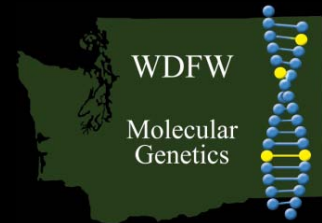


# Genetic Analysis of Natural-origin Spring Chinook in the Tucannon River and Comparison to a Supplementation And Captive Brood Program

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## Background

- Number of salmon returning to Tucannon River reduced
- 1985 - Tucannon River Supplementation program initiated
- 1989 - Supplementation program was integrated (H & W)
- 1992 - Snake River spring Chinook (including the Tucannon River) were listed “endangered” and then changed to “threatened” in 1995
- 1997 - Tucannon River Captive Brood Program began
- 1997 - Genetic samples were collected - Potential effects of supplementation and captive brood programs on natural-origin Chinook was unknown?

# Collections

- The following genetic samples were collected:
  - **Hatchery-origin (1997 – 2008)**  
Samples from 1999 were collected but not analyzed
  - **Natural-origin (1986, 1997 – 2008)**  
Samples from 1999 were collected but not analyzed

The same samples were then divided into two different categories  
(collection years are the same as shown above)

- **Supplementation Spawners (from hatchery broodstock)**
  - Supplementation Spawners included both hatchery- and natural-origin
- **In-River Spawners (naturally spawning)**
  - In-River Spawners included both hatchery- and natural-origin

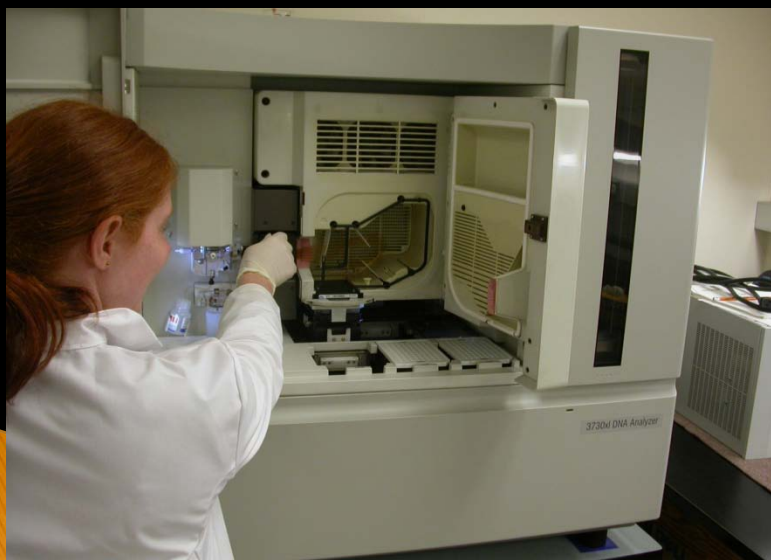
# Collections

- Three different groups were defined for the Captive Brood collections
  - **Adults used to produce the captive brood (1997 – 2002)**  
Adults used to produce the Captive Brood were from the Supplementation program
  - **Captive Brood (2000 – 2006)**  
Full sibs in the Captive Brood and Supplementation
  - **Captive Brood Returns (2008)**

## Laboratory Methods

- DNA was extracted from fin tissue
- PCR amplification - 13 microsatellite loci
- ABI-3730 Genetic Analyzer
- GENEMAPPER software v.3.7

# Laboratory Processes



## Locus Data

Locus	N Alleles	Allele Size Range (bp)	Reference
Ogo-2	11	202-232	Olsen et al. 1998
Ogo-4	14	132-166	Olsen et al. 1998
Oki-100	24	212-313	unpublished
Omm-1080	41	190-354	Rexroad et al. 2001
Ots-201b	32	141-302	unpublished
Ots-208b	35	158-322	Greig et al. 2003
Ots-211	28	208-327	Greig et al. 2003
Ots-212	21	131-231	Greig et al. 2003
Ots-213	28	214-334	Greig et al. 2003
Ots-3M	10	128-152	Banks et al. 1999
Ots-9	5	103-111	Banks et al. 1999
Ots-G474	9	156-204	Williamson et al. 2002
Ssa-197	27	189-305	O'Reilly et al. 1996
Ssa-408	28	184-304	Cairney et al. 2000

# History of Reporting for genetic analyses

- July 2005 - Hawkins and Frye (2003 collections)
- April 2006 – Kassler and Hawkins (2003 & 2004 collections)
- April 2007 – Kassler and Hawkins (2005 collections)
- April 2008 – Kassler and Hawkins (2006 collections)
- October 2010 – Kassler and Dean (consensus of all years)



# Groupings for Analysis

Eight different groupings of collections were analyzed to assess genetic relationship of collection type over time

- **Analysis #1** – All samples – collection year (1986, 1997 – 2008)
- **Analysis #2** – Analysis of the three captive brood groups
- **Analysis #3** – Analysis of spawner groups (in-river and supplementation) – collection year
- **Analysis #4** – Analysis of spawner groups (in-river and supplementation) – brood year

# Groupings for Analysis

- **Analysis #5** – Analysis of ancestral groups (hatchery and natural-origin) – collection year
- **Analysis #6** – Analysis of ancestral groups (hatchery and natural-origin) – brood year
- **Analysis #7** – Analysis by spawner groups (In-river and Supp) and ancestral groups (Hat and Nat) – collection year
- **Analysis #8** – Analysis of the adults used for production of the captive brood to their offspring (the captive brood) with the supplementation program and their offspring  
(captive brood and supplementation program offspring can be full siblings)

# Population Statistics

- HW equilibrium / Linkage Disequilibrium
- Allelic Richness / Heterozygosity
- Pairwise  $F_{ST}$
- Factorial Correspondance

# Results Summary for each Analysis

- **Analysis #1 – all samples/all years**
  - Significant differences among collections
  - Large number of significant locus comparisons with Linkage Disequilibrium
- **Analysis #2 – three Captive Brood collections**
  - Adults that produce the captive brood were not sig different
  - Significant differences among the captive brood collections
  - Low levels of relatedness among individuals
- **Analysis #3 – In-River and Supplementation collection year**
  - Fewer than two collections with 1 or 2 loci not in HW
  - Pairwise  $F_{ST}$  values were below 1.0%
- **Analysis #4 – In-River and Supplementation brood year**
  - Same as Analysis #3
  - Factorial Correspondance plot

# Results Summary/Analysis

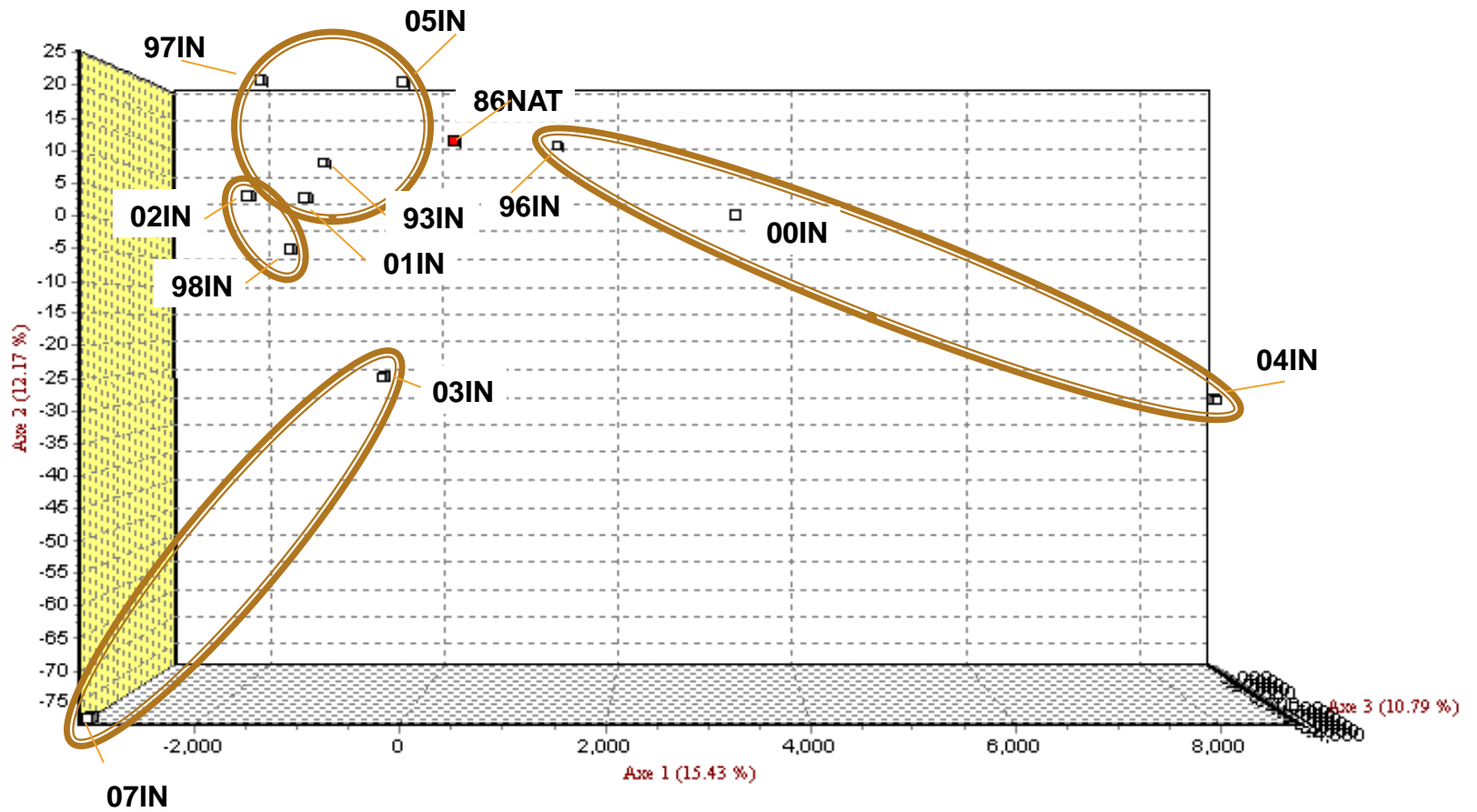
- **Analysis #5 – Hatchery and Natural-origin collection year**
  - **Mostly in HW**
  - **Pairwise  $F_{ST}$  values below 1.0%**
  - **Non-significant differences between most collections that were collected four years apart**
- **Analysis #6 – Hatchery and Natural-origin brood year**
  - **Same as Analysis #5**
- **Analysis #7 – In-River/Hatchery, In-River/Natural, Supp/Hatchery, and Supp/Natural**
  - **Mostly in HW**
  - **Small sample size for many collections**

## Results Summary/Analysis

- **Analysis #8 – Adults that produced the Captive Brood and offspring compared to Supplementation Spawners and offspring**
  - **Non-significant differences between the adults that produced the Captive Brood and Supplementation Spawners for each year**
  - **Non-significant difference between parents and the offspring they produced**
  - **Significant difference between Captive Brood (not released) and Supplementation offspring that had been released and then returned**

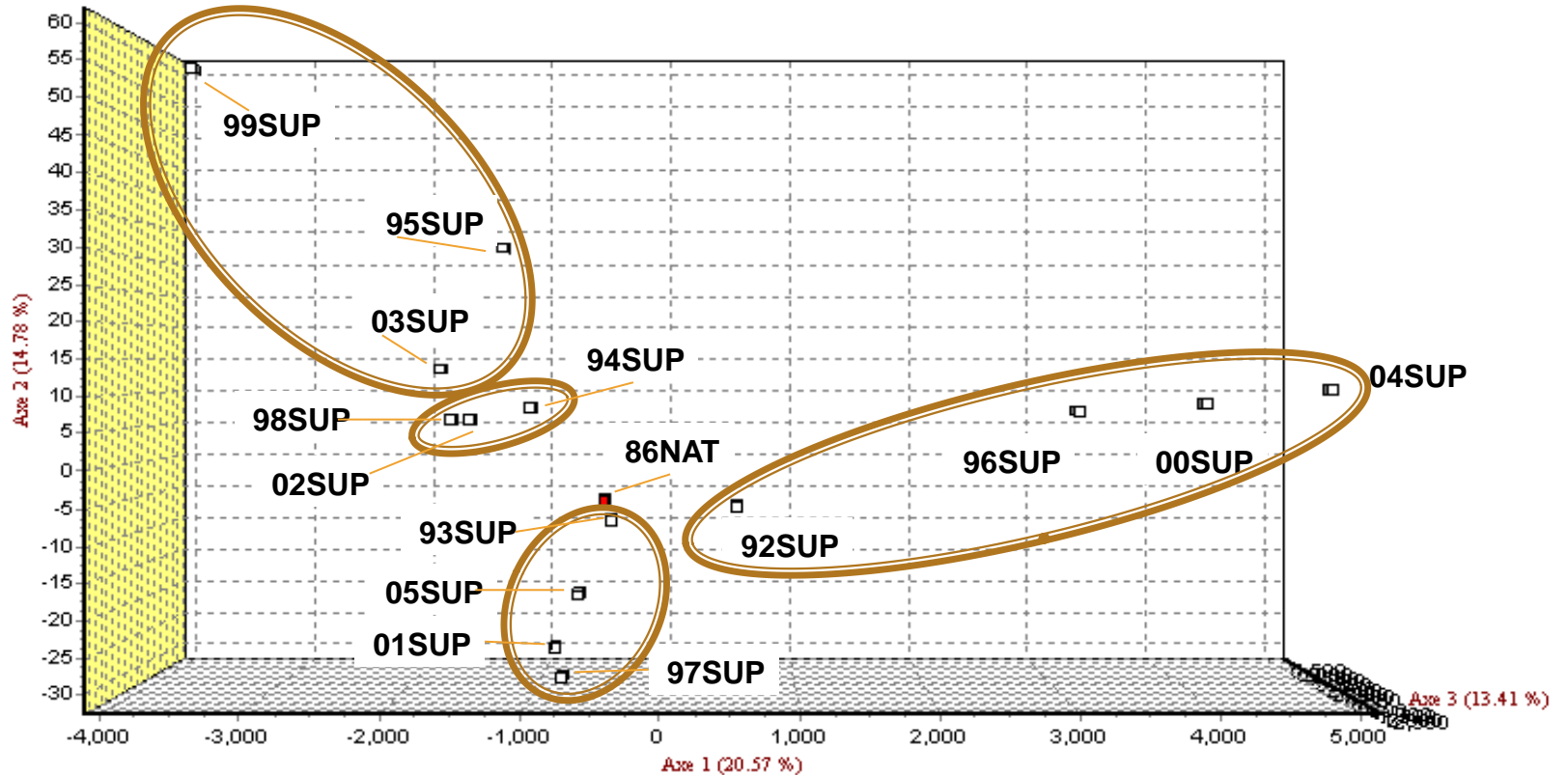
# Results – Factorial Correspondance Plot - In River

In-river by brood year.gtx



# Results – Factorial Correspondance Plot - Supplementation

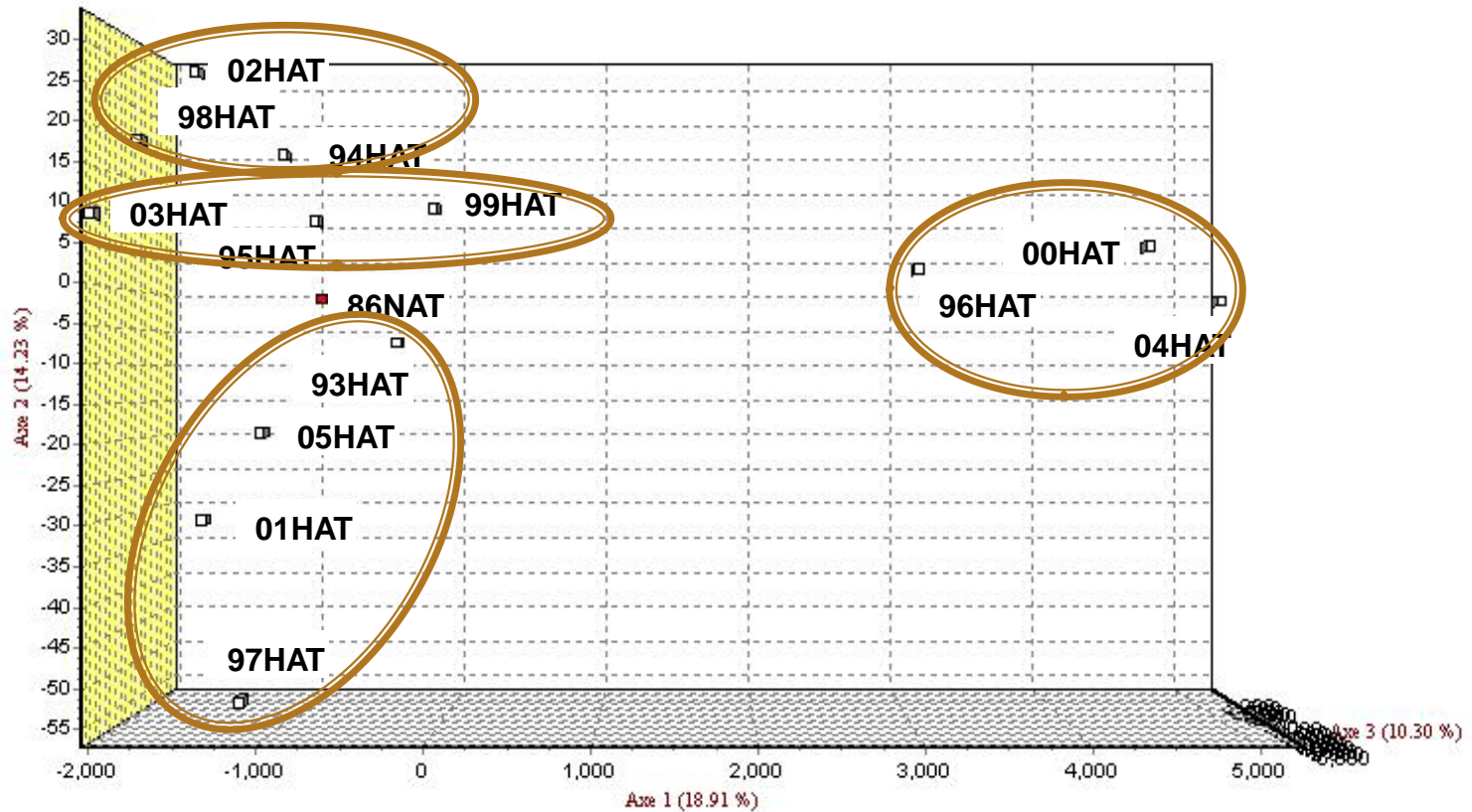
Supplementation by brood year.gtx



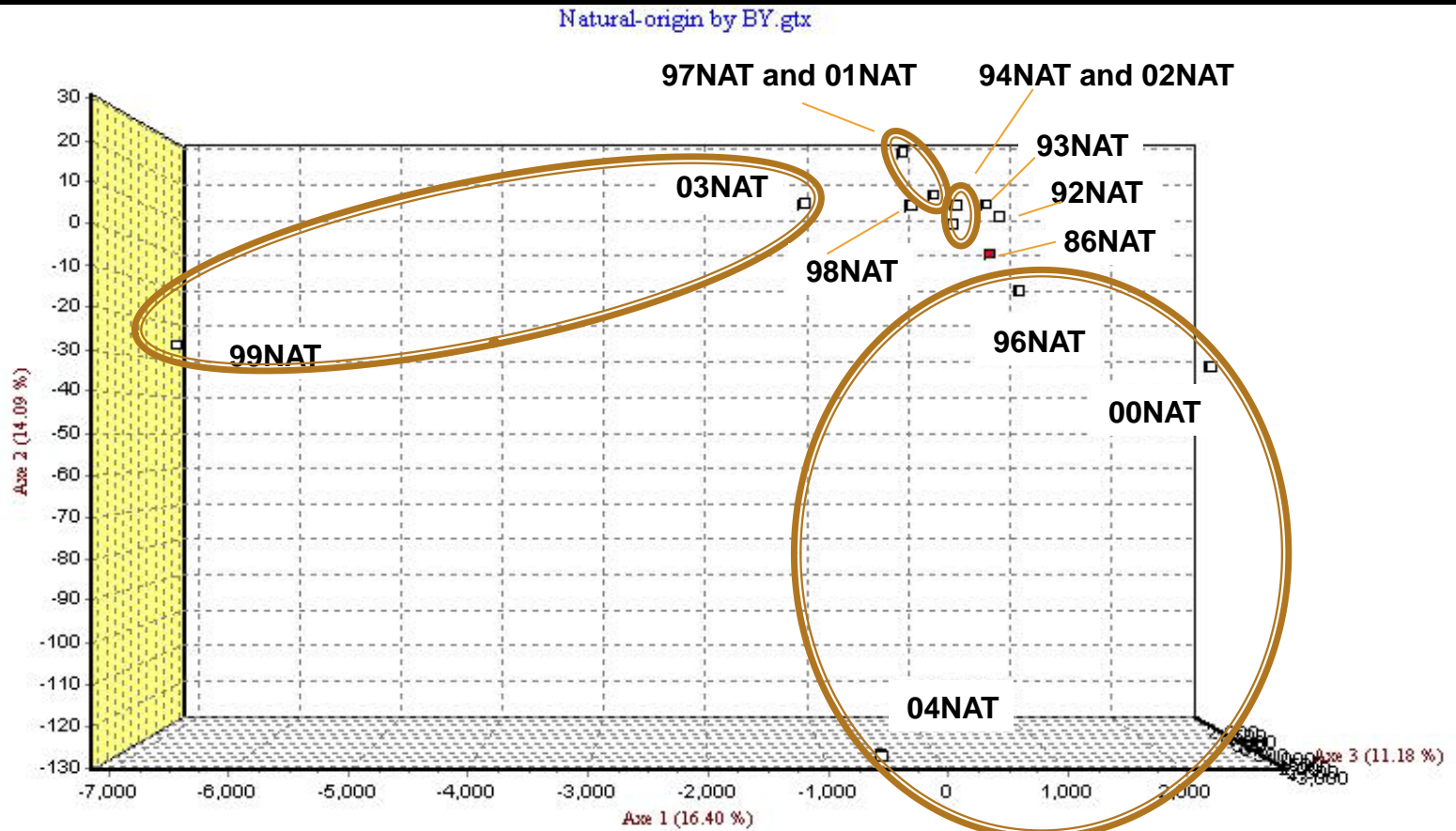


# Results – Factorial Correspondance Plot - Hatchery-origin

Hatchery-origin by BY.gtx



# Results – Factorial Correspondance Plot - Natural-origin



## Conclusions

- The genetic diversity of spring Chinook in the Tucannon River is different from year to year (Analysis #1)
- The only difference in the three collection groups of Captive Brood was between the captive brood collections when produced from equal numbers of individuals from two different brood years (2003 and 2004)
- The combination of Analyses 3-7 demonstrates that the genetic diversity of spring Chinook in the Tucannon River has not significantly changed as a result of the supplementation or captive brood programs
- Analyses using collection year or brood year did not result in any differences, both supported a conclusion that individuals that were four years apart were the most similar

# Conclusions

- Using different age groups of hatchery and natural-origin spring Chinook in the supplementation program has the potential of changing the genetic profile
- The genetic diversity of spring Chinook that are held captive have differential survival (selection) than spring Chinook that are released and then return four years later
- Captive Brood Returns (2008) were not different to the Supplementation collections

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