
- 3,201 / 10,523 = 0.3042 P ; 7,322 / 10,523 = 0.6958 Q
- 9.3% Hatchery-origin (H X H) P²
- 42.3% Hatchery & Natural-origin (H X N & N X H) 2PQ
- 48.4% Natural-origin (N X N) Q²

Observed returns 2007 -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%)

Observed returns 2008 -Hatchery- and Natural-origin Chinook

- 21 / 799 offspring were assigned parental pair Hatchery X Hatchery (2.6%)
- 67 / 799 offspring were assigned a mother only Hatchery X Natural (8.4%)
- 60 / 799 offspring were assigned a father only Natural X Hatchery (7.5%)
- ??? / 799 offspring did not assign a mother or father Natural X Natural (?.??%)

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

2003 / 2007	Expected	Observed
НХН	45.9%	19.9%
HXN&NXH	43.7%	52.5%
NXN Contingency table X ² test p-va	10.4%	27.6%
2004 / 2008	Expected	Observed
2004 / 2008 H X H	Expected 9.3%	Observed 2.6%
	-	

Conclusions

The number of observed natural-origin Chinook is higher than expected while the number of observed hatchery-origin Chinook is lower than expected in the 2003 / 2007 collections

 More hatchery-origin females assigned as a parent than hatchery-origin Males in the 2003 / 2007 collections

 Results from the 2004 / 2008 collections incomplete without the analysis of the remaining hatchery-origin parents (# of N X N likely inflated)

 Number of natural-origin adults returning in 2004 was 10X greater than 2003

Future Work

- Statistical analyses using COLONY to error check the number of natural origin parents from the 2003 and 2004 collection years
- Completion of the 2004 adults and 2008 offspring
- Analysis of the third generation 2011 returning 4 yr olds
- Estimation of impacts (potential bias) from fisheries harvest

Acknowledgements

- Funds from the Yakama Nation supported this work effort
- Mark Johnston and crew from the Yakama Nation at Roza Dam for collecting samples
- Jennifer VonBargen for laboratory analysis