9.1 Genomic Adaptation and Conservation of Life-History Variation

NOAA FISHERIES
Southwest Fisheries Science Center

Devon Pearse

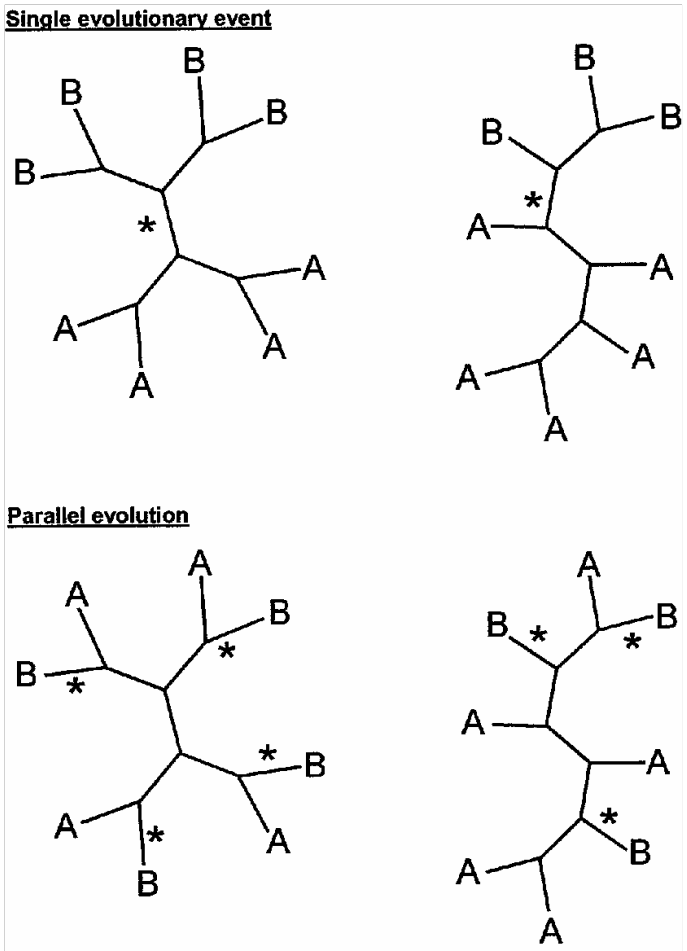
May 6, 2015

>What is the role of **population genetics** in conservation?

Delineate ESU/DPS boundaries, stock identification, parentage.

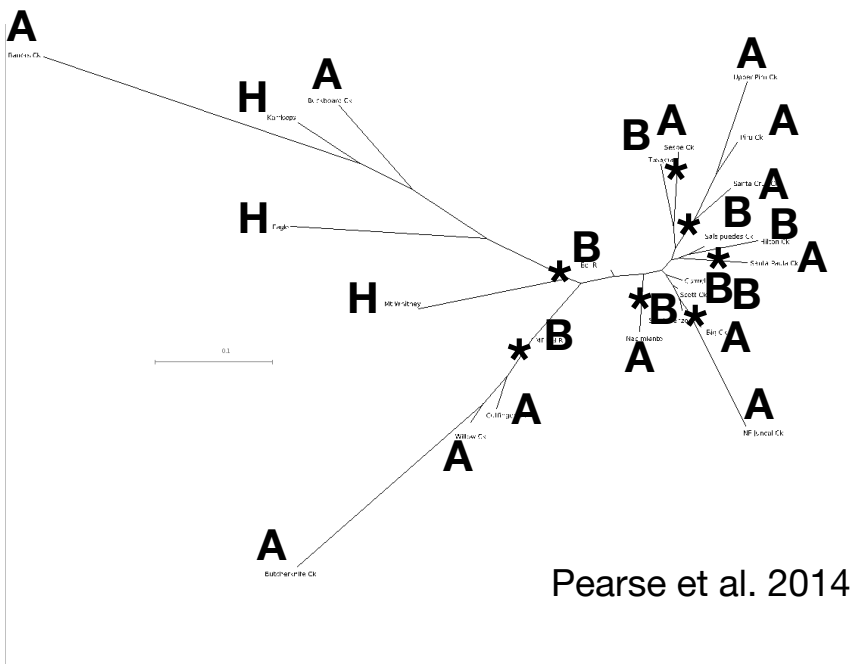
>How is **‘adaptation genomics’** different?

Parallel evolution of life-history traits:



Waples et al. 2004

"…all naturally spawned **anadromous** *O. mykiss* (steelhead) **populations below** natural and manmade impassable barriers…" NMFS 2006

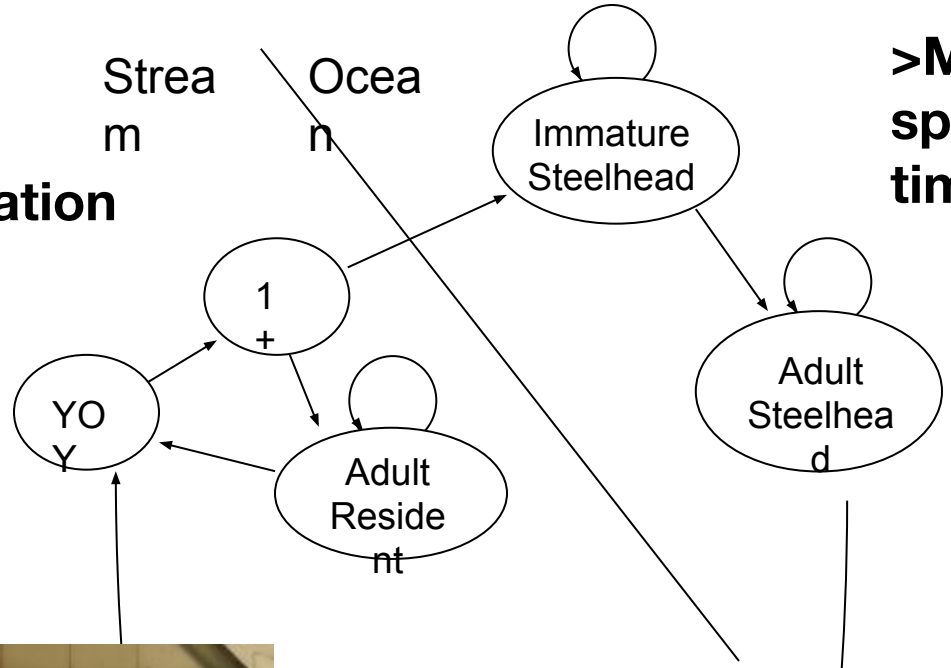


Pearse et al. 2014

Smoltification is a complex, plastic, phenotype, involving morphological, physiological, and behavioral changes.

>Partial migration

>Marine survival, spawning migration, timing



Beakes et al. 2010; Berejikian et al. 2013, 2014
Hayes et al. 2012; Satterthwaite et al. 2012; Sogard et al. 2012

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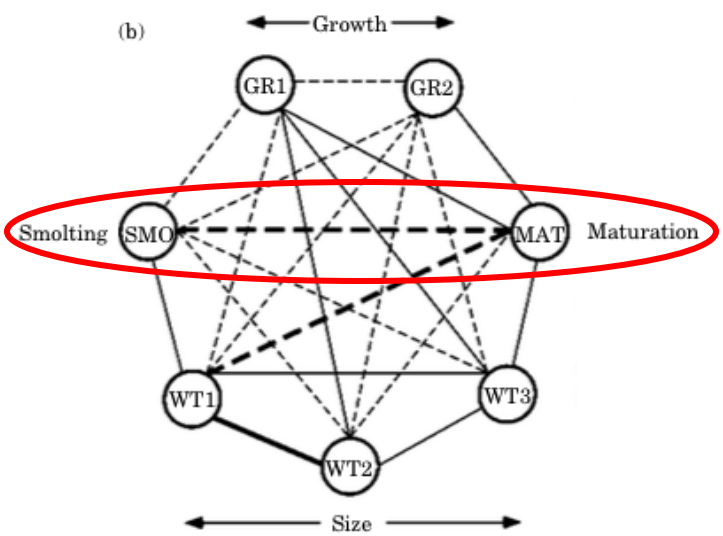
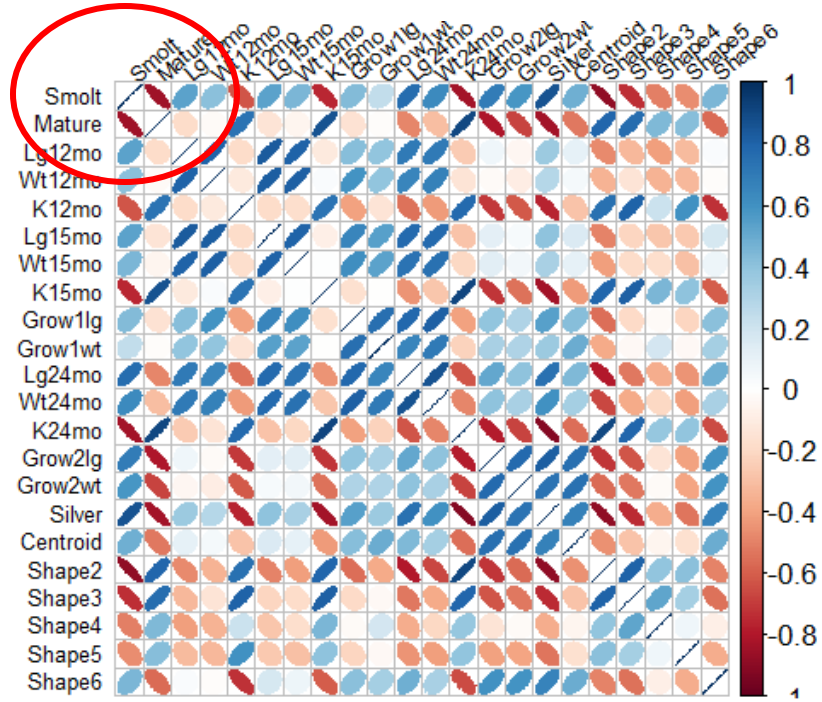
Genetic architecture of anadromy/residency in *O. mykiss*

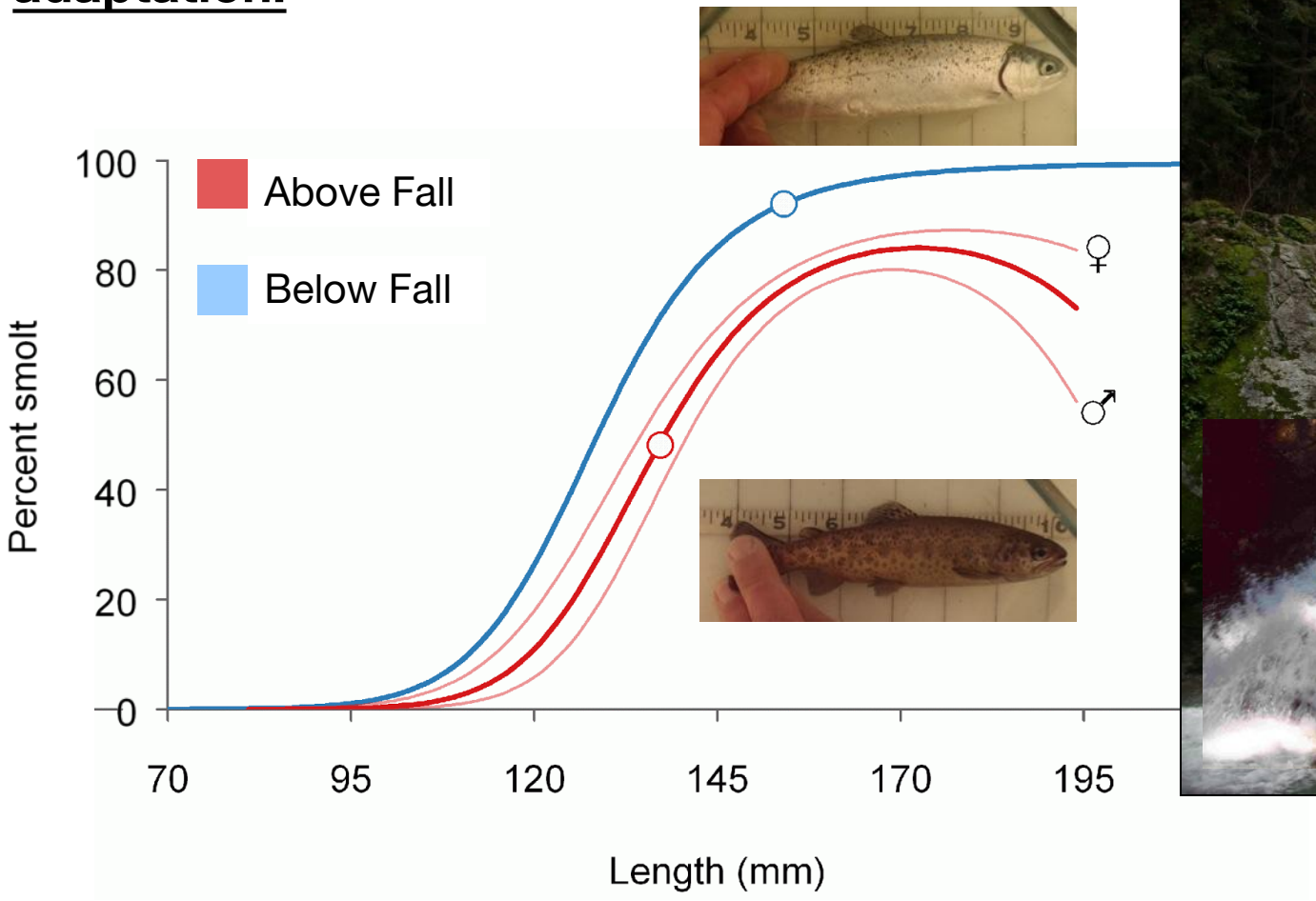
>Heritable (Neave 1944)

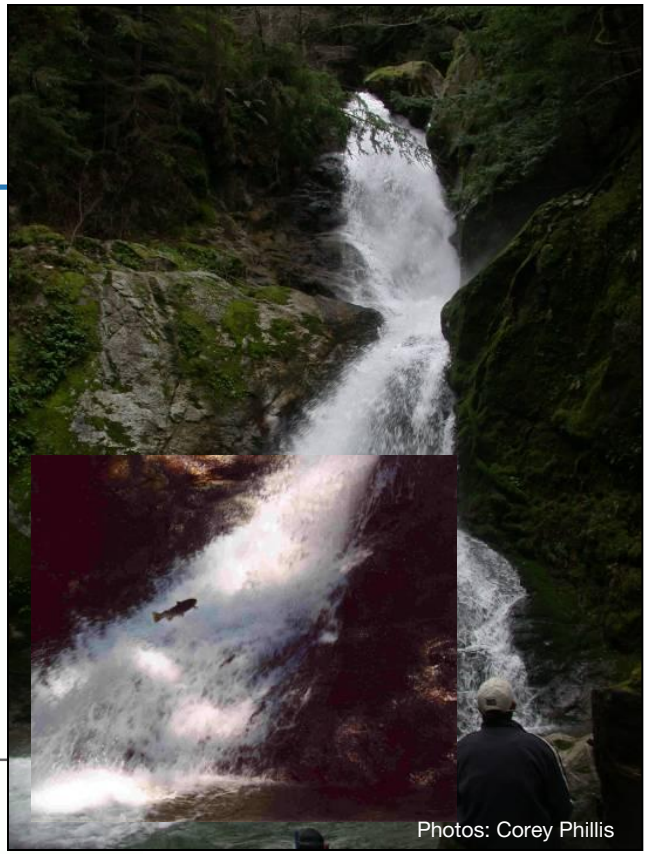
>Negative genetic correlation between anadromy and residency in Sashin Creek, AK (NWFSC: Thrower et al. 2004; Hecht et al. 2015)





Big Creek Falls: Strong selection on fish introduced above the falls not to migrate downstream over the falls leads to **rapid resident adaptation:**

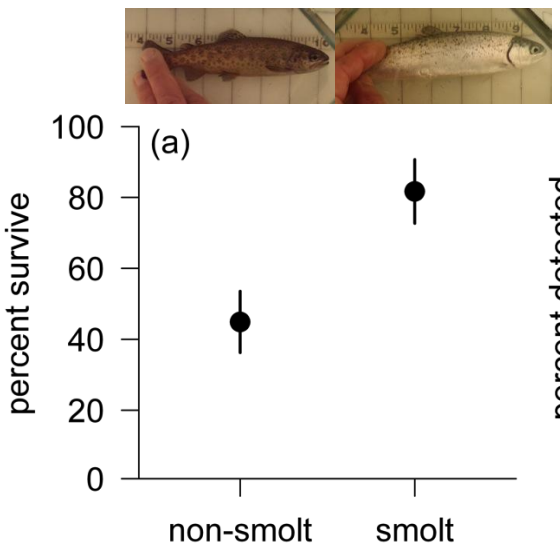




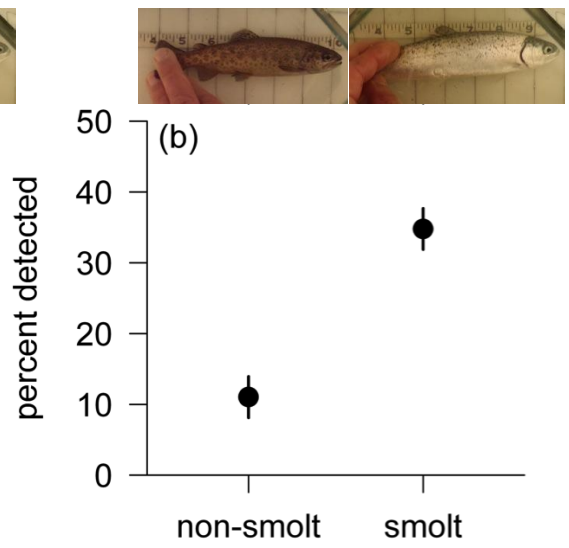
Pearse et al. 2009; Phillis et al. *accepted*

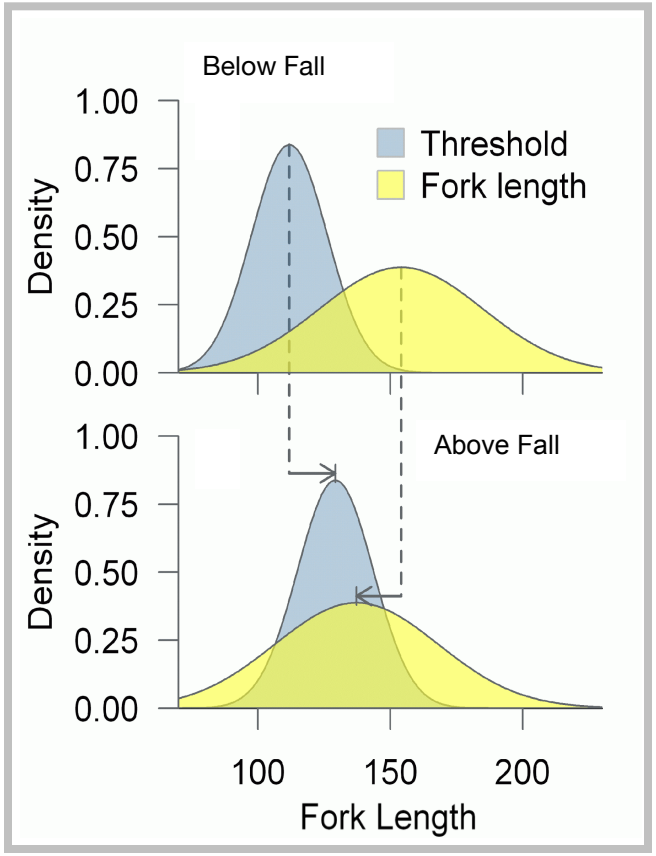
Correlated phenotypes, regardless of above- or below origin

Seawater Challenge



Downstream Movement





>Note low **marine survival** of above-barrier fish. (Thrower & Hard 2009)

Phillis et al. *accepted*

Smoltification is a **complex**, plastic, phenotype, involving morphological, physiological, and behavioral changes.

What is the **genomic basis** of this trait?

>Numerous genomic studies of life-history in *O. mykiss*:

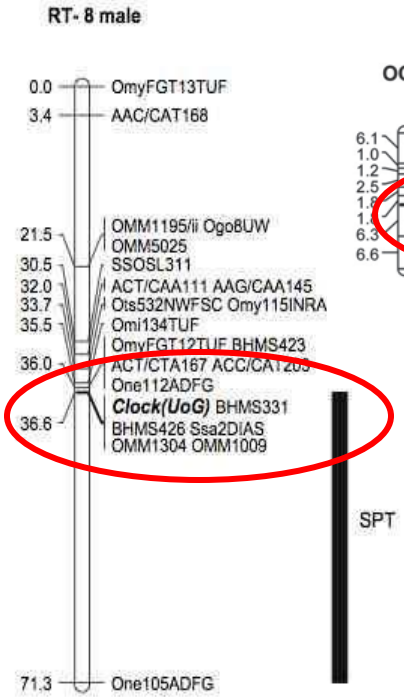
Robison et al. 2001; O'Malley et al. 2003; Leder et al. 2006; Phillips et al. 2006;
Nichols et al. 2007, 2008; Haidle et al. 2008; Colihueque et al. 2010
Paibomesai et al. 2010; Easton et al. 2011; Le Bras et al. 2011
Martínez et al. 2011; Miller et al. 2012; Narum et al. 2011
Limborg et al. 2012; Hecht et al. 2012a,b; Hale et al. 2014; Pearse et al. 2014; McKinney et al. 2015

>Results highly variable, but many have associated one region of chromosome Omy5 with correlated life-history traits:

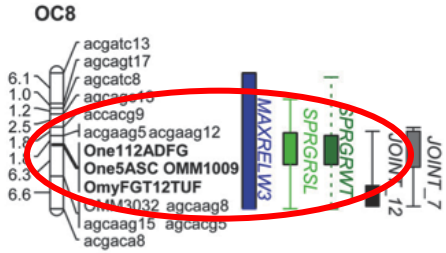
Spawn timing: O'Malley et al. 2003; Leder et al. 2006; Colihueque et al. 2010
Smoltification or **migration**: Nichols et al. 2008, Martínez et al. 2011
Development rate and/or **early maturation**:
Nichols et al. 2007; Haidle et al. 2008; Easton et al. 2011, Miller et al. 2012

>This region contains QTL for smolting, spawn timing, development rate, and the *Clock* gene, and has **reduced recombination**. (Phillips et al. 2006)

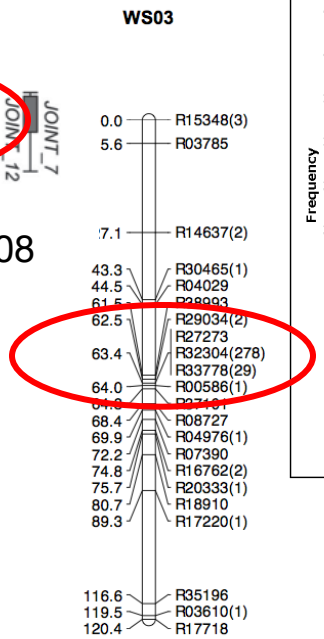
>Resident and Anadromous life-history variation is strongly associated with alleles in a single, **large**, region of **Omy5**.



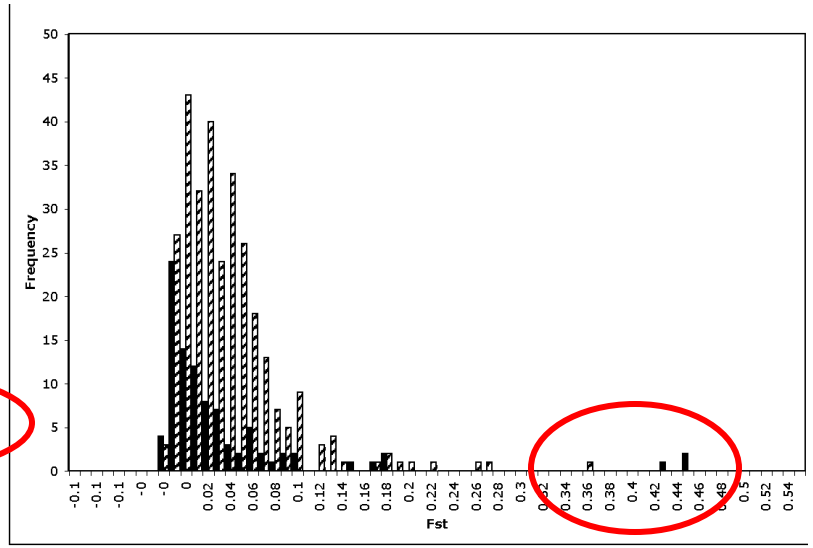
Leder et al. 2006



Nichols et al. 2008

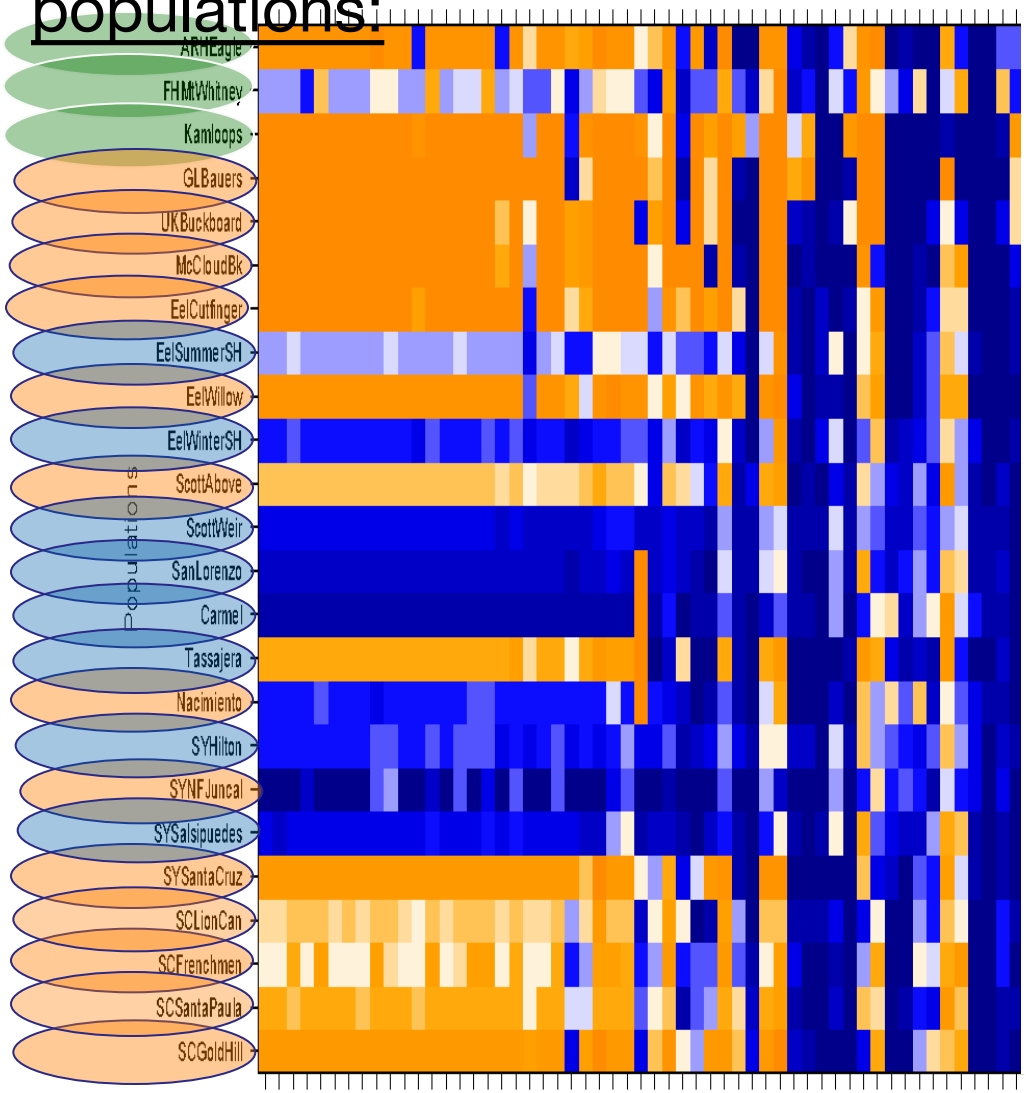


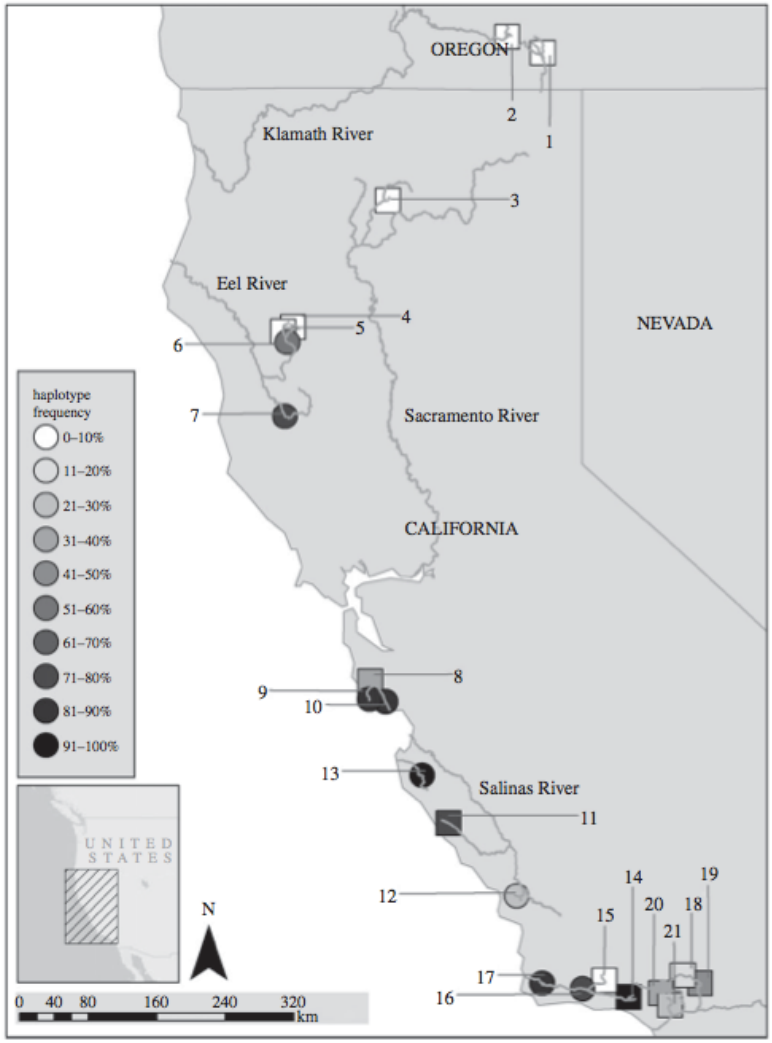
Miller et al. 2012



Martinez et al. 2011
Abadía-Cardoso et al. 2011

Omy5 variation among above- and below-barrier populations:

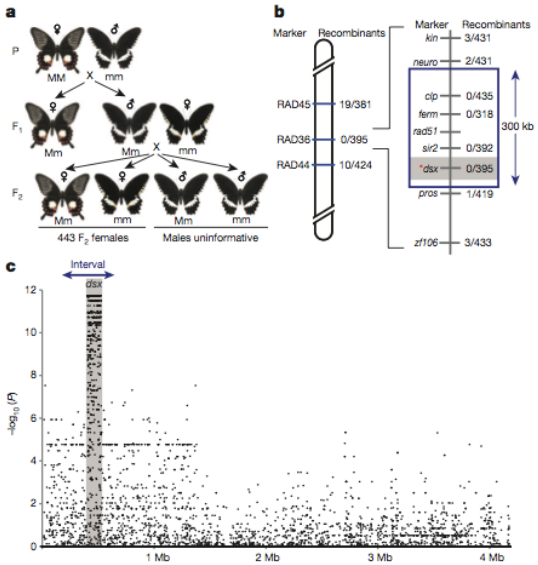




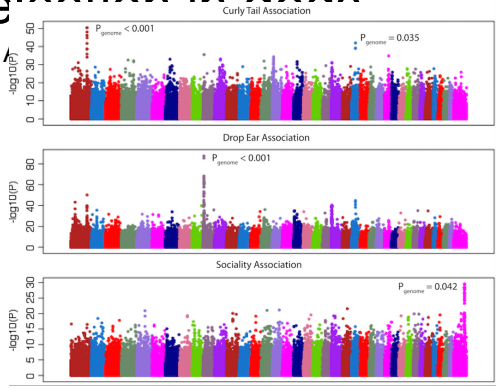
Pearse et al. 2014

Chromosomal inversions suppress recombination, supporting evolution of “supergenes” associated with many adaptive traits:

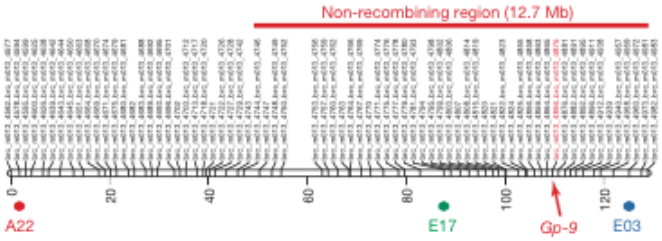
>Butterfly mimicry in *Heliconius* and *Papilio*.
(Joron et al. 2011, *Nature;* Kunte et al. 2014, *Nature;* Reed et al. 2011, *Science*)



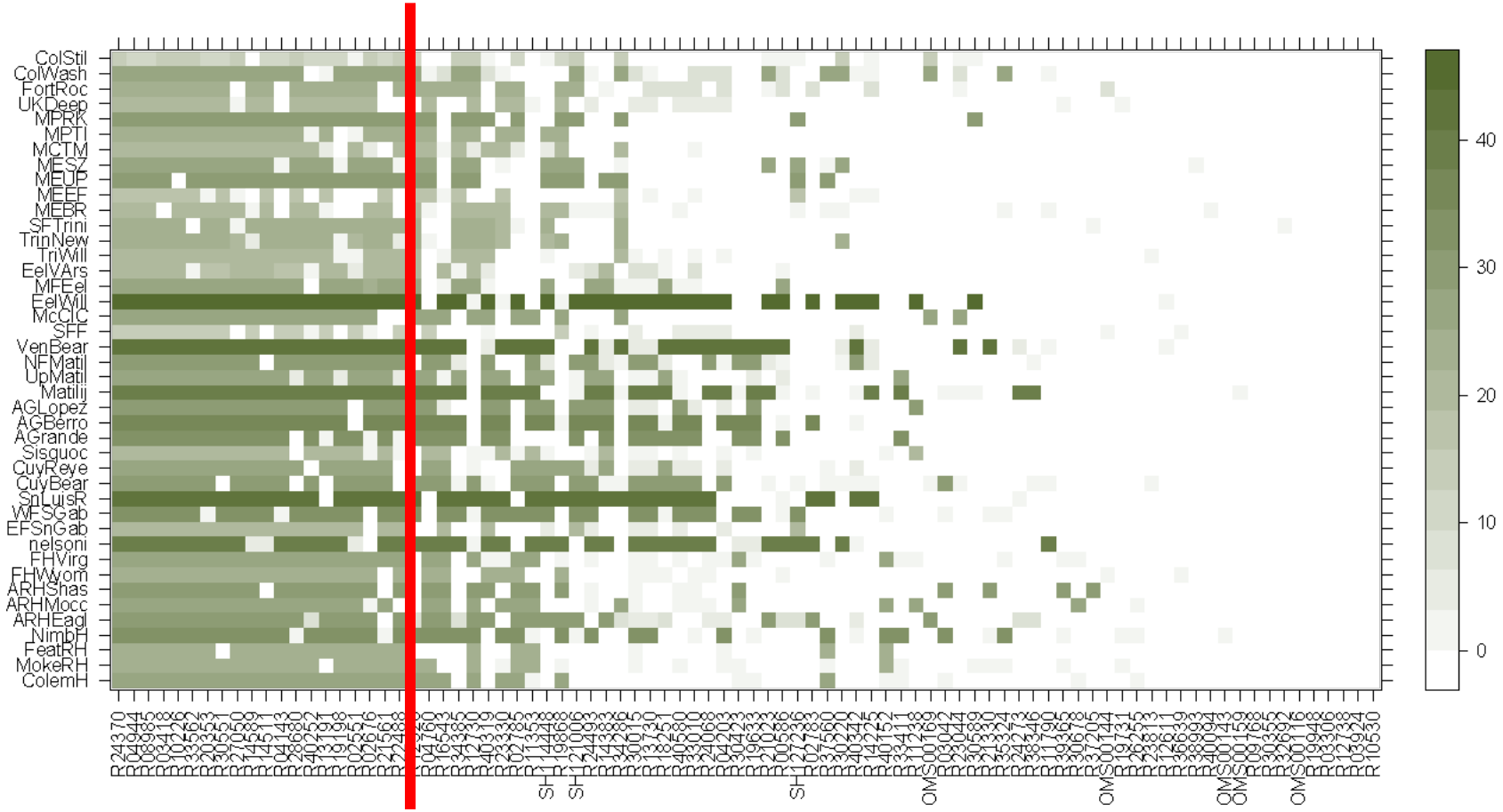
>Domestication selection in dogs



>Social structure in fire ants (*GP9)*
(Wang et al. 2013, *Nature*)



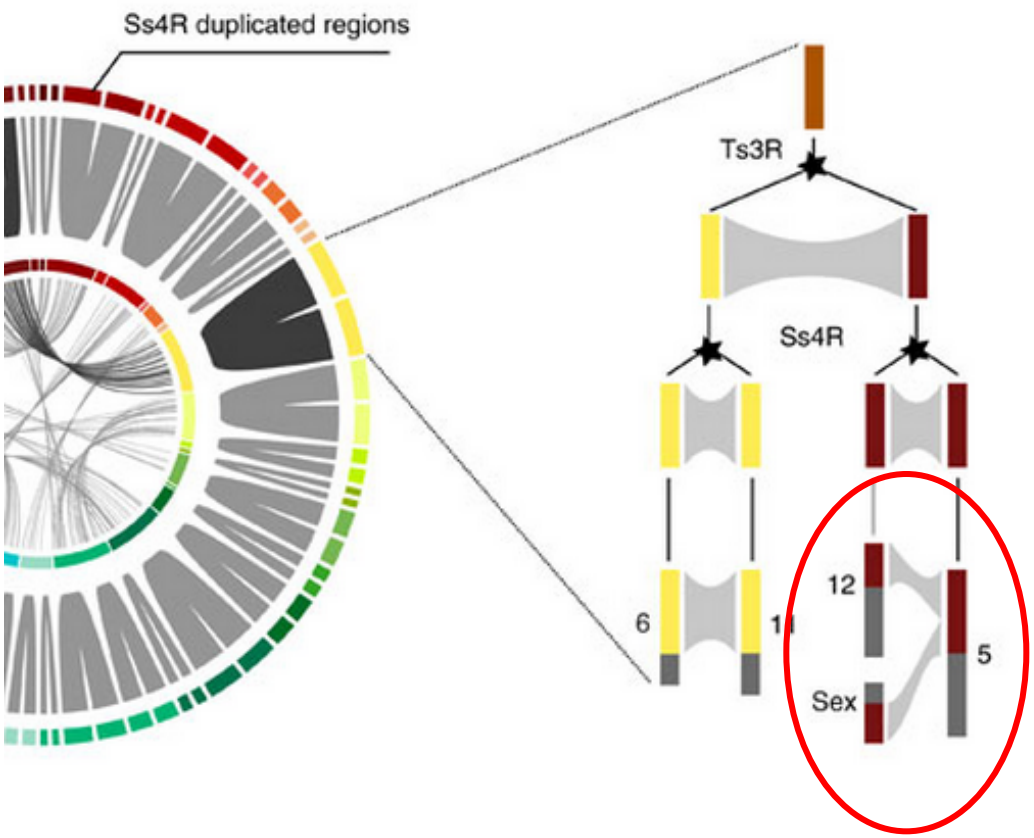
> Pairwise linkage disequilibrium across populations:



Abadía-Cardoso et al. In Prep

***O. mykiss* genome:**

Berthelot et al. 2014



>**Large** genome.

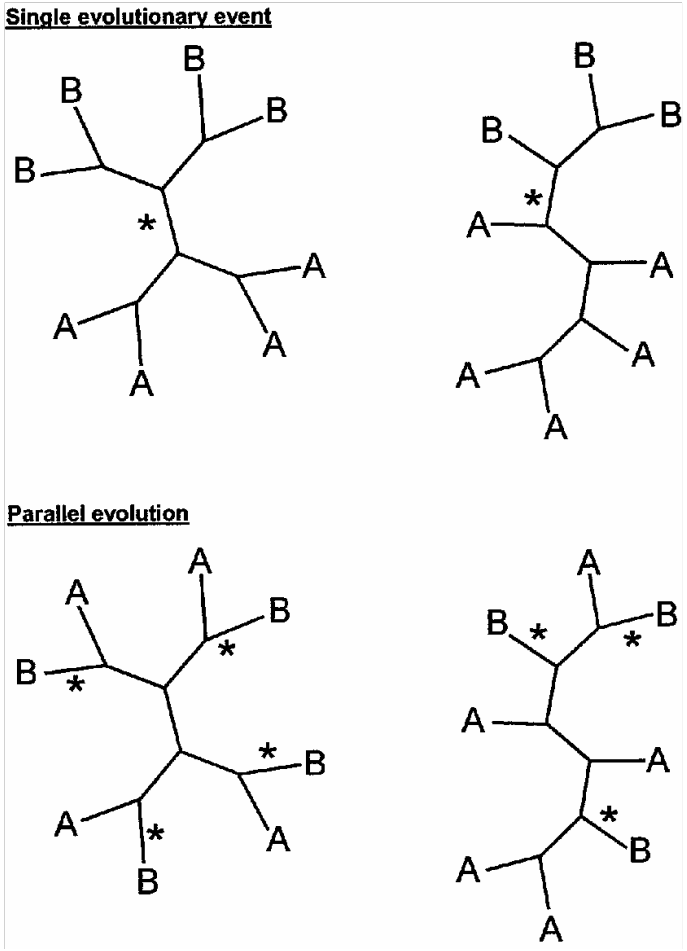
>Highly **duplicated**.
(ancestral tetraploidy)

>Transposable elements.

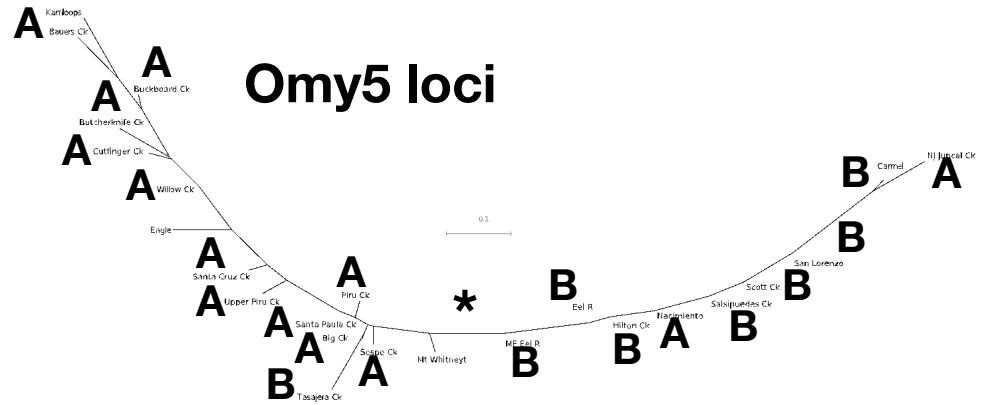
>Difficult assembly.

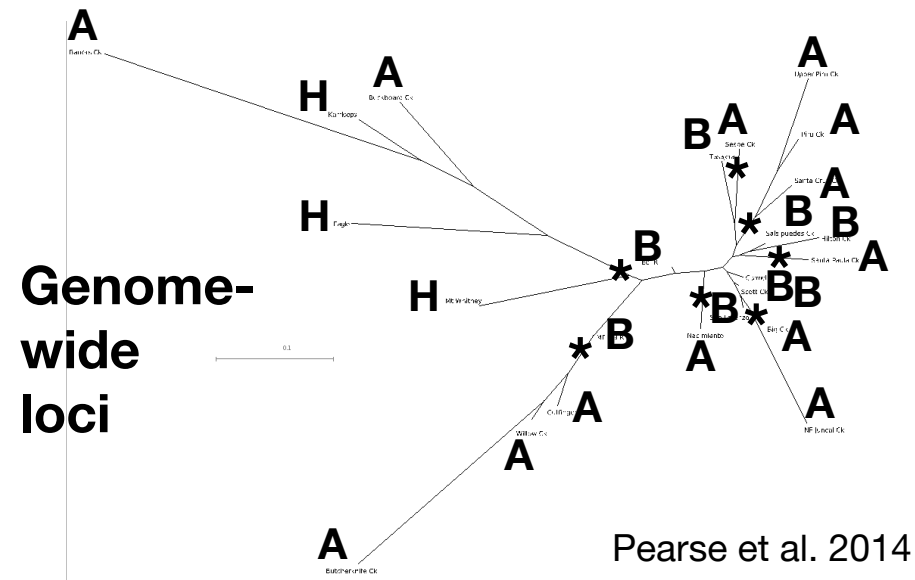
Omy12: Le Bras et al. 2011; Hecht et al. 2012a,b; Hale et al. 2014; McKinney et al. 2015

Parallel evolution of residency in *O. mykiss*



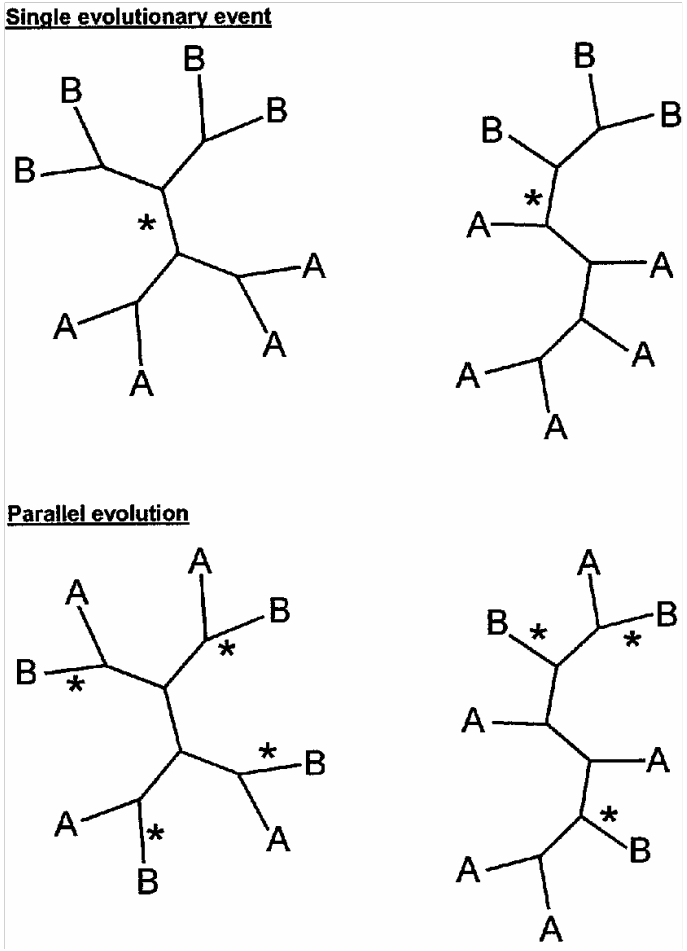
Waples et al. 2004



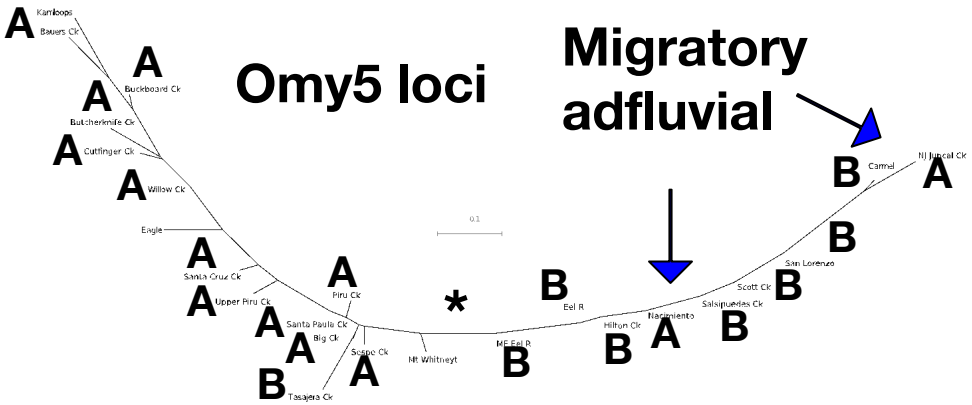


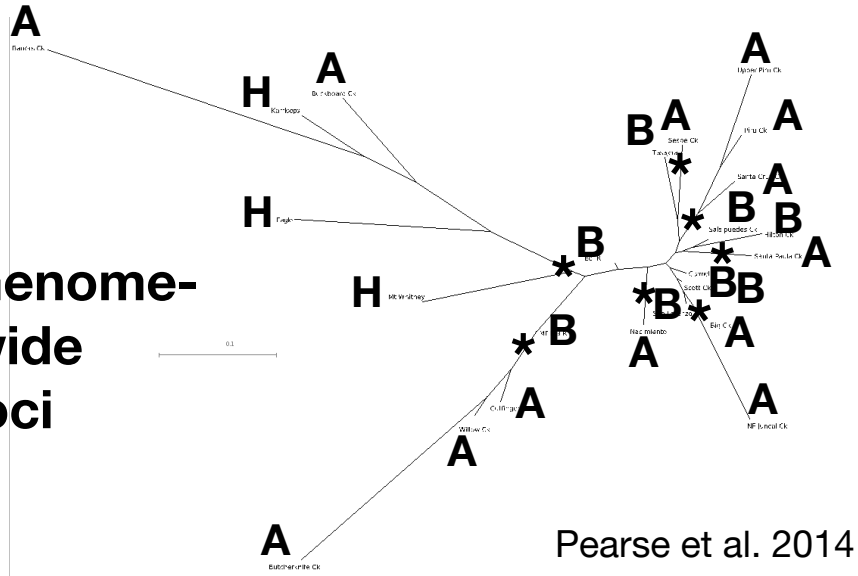
Pearse et al. 2014

Parallel evolution of residency in *O. mykiss*



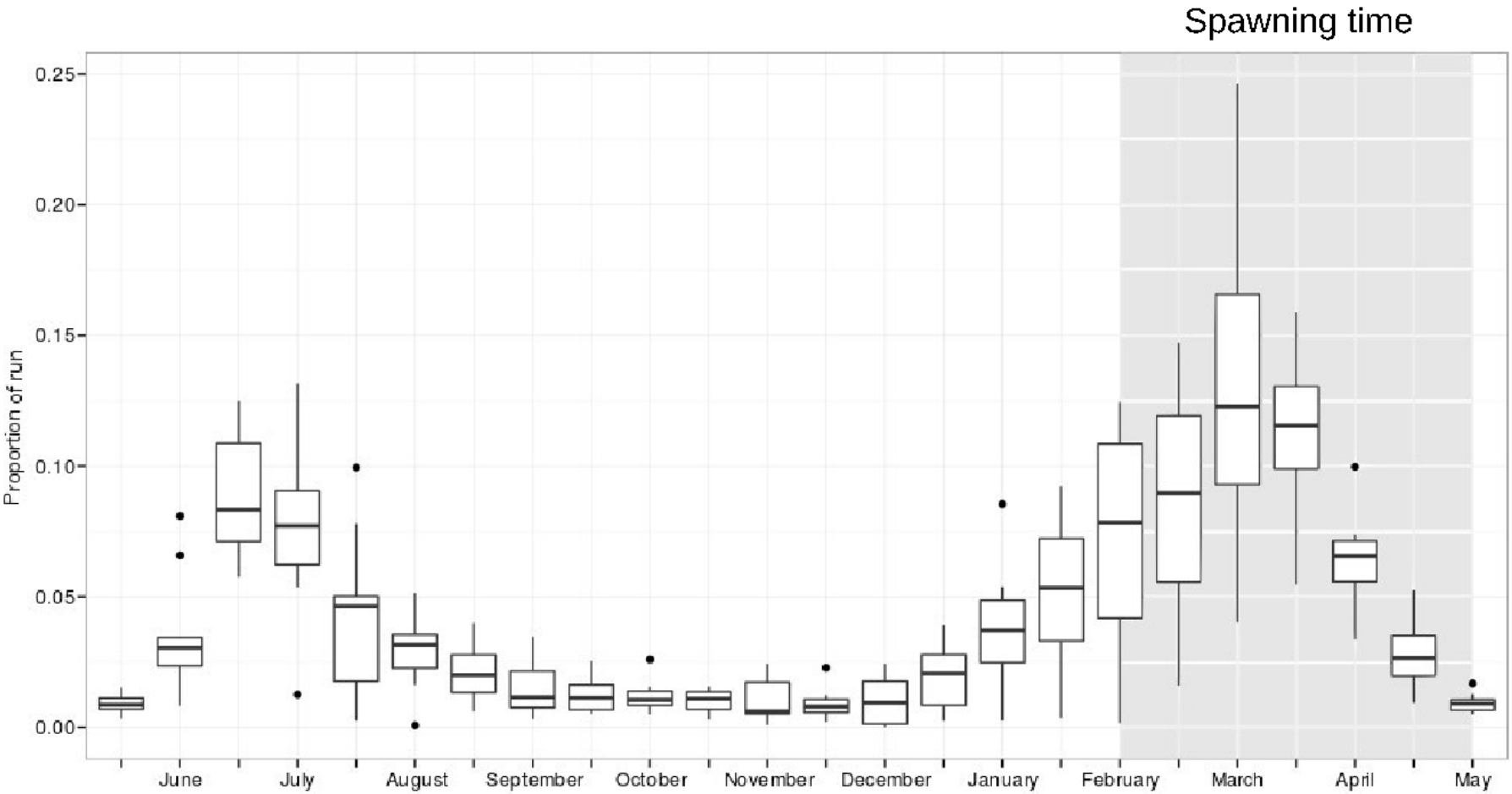
Waples et al. 2004



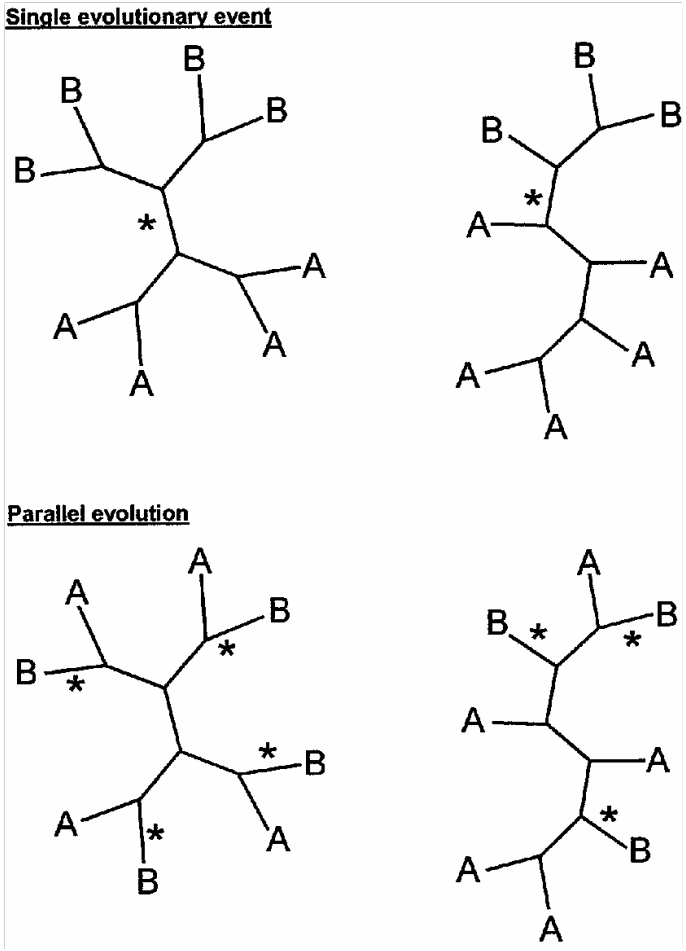


Pearse et al. 2014

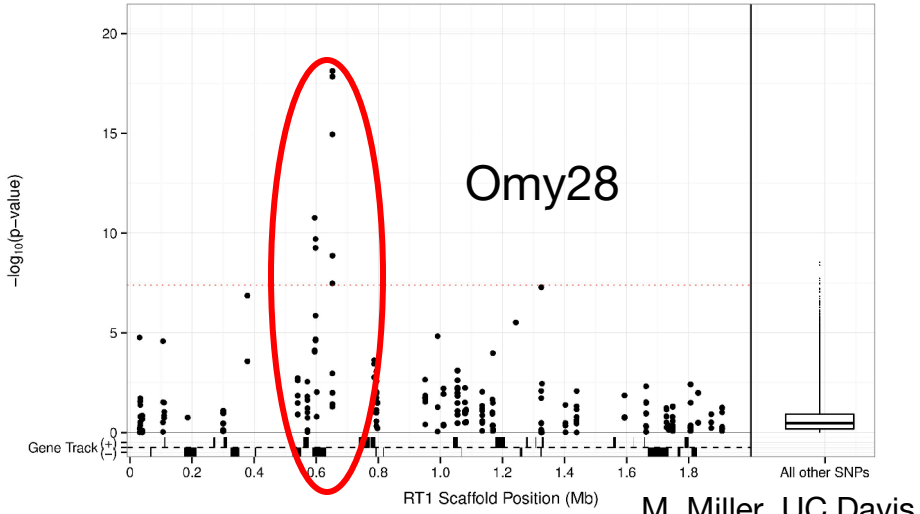
Genomics of anadromous run timing life-history:



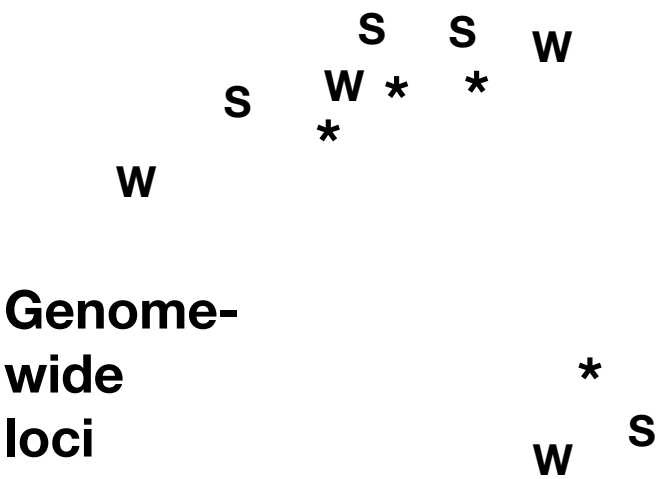
Parallel evolution of Summer run timing in steelhead



Waples et al. 2004



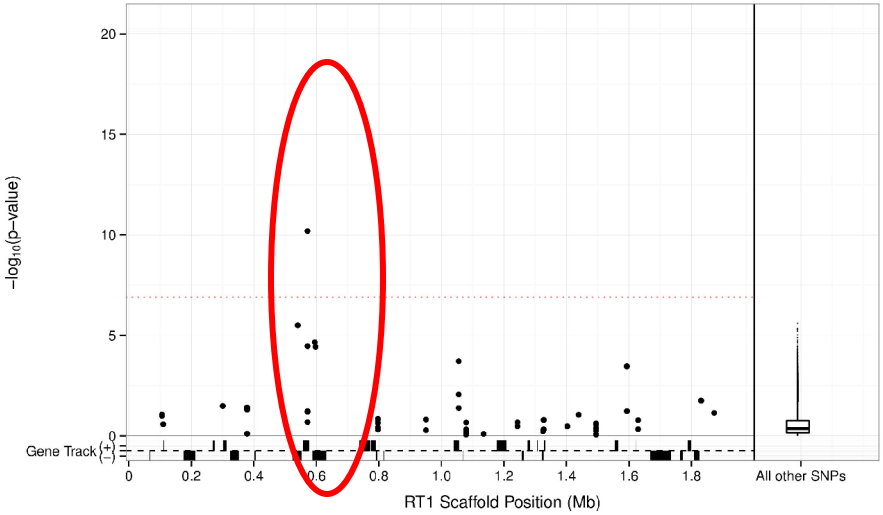
M. Miller, UC Davis



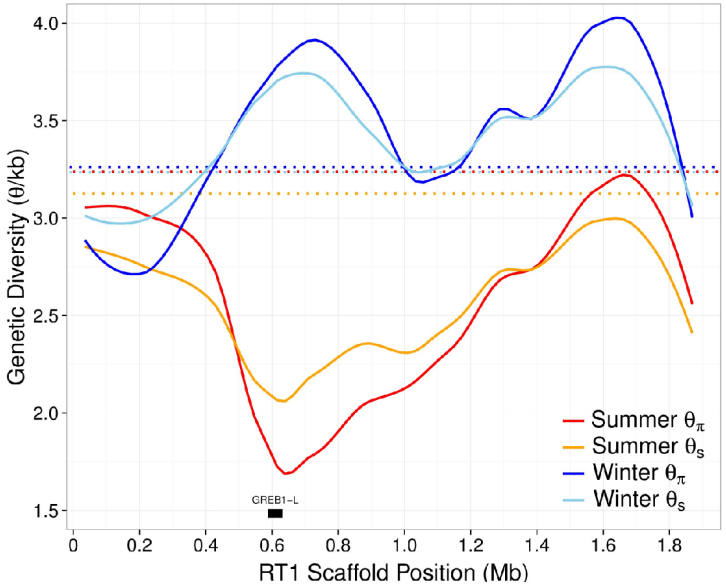
Arciniega et al. *submitted*

Parallel evolution of Spring run timing in Chinook

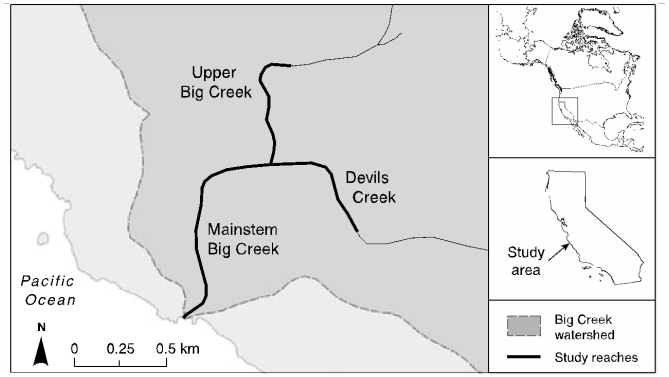
>The same genomic region is associated with run-timing in **Chinook.**



>Changes in the **same gene** in both species influence alternative run timings.



Genomic basis of **individual** life-history dynamics:



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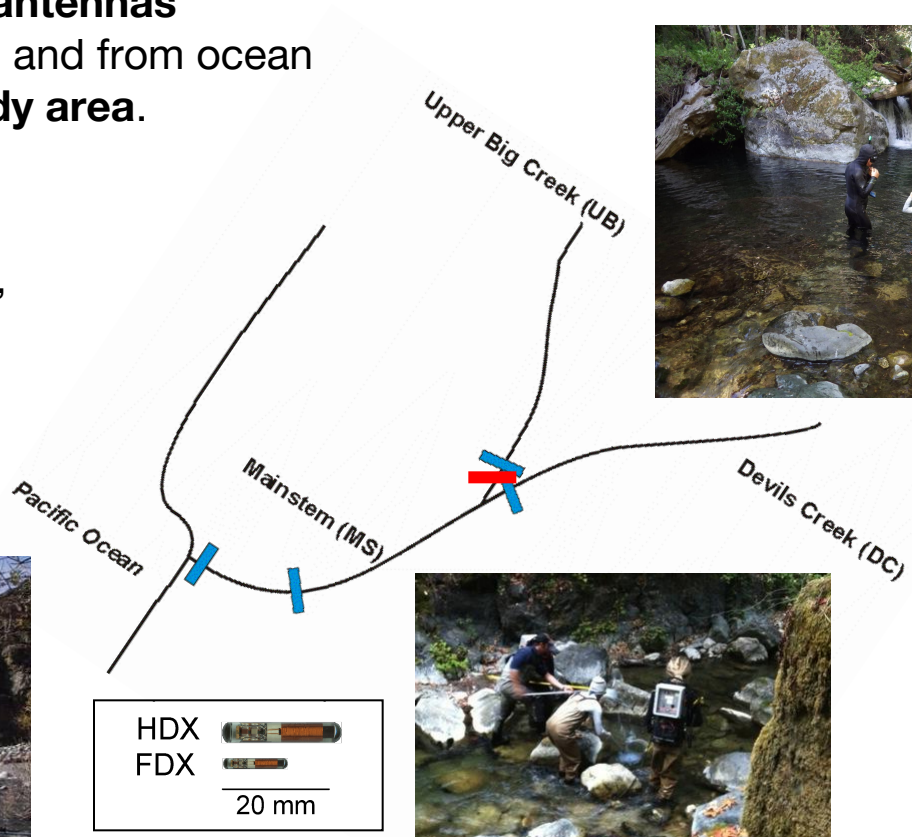
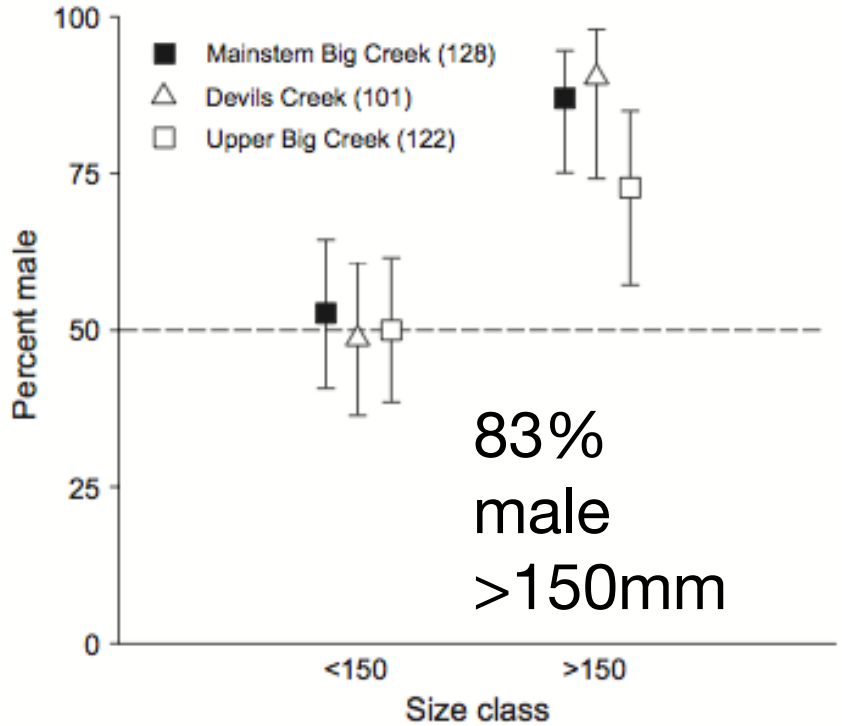
- **Juvenile** capture-recapture sampling using PIT tags
  - Fall and Spring since fall 2005; Intensive genetic sampling since 2009.
  - Re-sampling and monitoring 2010-2015.

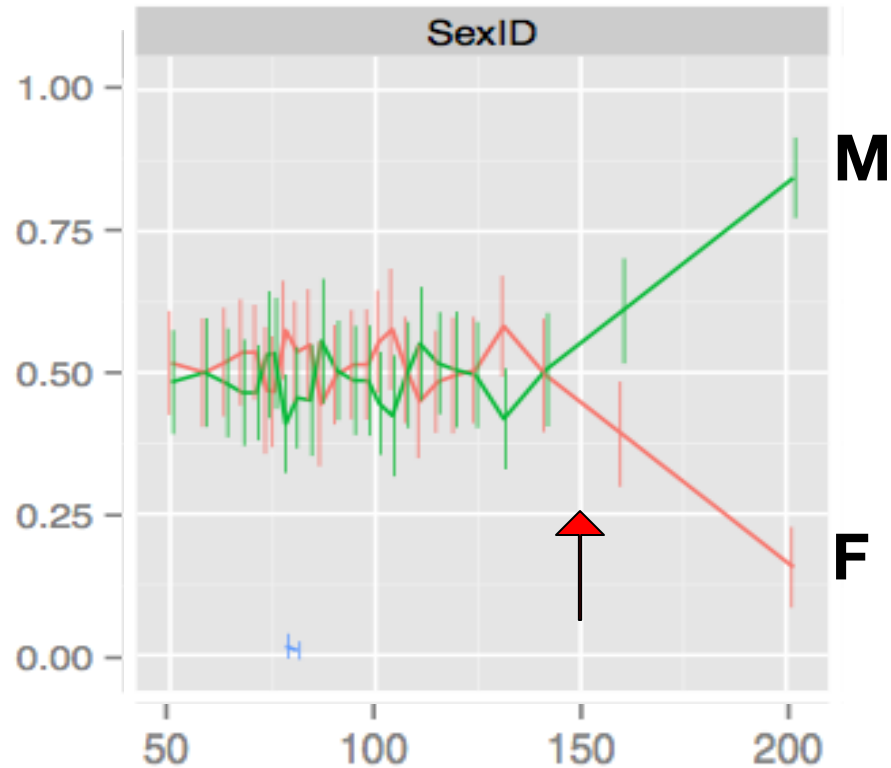
- Track fish **with PIT tag antennas**
  - Within basin and to and from ocean
  - **No barriers in study area**.

- Genetic analysis for
  - -Population genetics,
  - -Family structure
  - -**Gender**
  - -**Omy5**.



Highly skewed sex ratio in post-smolt population:

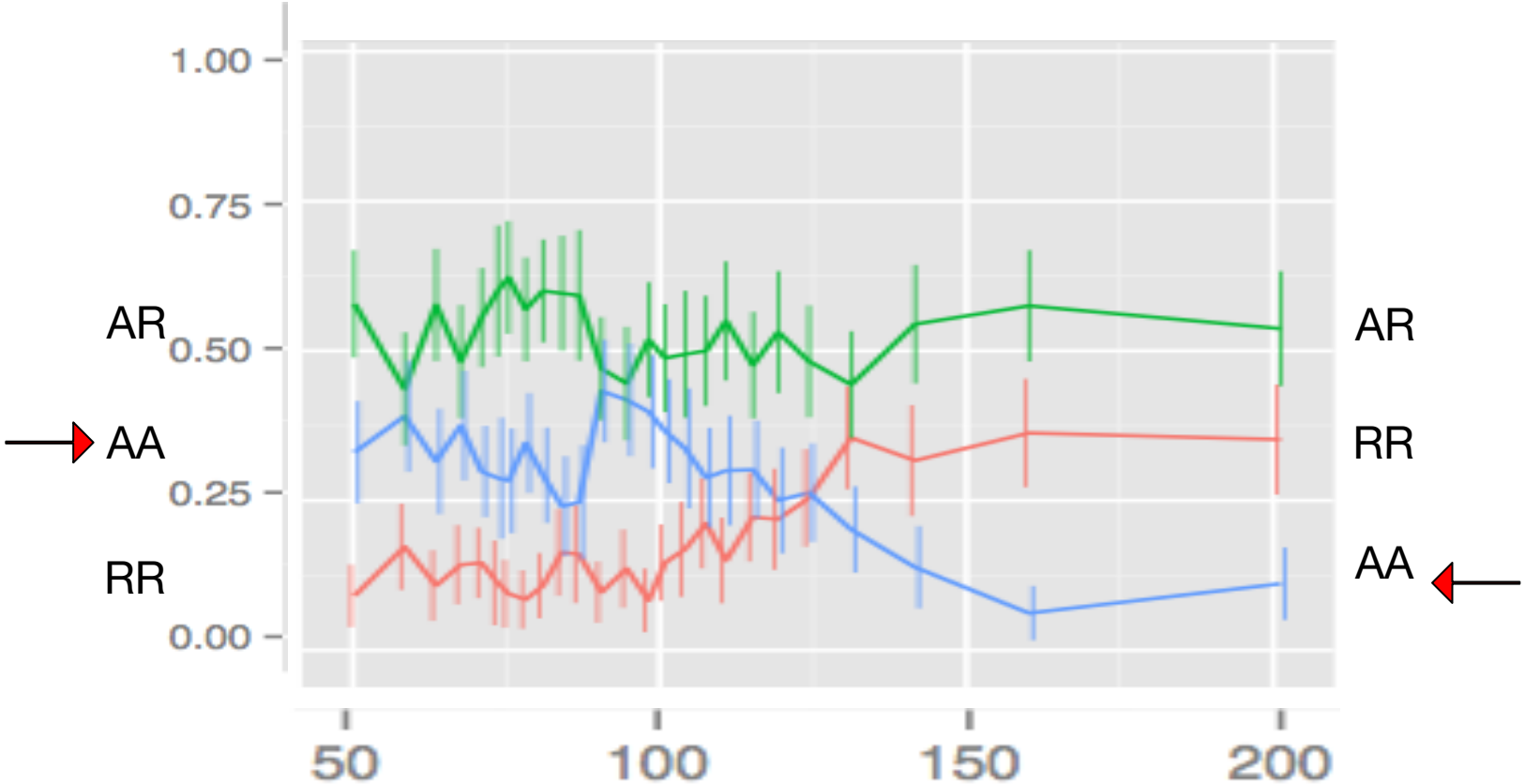




Rundio et al. 2012

Pearse, Anderson, Garza, Rundio, Williams, Lindley, *In Prep*

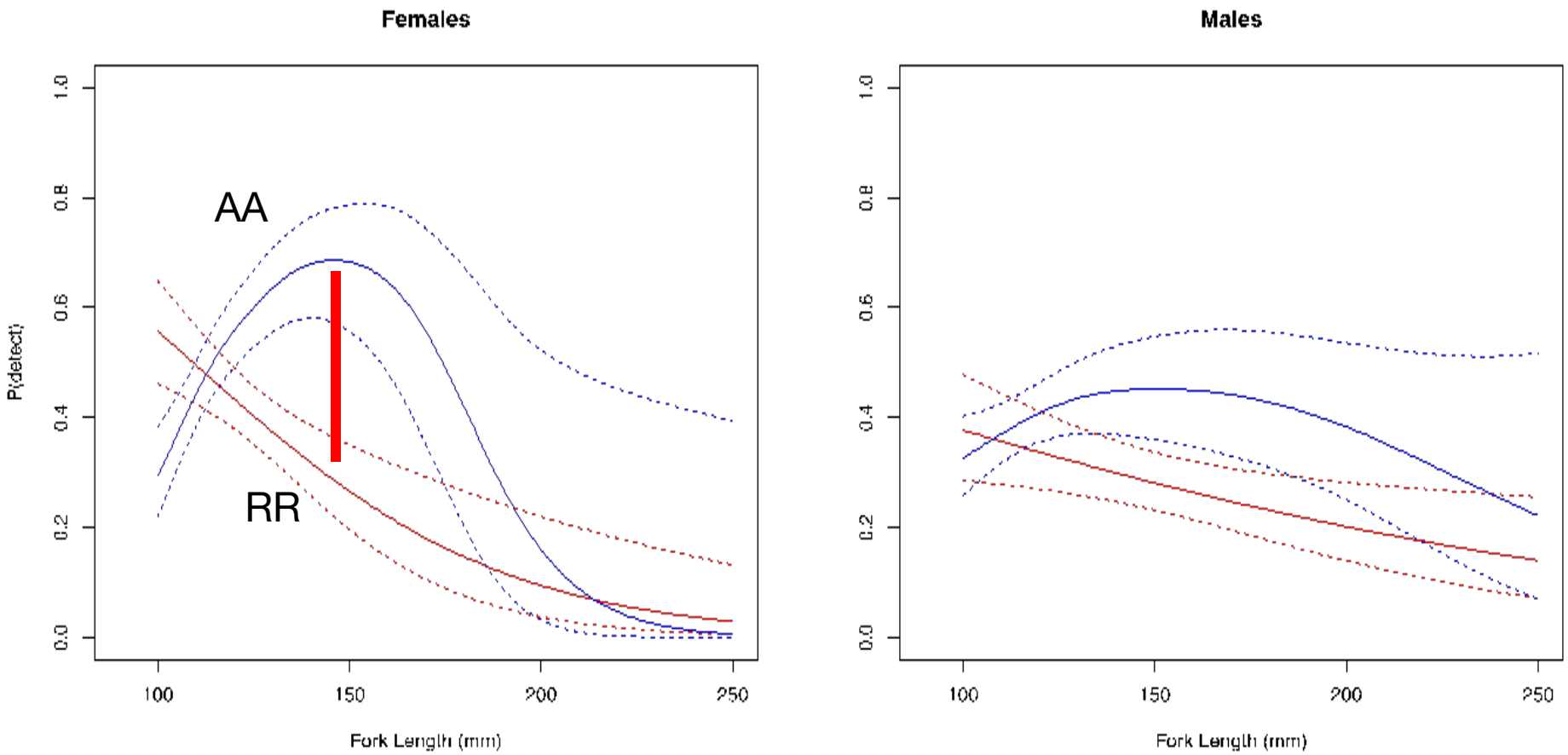
Omy5 **genotype** frequencies associated with size due to **partial anadromy.**



Pearse, Anderson, Garza, Rundio, Williams, Lindley, *In Prep*

>Downstream antennae detections, 2010-2012.

>Highly significant **individual** effect of *Omy5* genotype.



Pearse, Anderson, Garza, Rundio, Williams, Lindley, *In Prep*

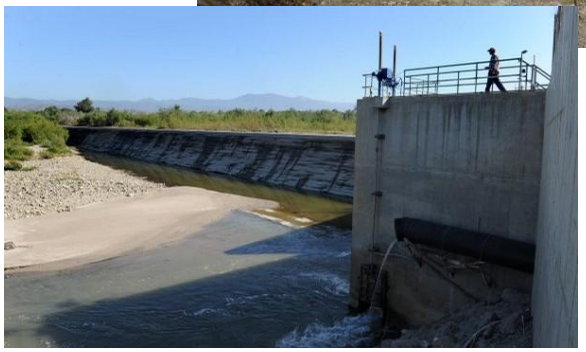
Adaptive genomic variation reflects ecological conditions:

>Relative reproductive success of individuals with alternative life-history forms.

>Individual, gender-specific.

>Drift, ‘barriers’ to action of selection.

>Non-equilibrium populations.



Summary: What should we do with this information?

- ‘Rescue’ of anadromous populations from above-barrier reservoirs? But, significant effect of above-barrier population age. Adfluvial populations.

- Should identified adaptive genomic variation be targeted for conservation? Above-barrier populations as a ‘seed bank’.

- Even genes of major effect are probabilistic indicators of individual phenotype.

- Focus on evolutionary *processes* that promote diversity rather than an idealized genetic composition. Evaluate that diversity using neutral and adaptive loci.

Acknowledgements

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