Reducing genetic risks to wild populations: Evaluating the degree of genetic change in an integrated hatchery population compared to a segregated line

A collaborative project between UW, the Yakama Nation, WDFW, & NOAA

Charlie Waters

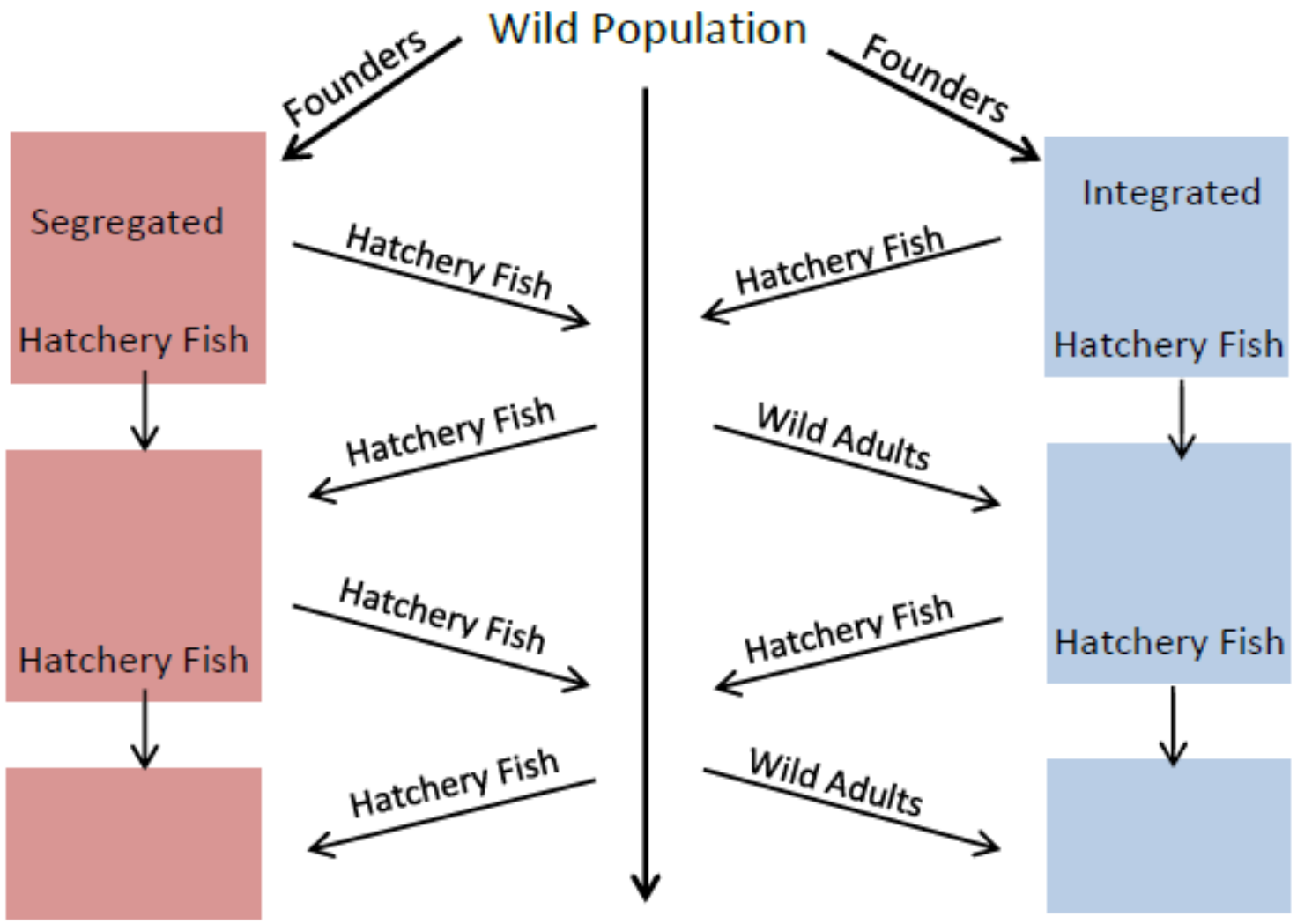
School of Aquatic and Fishery Sciences

University of Washington

Collaborators and Acknowledgments

- Kerry Naish, UW
- Jeff Hard, NOAA
- Steve Schroder, WDFW (ret.)
- Ken Warheit, WDFW
- Todd Seamons, WDFW
- Sewall Young, WDFW
- Jim Seeb, UW
- Curt Knudsen, Oncorh Consulting
- Bill Bosch, Yakama Nation
- Dave Fast, Yakama Nation
- Charlie Strom, Yakama Nation
- All CESRF staff
- NOAA

Segregated vs. Integrated Hatcheries



- What are the differences between these lines?

Aims and Objectives

Aim: To evaluate the degree, if any, of genetic change in an integrated hatchery population compared to a segregated line

Objectives:

1. Analyze DNA from three generations of Chinook salmon within segregated and integrated hatchery lines and compare to the founders from the wild population
2. Identify differences between the lines, including signatures of selection
3. Quantify the rate at which domestication can occur in both segregated and integrated hatchery lines
4. Perform genome wide association analyses with phenotypes

Cle Elum Supplementation and Research Facility

- Model system...maintain both segregated and integrated hatchery lines (best practices)

- Collect tissue samples and phenotypic data from every fish used for broodstock

- Ideal for tracking genetic changes over time

Photo: www.nwcouncil.org

Previous Studies on CESRF Populations

Study	Evidence for Domestication
Knudsen et al. 2006	Yes
Busack et al. 2007	Small
Fritts et al. 2007	Small
Pearsons et al. 2007	Small
Knudsen et al. 2008	No
Schroder et al. 2008	No
Dittman et al. 2010	No
Schroder et al. 2010	Small

- All compared wild Yakima Chinook to 1st generation hatchery Chinook
- Conclusion: domestication may be present but effect is small

Experimental Approach

- Sub-sample fin clips from approx. 100 fish (50 males and 50 females) within each hatchery line for 2002, 2006, and 2010 and from the 1998 founders
- Extract, qualify, and quantify DNA from fin clips
- Sequence DNA fragments using restriction site-associated (RAD) sequencing
- Compare DNA from hatchery lines of each generation to founding population to identify differences, including loci under selection, and quantify rate of change

Restriction Site-Associated (RAD) Libraries

- Libraries contain 6 or 12 individuals
- Samples distributed evenly (year, origin, sex)
- Libraries pooled into “lanes” of 36 individuals
- Sequenced on Illumina HiSeq 2000

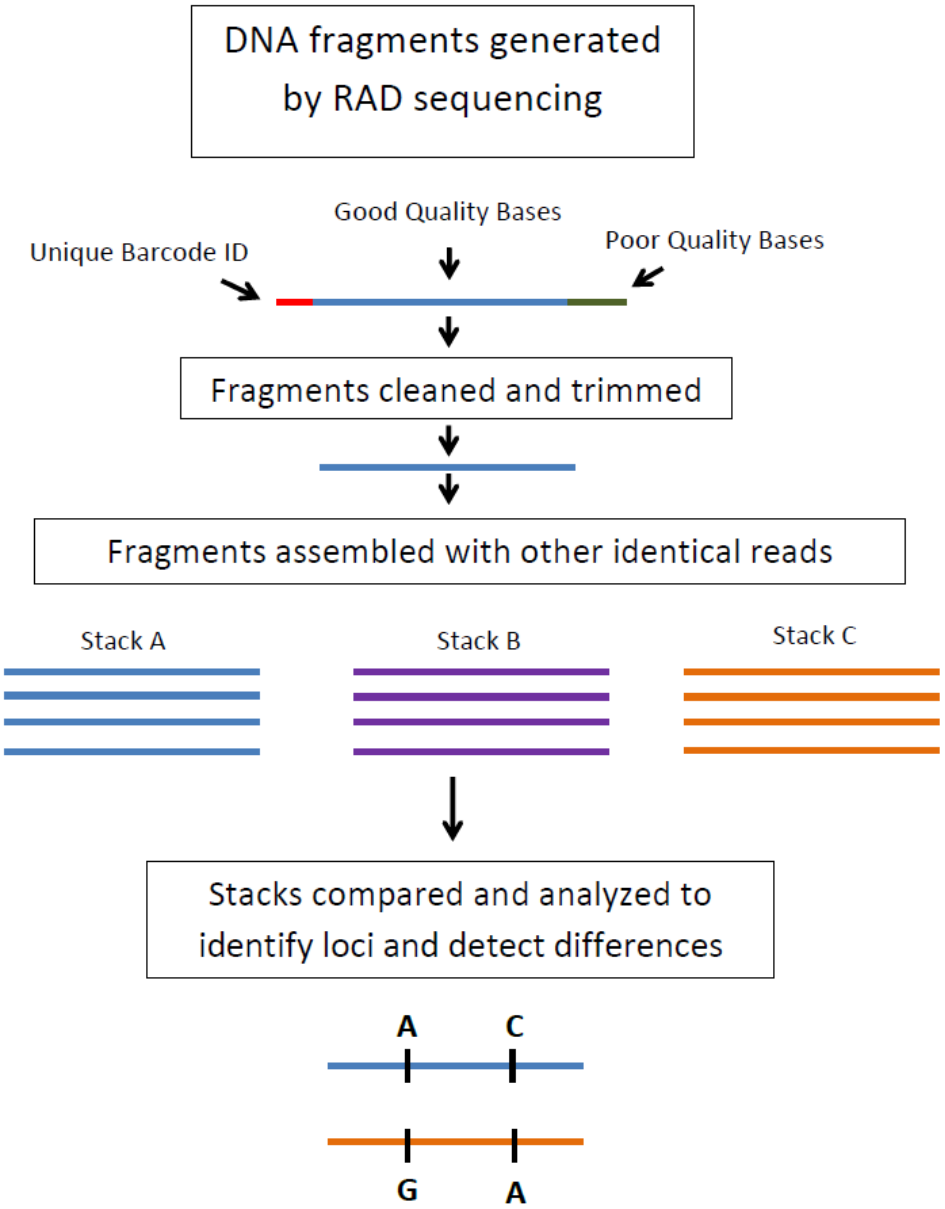
Samples Currently Sequenced

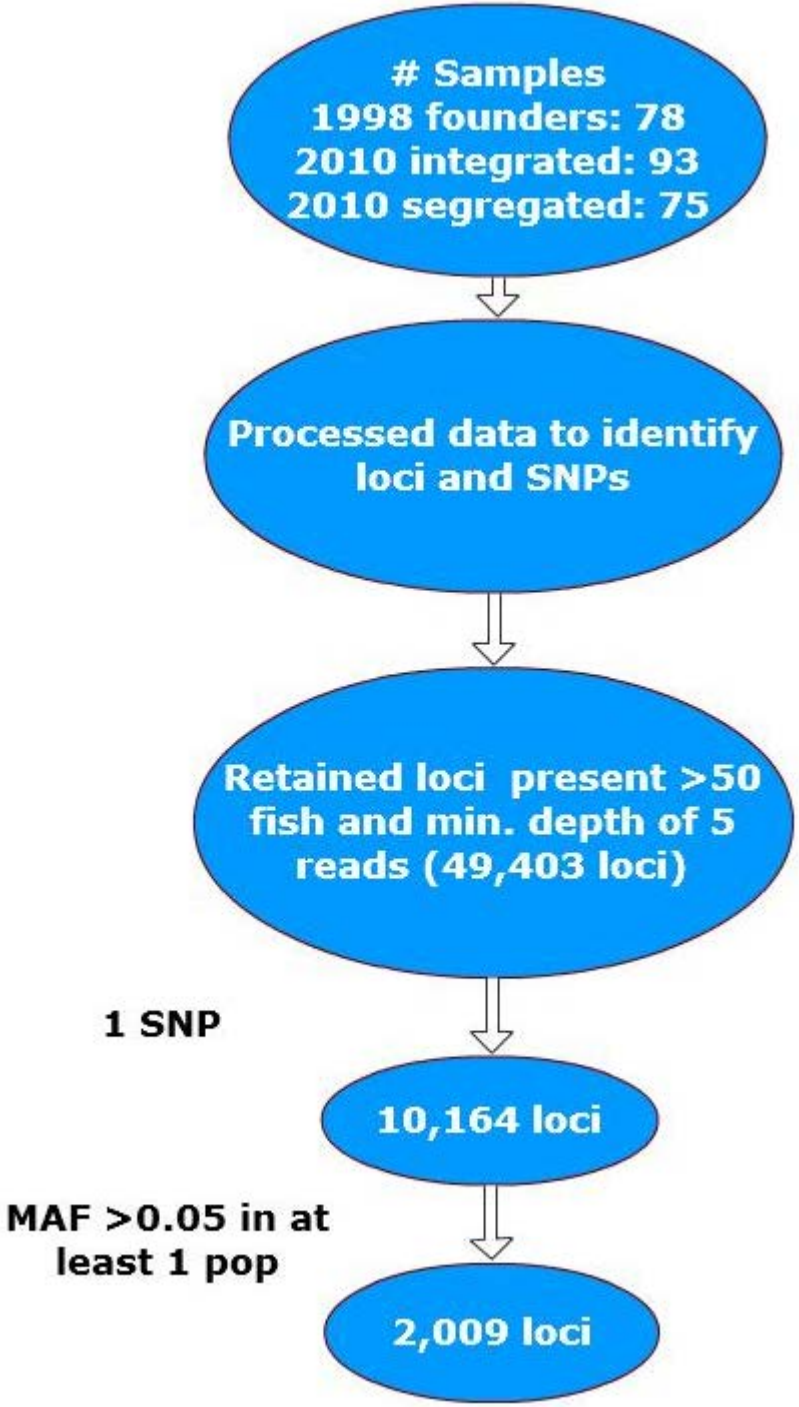
Year	Source population	Integrated hatchery fish	Segregated hatchery fish	Haploids
1998	78			
2002		76	61	
2006		89	65	
2010		93	75	
2011				167

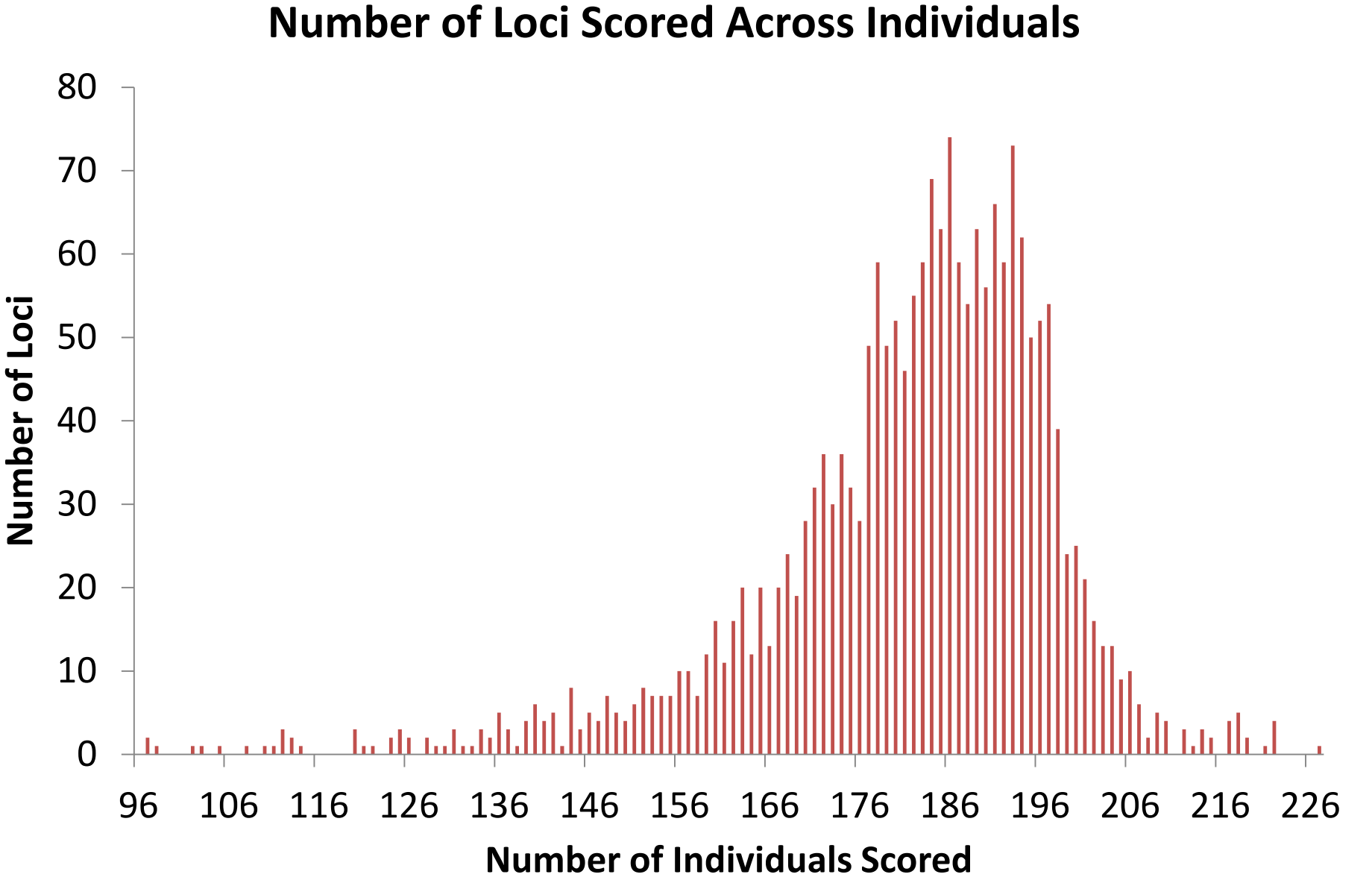
Samples Sequenced (N=704)

**Majority of population (80%) matures at age 4

Overview of Analysis




Samples
1998 founders: 78
2010 integrated: 93
2010 segregated: 75
Processed data to identify loci and SNPs
Retained loci present >50 fish and min. depth of 5 reads (49,403 loci)
1 SNP
10,164 loci
MAF >0.05 in at least 1 pop
2,009 loci



* Most loci were scored in at least 70% of the individuals

Population-Wise Comparisons

Pairwise population differentiation across all loci (distribution of genotypes)			
Population pair	**X^2**	**df**	**p-value**
1998-2010 integrated	3731.40	4002	Highly sign.
1998-2010 segregated	Infinity	4000	Highly sign.
2010 integrated-2010 segregated	Infinity	4014	Highly sign.

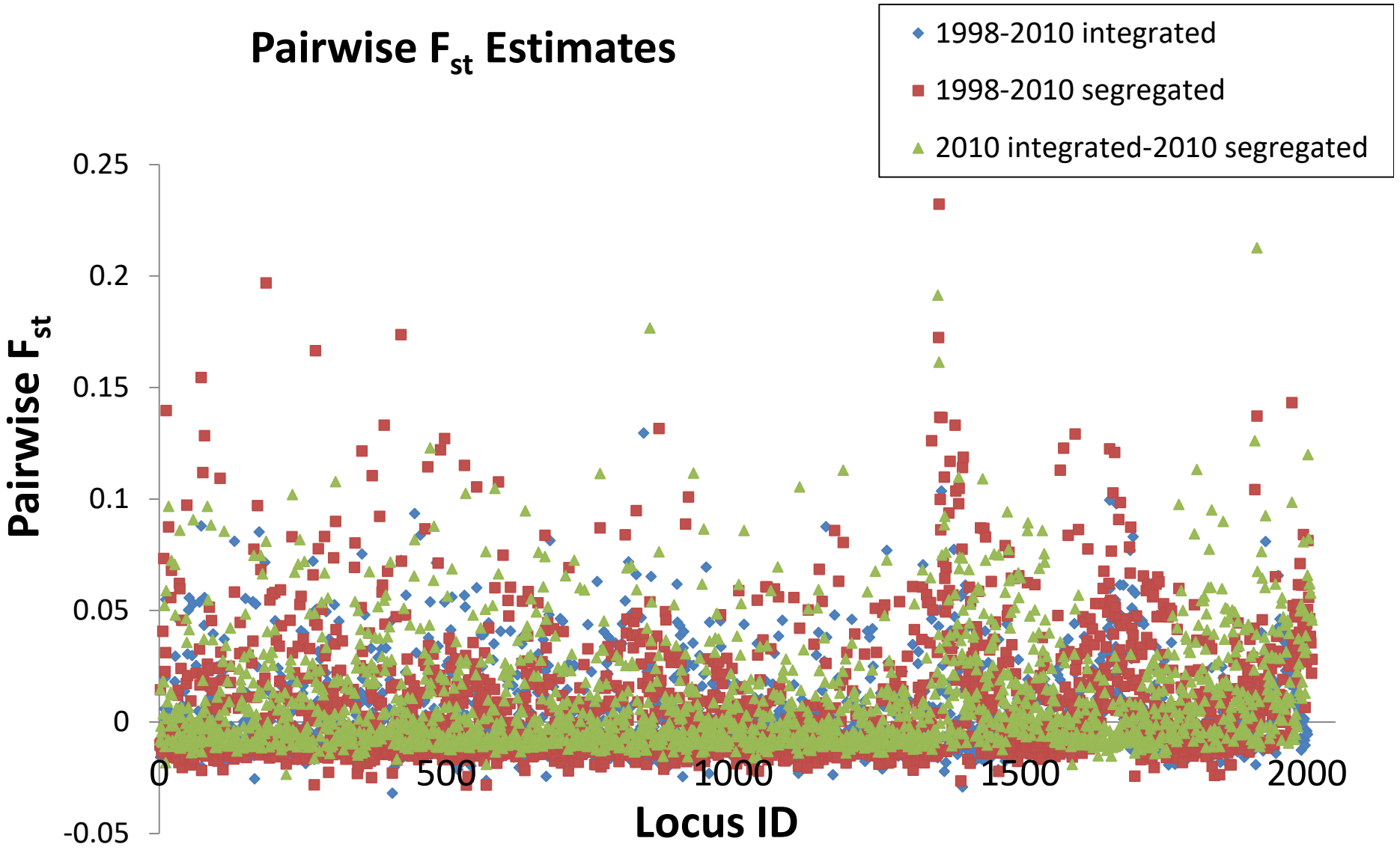
- Calculations performed in GENEPOP 4.1 (Raymond and Rousset, 1995)
- All populations are significantly different from each other in terms of distribution of genotypes
- But how much differentiation?

Genetic Differentiation

- F_{st} is a common measure of genetic differentiation
  - 0 = same
  - 1 = completely different

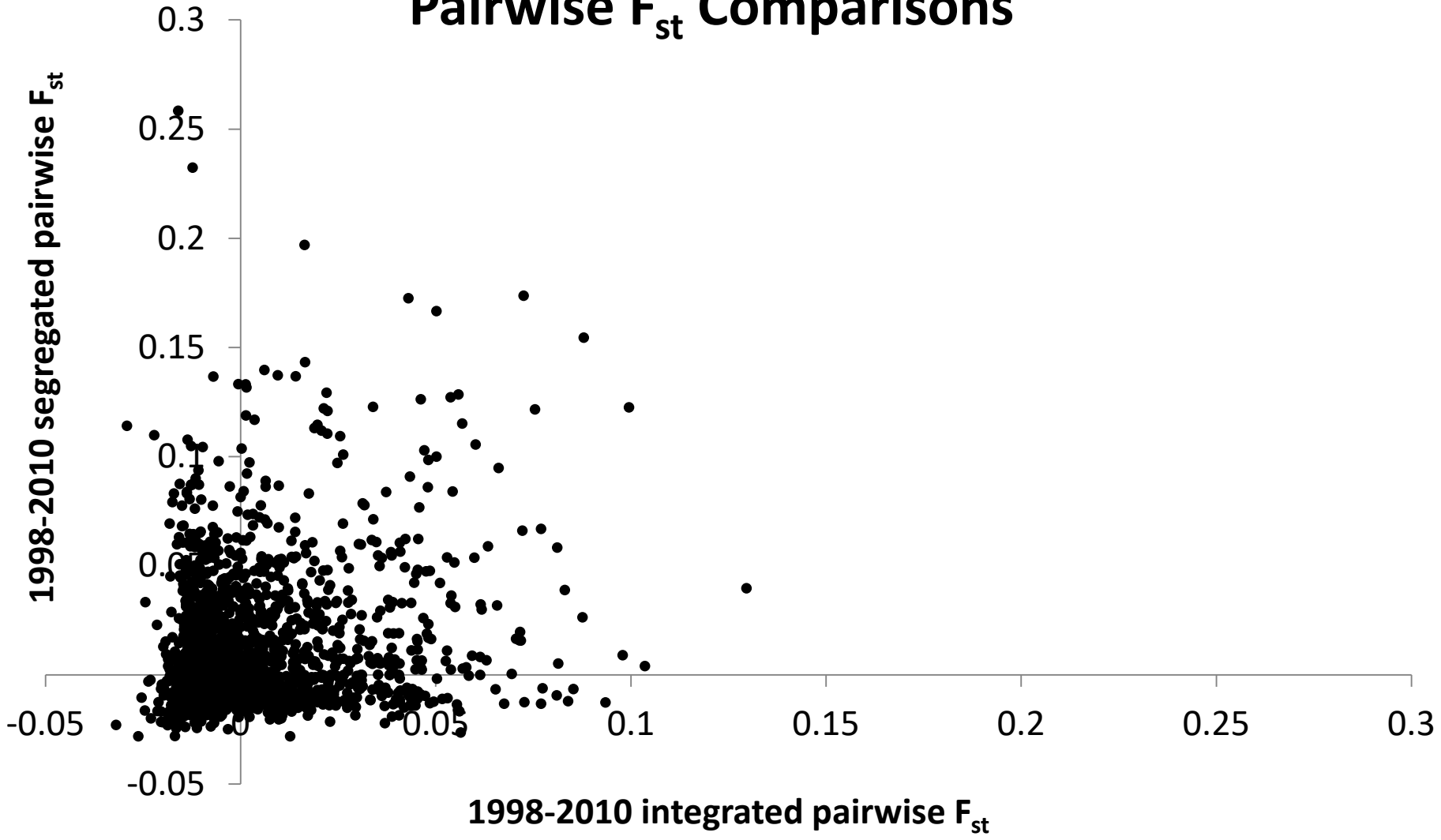
Pairwise F_{st} estimates across all loci:		
Population	**1998 Founders**	**2010 integrated**
2010 integrated	0.0008	
2010 segregated	0.0079	0.0085

* Little differentiation in both the integrated and segregated lines when compared to 1998 founders, but it seems to be higher in segregated line

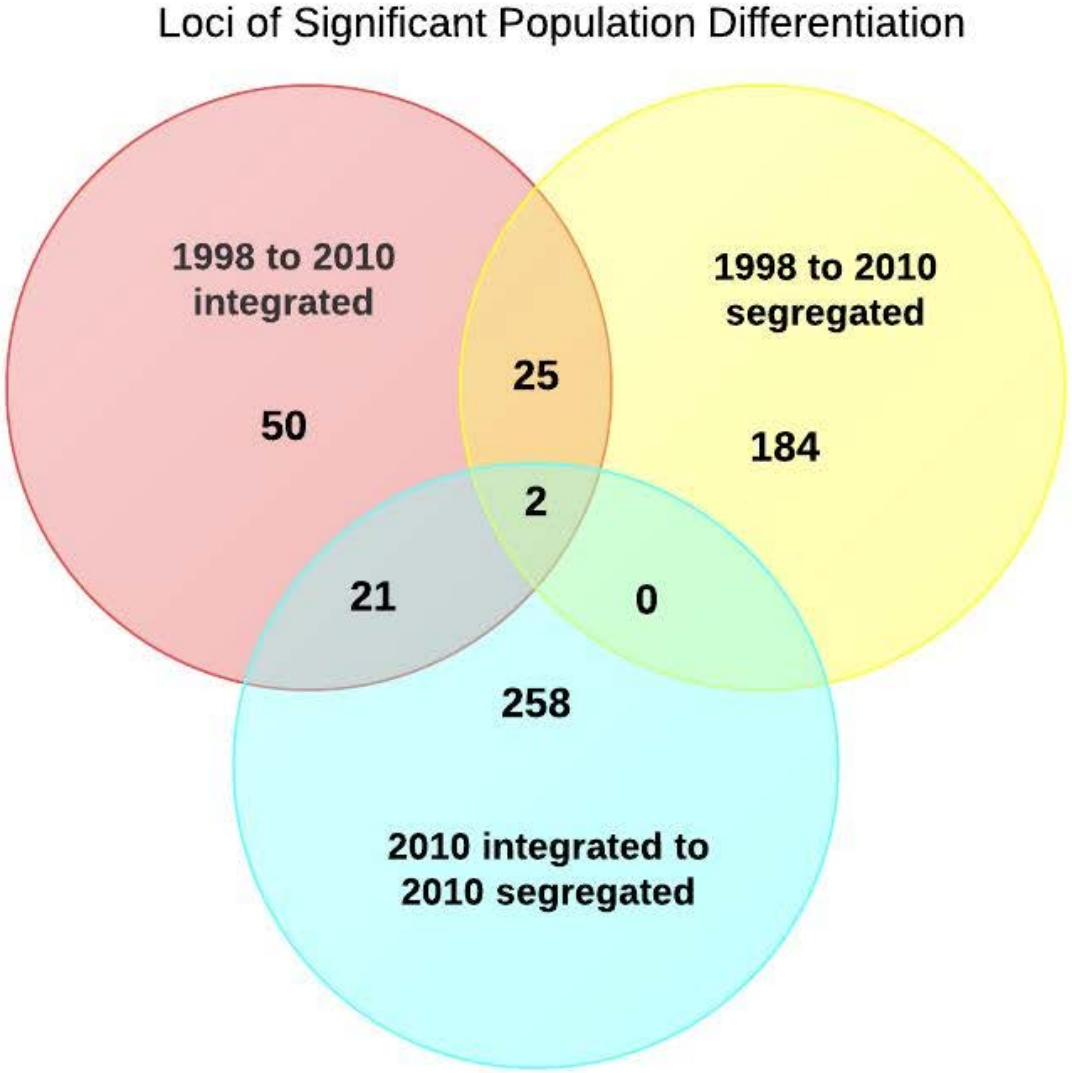


*Segregated line has more loci that have differentiated from founders than the integrated line

*1998 founders and 2010 integrated seem to have least number of loci with high F_{st}



* Segregated and integrated lines share some loci that have diverged from 1998 founders; have also diverged at unique loci

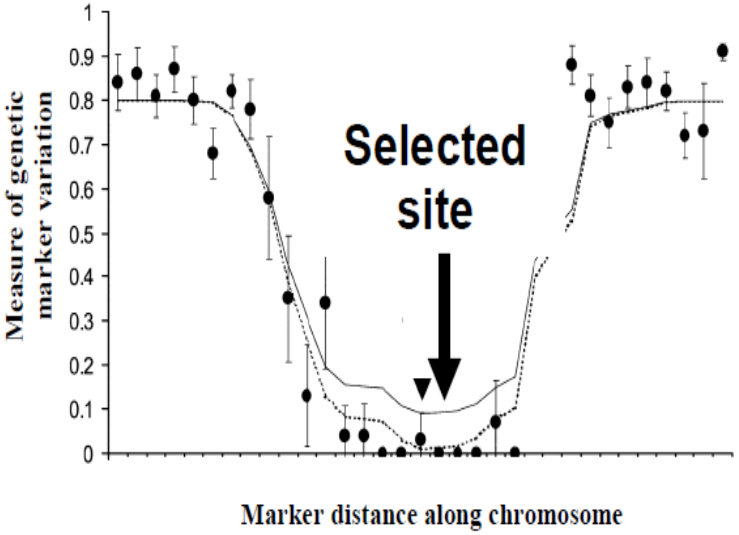


* Integrated hatchery line has the least number of differentiated loci
* 2010 segregated and integrated lines seem to be diverging

Next Steps

- Process sequence data for 2002 and 2006 samples
- Compare all generations to quantify rate of differentiation
- Identify loci under selection and map to genome locations

- Estimate amount of genetic change due to random variation for each population (N_e)
- Estimate level of relatedness and inbreeding within each population
- Genome wide association analysis

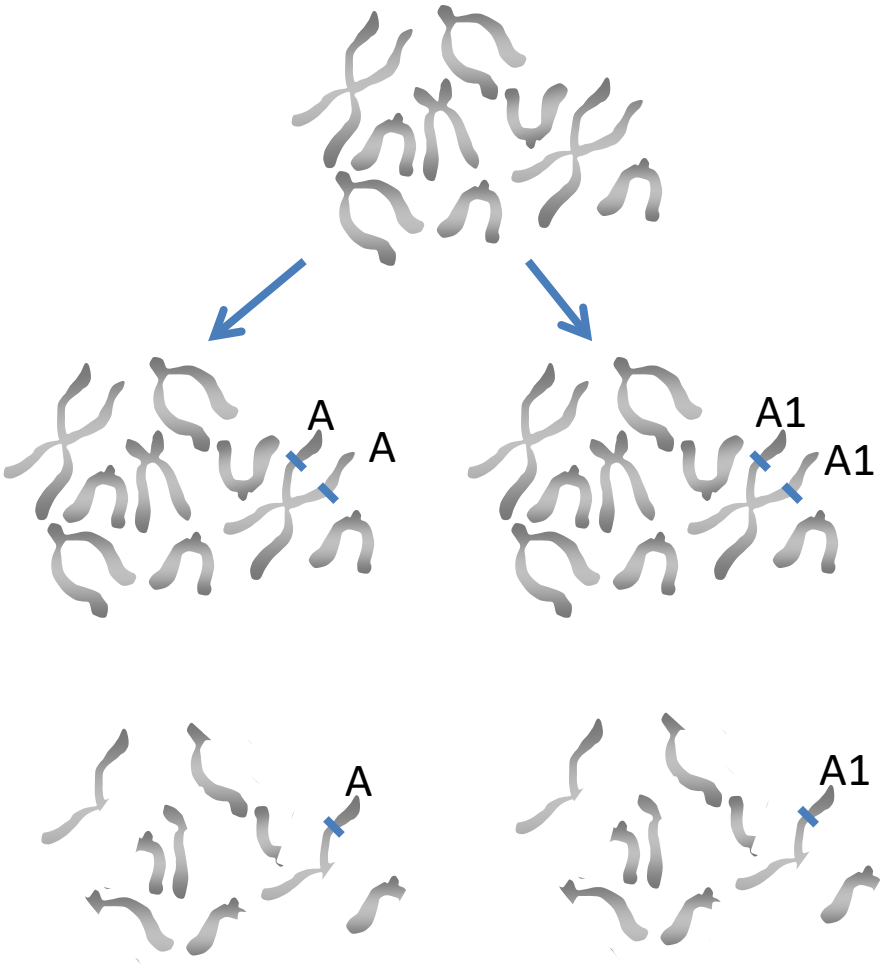


Genetic variation is reduced at sites under directional selection. Adopted from Nair et al. (2003).

Thanks!

- Our collaborators at CESRF and Yakama Nation
- Washington Department of Fish and Wildlife
- NOAA Northwest Fisheries Science Center
- Colleagues at UW
- Funded by Federal Biop funds “Hatchery reform”

Why are we creating haploids?



The salmon genome is duplicated (occurred about 20 million years ago)

Problem in genetic studies – are we studying variation at one site or at two separate sites (have different evolutionary processes)

Haploids have half the genome, so we can separate the sites and study them independently