

Using genomics to study segregated hatchery effects in western Washington steelhead



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Image credit: <http://www.worldfamilies.net/dnatesting>

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Outline

- Overview of study
- Introduction to important terms and concepts
- Why use genomics to study hatchery effects?
- Steelhead lineages and hatchery lines in western Washington
- Linkage maps of the steelhead genome in western Washington
- The future

Overview

- We are using genomic methods to identify and track hatchery effects in Lower Columbia River steelhead.
- Improve estimates of p_{HOS} – specifically from segregated early winter (Chambers Creek strain)
- Discover genetic markers of domestication to improve detection of introgression

Approach

- High-resolution marker discovery
- Develop genetic linkage maps
- Select uniformly distributed markers for scanning population samples
- Look for genomic signatures of selection during development of the segregated strains

Genomics 111 – key concepts

- Genomic studies incorporate information about patterns of genetic variation across a genome. Requires a map.

Population Genomics of Parallel Adaptation in Threespine Stickleback using Sequenced RAD Tags

Paul A. Hohenlohe^{1,3}, Susan Bassham^{1,3}, Paul D. Etter², Nicholas Stiffler³, Eric A. Johnson², William A. Cresko^{1*}

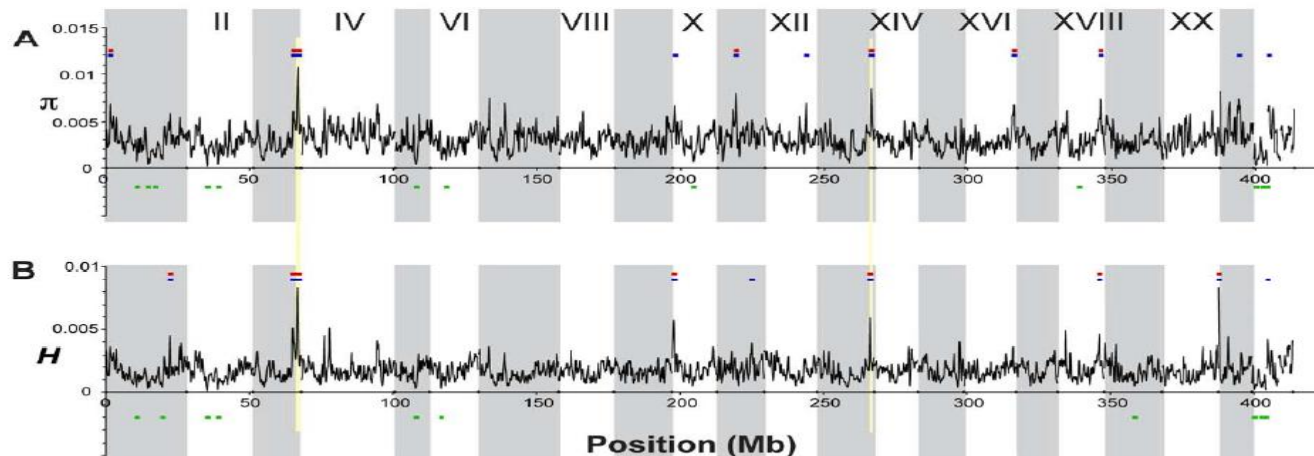
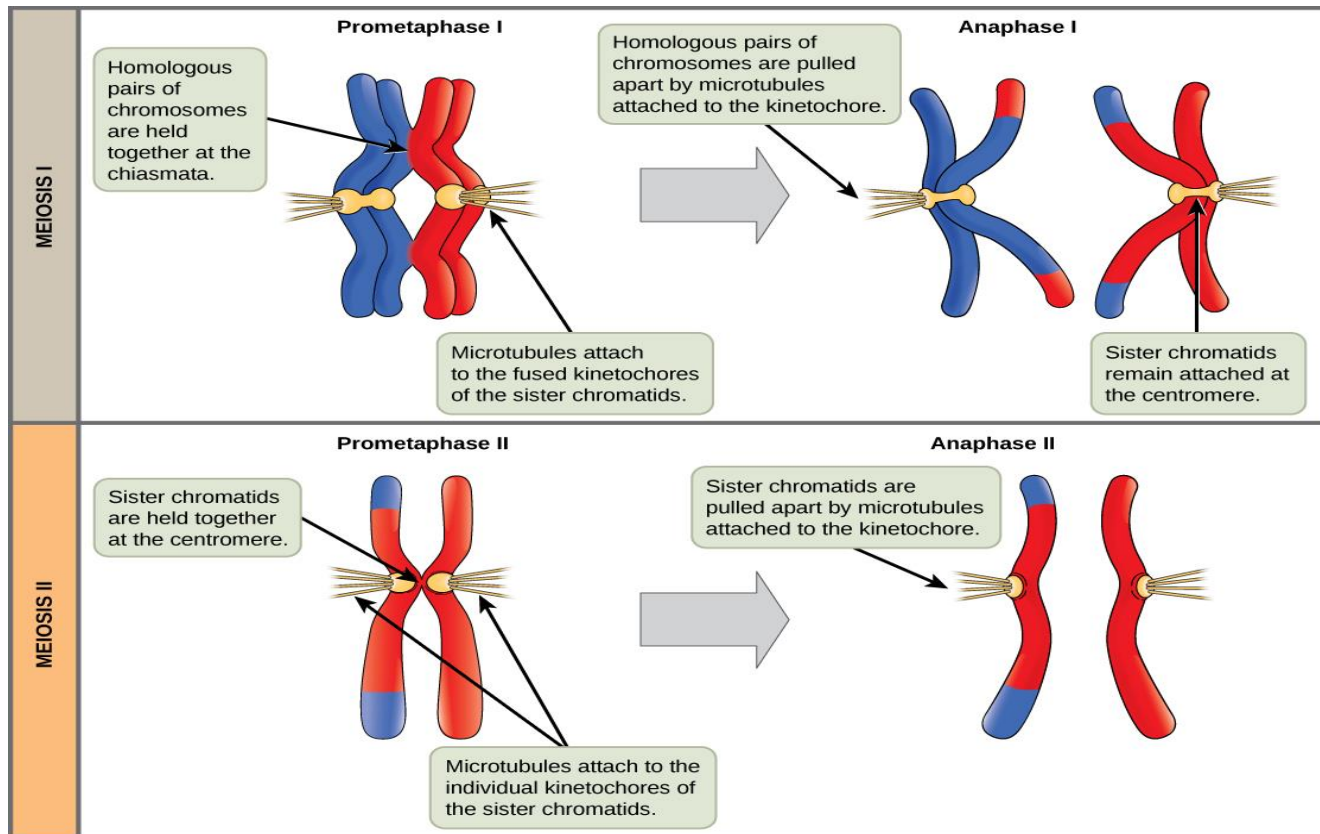


Figure 4. Genome-wide patterns of nucleotide diversity. Each plot shows a smoothed distribution of the statistical measure across the genome (black lines). Colored bars above and below the distributions indicate regions of significantly elevated ($p \leq 10^{-5}$, blue; $p \leq 10^{-7}$, red) and reduced ($p \leq 10^{-5}$, green) values, assessed by bootstrap resampling. Vertical shading indicates the 21 linkage groups and the unassembled scaffolds greater than 1 Mb in length, and gold shading indicates two regions showing evidence of balancing selection as discussed in the text. (A) Nucleotide diversity (π) across all five stickleback populations sampled. (B) Heterozygosity (H) across all five populations. doi:10.1371/journal.pgen.1000862.g004

Genomics 111 – key concepts

Crossovers during meiosis reveal the relative locations of genes and distances between them



Genomics 111 – key concepts

- Genetic linkage mapping uses the frequencies of crossovers to estimate the ordering of genes and the distances between them.

Everett *et al.* *BMC Genomics* 2012, **13**:521
<http://www.biomedcentral.com/1471-2164/13/521>



RESEARCH ARTICLE

Open Access

Meiotic maps of sockeye salmon derived from massively parallel DNA sequencing

Meredith V Everett^{1*}, Michael R Miller² and James E Seeb^{1*}

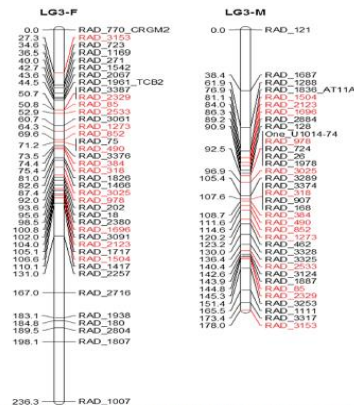


Figure 4 Female (F) and Male (M) consensus maps for linkage group LG2. Markers shared between the male and female maps are in red. Marker names beginning with 'RAD_' are red tag maps and names beginning with 'CR_' are from the reference genome.

Genomics 111 – key concepts

- Structural chromosomal differences between lineages within species can serve as persistent tags that identify the lineages

Brenna-Hansen *et al.* *BMC Genomics* 2012, **13**:432
<http://www.biomedcentral.com/1471-2164/13/432>

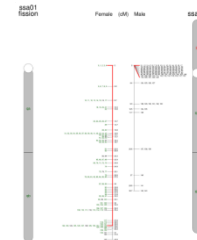
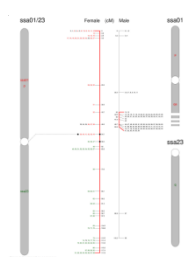


RESEARCH ARTICLE

Open Access

Chromosomal differences between European and North American Atlantic salmon discovered by linkage mapping and supported by fluorescence *in situ* hybridization analysis

Silje Brenna-Hansen¹, Jieying Li², Matthew P Kent¹, Elizabeth G Boulding³, Sonja Dominik⁴, William S Davidson² and Sigbjørn Lien^{1*}



Genomics 111 – key concepts

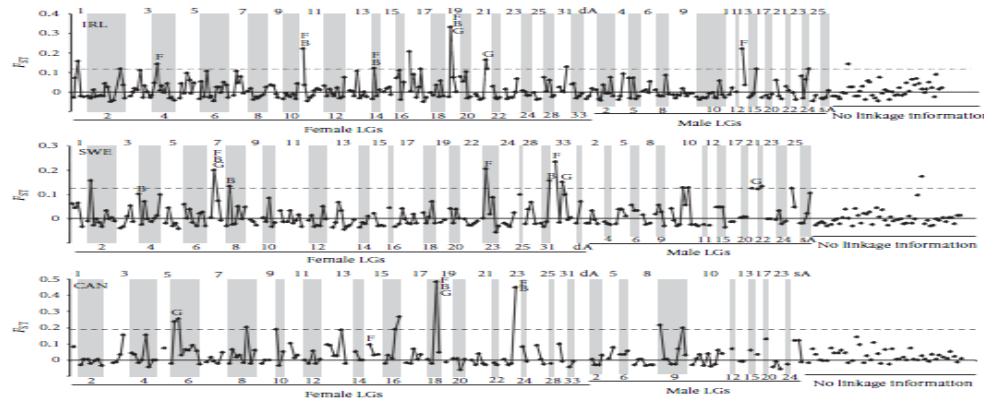
- Positive selection skews the distribution of reproductive success within a population and leaves genomic “footprints”

Hindawi Publishing Corporation
Comparative and Functional Genomics
Volume 2012, Article ID 628204, 14 pages
doi:10.1155/2012/628204

Research Article

Screen for Footprints of Selection during Domestication/Captive Breeding of Atlantic Salmon

Anti Vasemägi,^{1,2} Jan Nilsson,³ Philip McGinnity,^{4,5} Tom Cross,⁴ Patrick O'Reilly,⁶
Brian Glebe,⁷ Bo Peng,⁸ Paul Ragnar Berg,⁹ and Craig Robert Primmer¹



Why use genomics to study hatchery effects?

- Several long-term studies have implicated inter-breeding between hatchery- and wild-origin steelhead in the declining abundance of wild populations but specific causal genetic changes remain elusive.
- Current management emphasizes natural production and requires robust tools to monitor the interactions between hatchery- and natural-origin populations.
- Recent advances in DNA sequencing technology have made collection of genome-wide data on genetic variation practical.
- A large body of evolutionary theory provides the bases for detecting characteristic patterns of selection in genome-wide data sets.
- Knowing when selection occurred might allow us to calibrate models of recent adaptive evolution that could be used in other situations.

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- Positive selection can create characteristic patterns of variation in a genome

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Two distinct chromosomal lineages exist in western Washington steelhead

Copeia, 1983(3), pp. 650–662

Chromosomal Differences Among Rainbow Trout Populations

GARY H. THORGAARD

Chromosome numbers varied from 58 to 64 among rainbow trout sampled from 29 locations ranging from Alaska to California. The differences were associated with centric fusions or fissions; the chromosome arm number was constant at 104 while the chromosome number varied. A 58 chromosome karyotype similar to that found in the golden and redband trout was the most commonly observed karyotype over the species range. The similar karyotypes in the rain-

Copeia, 1999(2), pp. 287–298

Geographic Distribution of Chromosome and Microsatellite DNA Polymorphisms in *Oncorhynchus mykiss* Native to Western Washington

CARL O. OSTBERG AND GARY H. THORGAARD

Chromosome studies of native populations of *Oncorhynchus mykiss* (steelhead and rainbow trout) in western Washington and southern British Columbia revealed the presence of two evolutionarily distinct chromosome lineages. Populations between, and including, the Elwha River, Washington, and Chilliwack River, British Columbia, contained $2n = 60$ chromosomes. Populations on the central Washington coast contained $2n = 58$ chromosomes. The north Washington coast and western Strait of

Distribution of steelhead chromosomal lineages



Ice Age Floods in the Pacific Northwest.

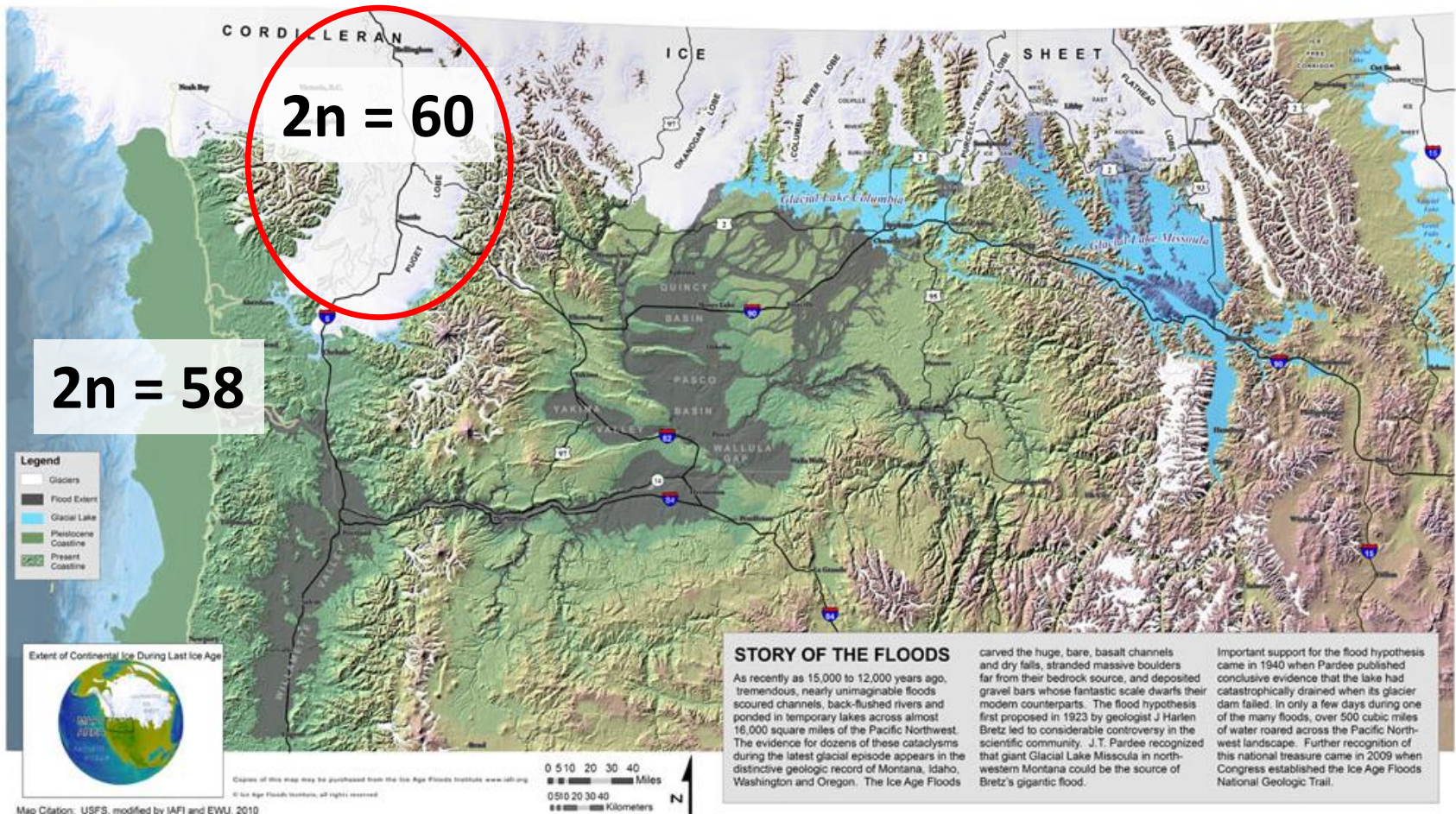
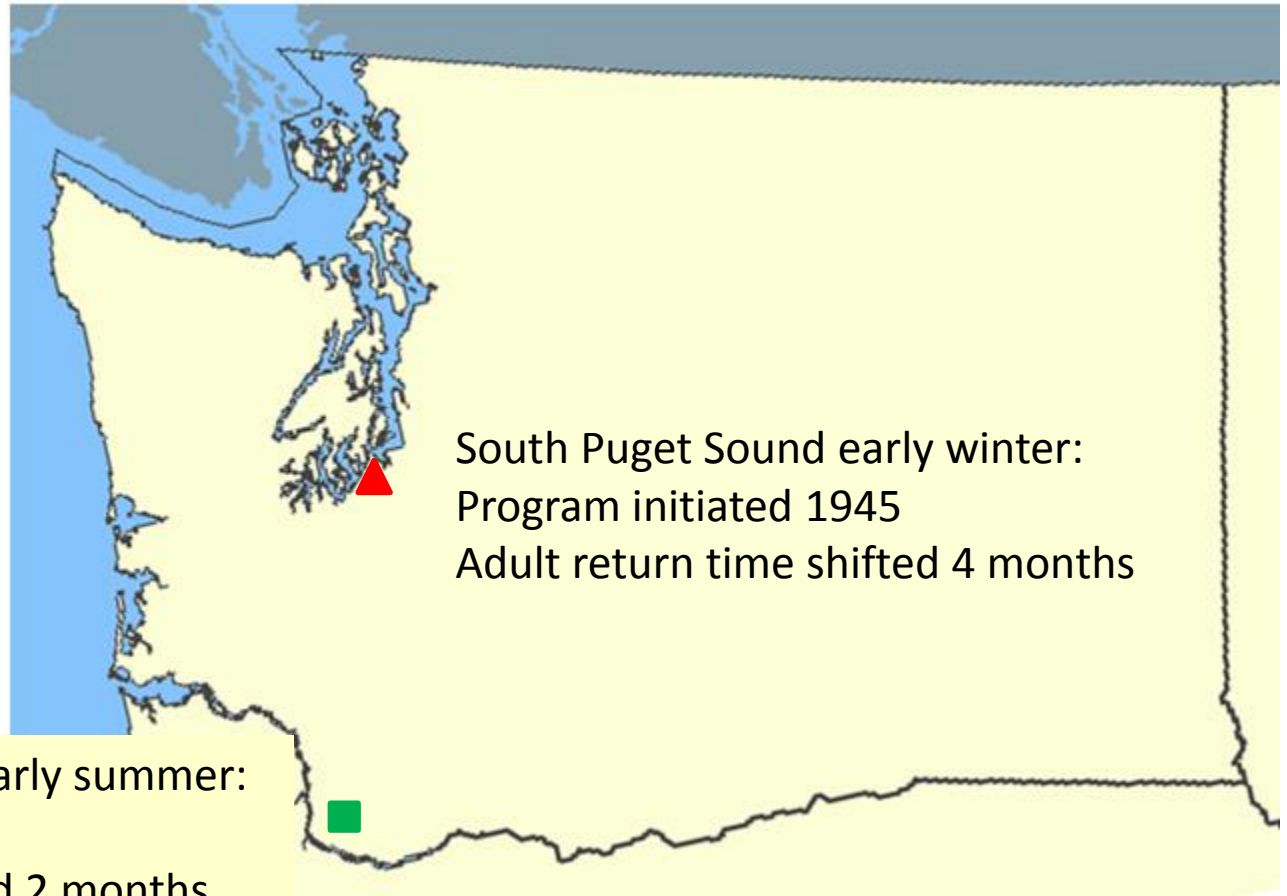


Image source: http://www.iafi.org/images/floodsmap_lg.jpg

Segregated steelhead hatchery lines in western Washington were bred for aquaculture

Selection criteria:

- 1) Early spawners
- 2) Adult returns from yearling releases



Lower Columbia River early summer:
Program initiated 1956
Adult return time shifted 2 months

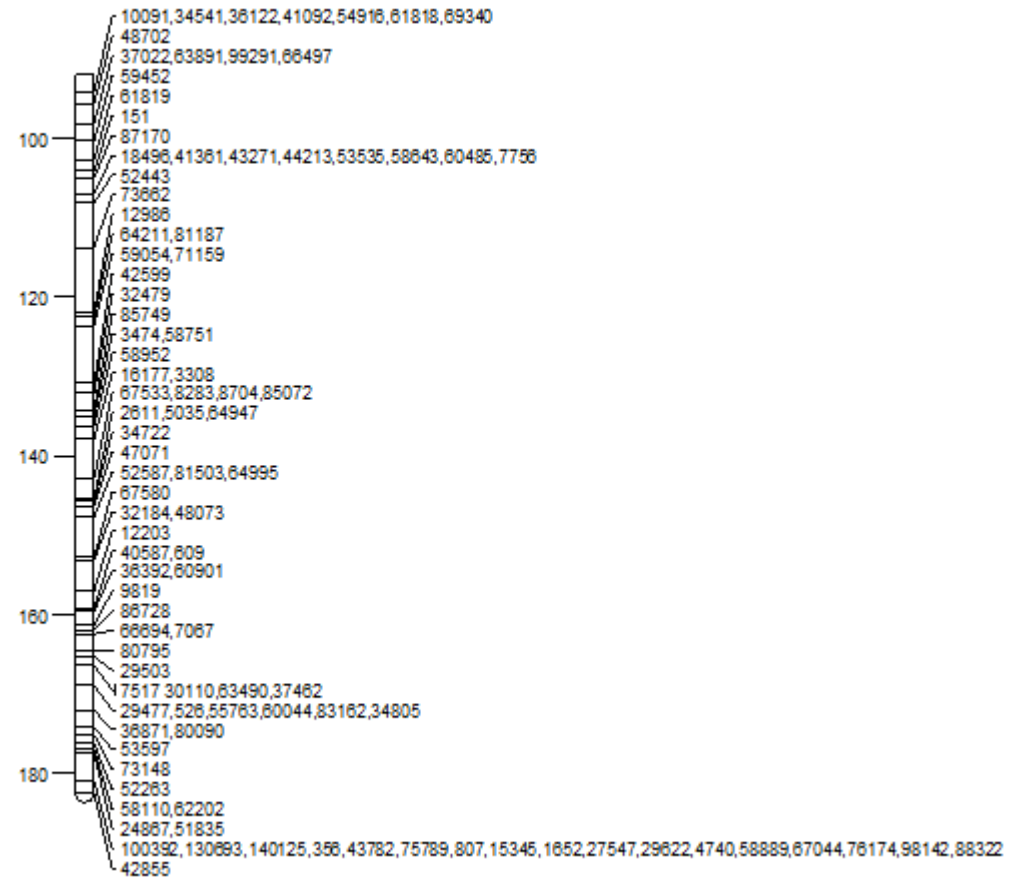
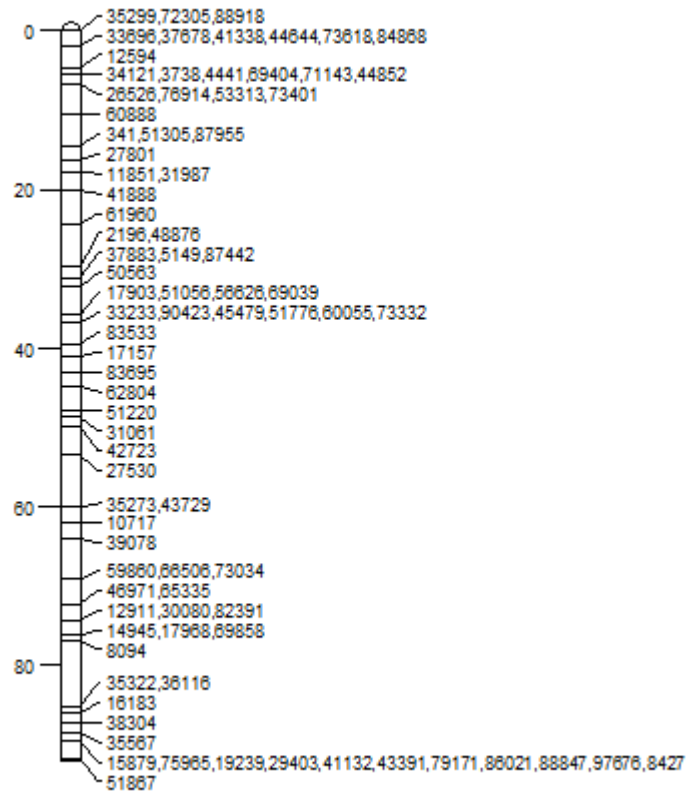
Genetic linkage maps

- Created gynogenetic haploid mapping families
- Enzymatically cut genomic DNA at specific sequence motifs
- Attached 6-nucleotide, individual-specific “barcodes”
- Sequenced DNA fragments at UO Genomics Core Facility
- Screened the raw sequence reads for quality and generated a catalog of loci and alleles
- Assigned haplotypes for each haploid offspring at all observed loci
- Deduced linkage relationships from pair-wise recombination fractions to generate linkage maps.

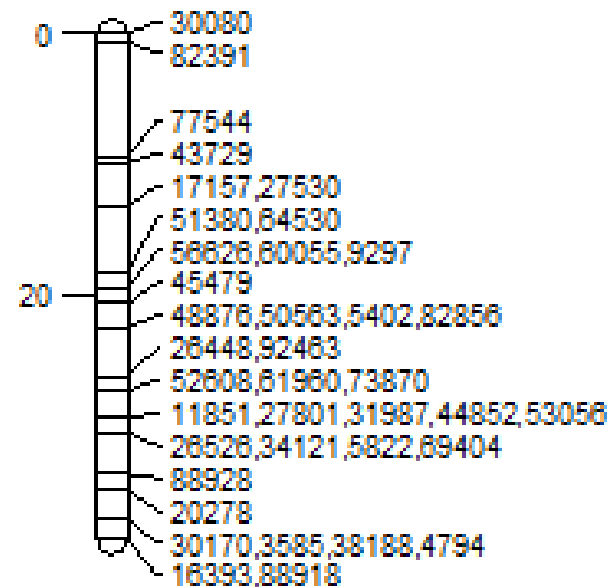
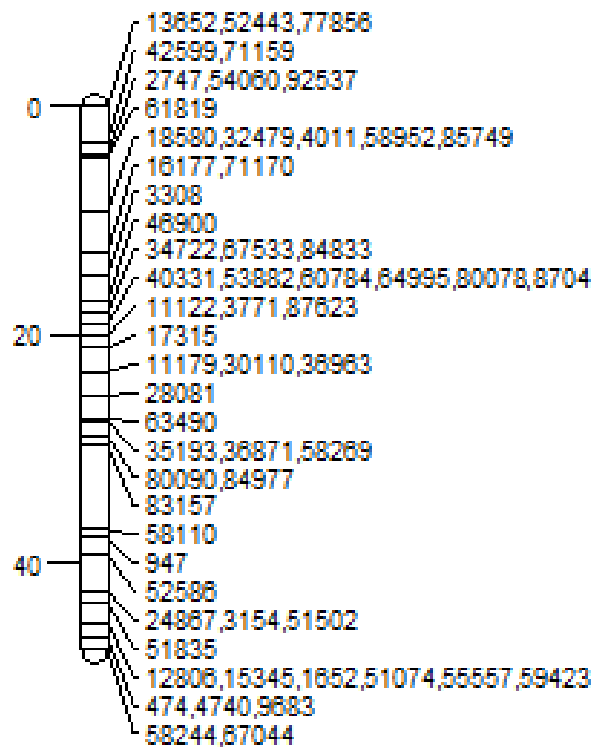
Preliminary mapping results

- 5646 markers mapped
- 29 linkage groups in the indigenous Kalama River families; 30 linkage groups in the out-of-basin early winter (Chambers Creek strain)

Linkage group W-29 in indigenous Kalama River winter steelhead



Linkage groups W-29_{PS} and W-30_{PS} in out-of-basin early winter steelhead



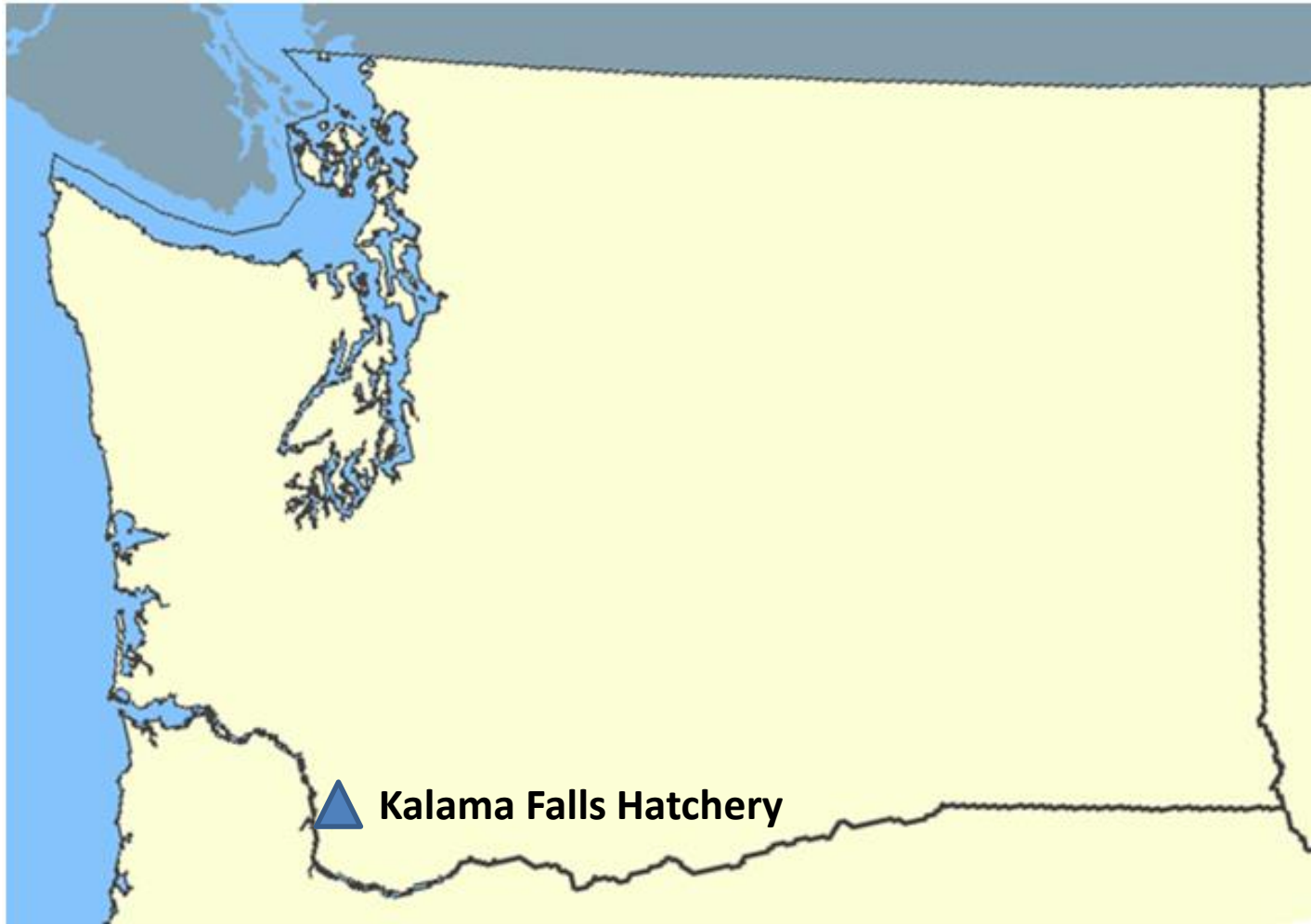
Still to do ...

- Merge our maps with existing ones
- Identify the locations of known genes
- Select a subset of loci to use in population screening
- Estimate p_{HOS} in the Kalama River
- Look for signs of recent positive selection

Acknowledgements

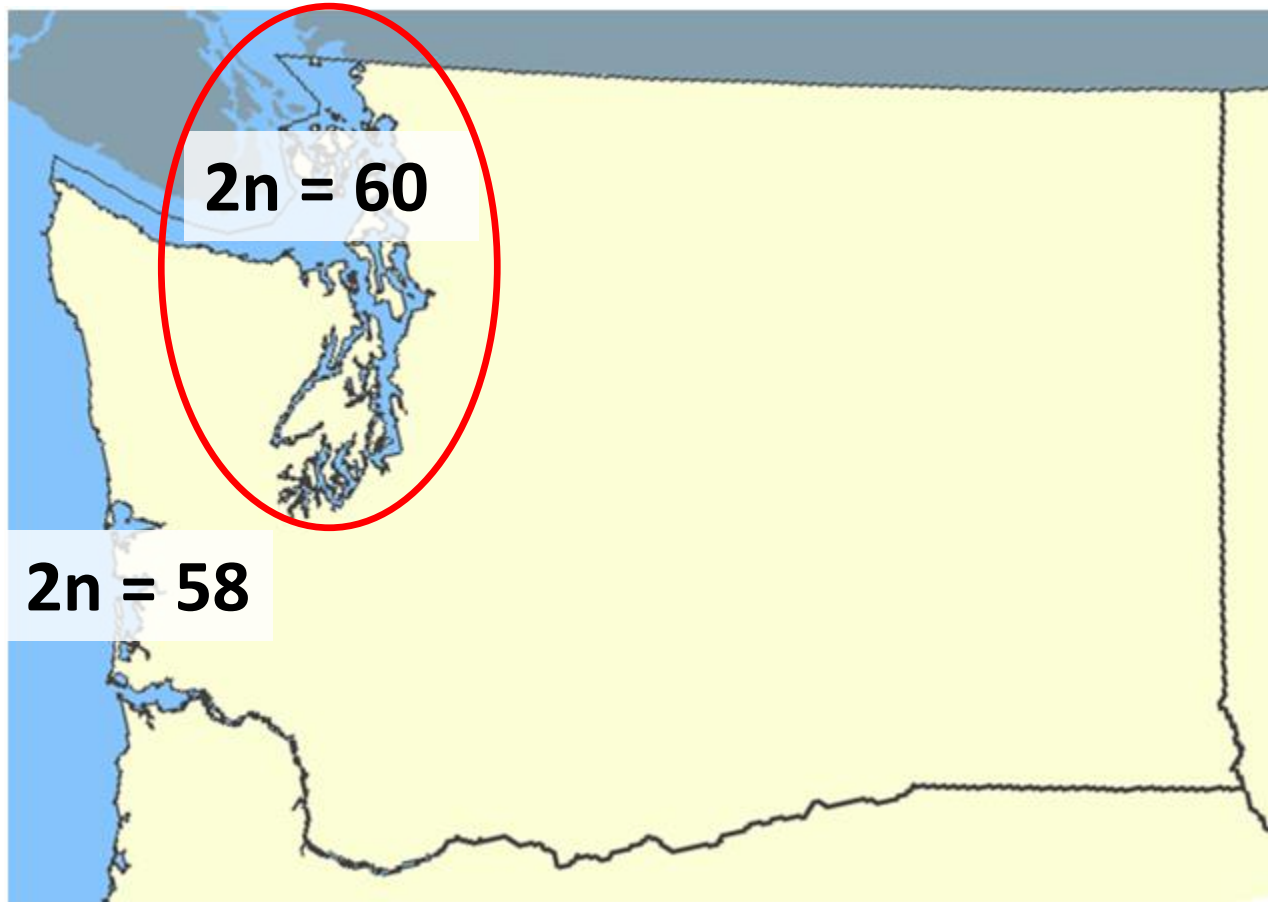
- Financial support from the Washington State General Fund, a Lauren Donaldson scholarship, the Wild Steelhead Coalition
- The crew at Kalama Falls Hatchery
- Sampling assistance – Marissa Jones, Cherril Bowman, Edith Martinez, Todd Seamons, Cheryl Dean, Helen Niemi-Warheit
- Sequencing library preparation- Edith Martinez and Carita Pascal
- Data analysis discussions – Ryan Waples

Source of mapping families used in this study



Early winter and early summer hatchery steelhead strains in western Washington

Distribution of steelhead chromosomal lineages



Note on terminology

Convention on Biological Diversity: Article 2. Use of Terms

"Domesticated or cultivated species" means species in which the evolutionary process has been influenced by humans to meet their needs.