The genetic basis of life-history variation in *O. mykiss*

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>Genetics 101: Units

A LOCUS is a region, gene, or SNP in the genome.

Single Nucleotide Polymorphism (SNP)

A single locus can have multiple ALLELES, e.g. A and a.
multiple haplotypes-- SARS-CoV-2 variants!

Unlike SARS-CoV-2, in most animals ALLELES combine within individuals into three GENOTYPES: AA, Aa, aa

>Genetics 101: Definitions of evolution

1. Molecular evolution changes DNA sequence or structure.

Creates new variants

2. Allele frequencies change over time (generations).

Standing genetic variation

>Genetics 101:

The distributions of these ALLELES and GENOTYPES among populations and individuals are used to understand:

- **ANCESTRY → Parentage, populations or species**
  'neutral' loci

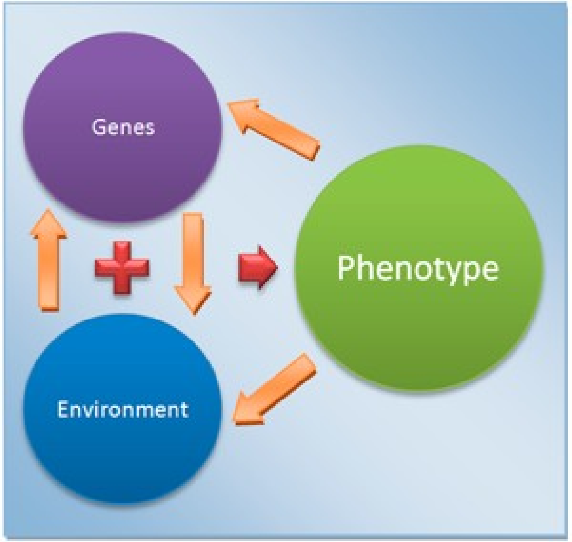
- **ADAPTATION → Functional traits or phenotypes associated with a specific locus or loci**
  >Adaptive Genomic Variation (AGV)

>Genetics 101:

>Adaptive Genomic Variants are variable, and their connection with specific phenotypes varies**:**

Many genes (Polygenic) → Single locus (major effect)

Effect strength



Salmonid Life-History traits:

>**Age-of-Return**: How many years at sea?

Early = 1 or 2 years **Late = 2 or 3 years**

>**Run-Timing**: When do adults migrate into freshwater?

Early=Spring/Summer, **Late=Fall/Winter**

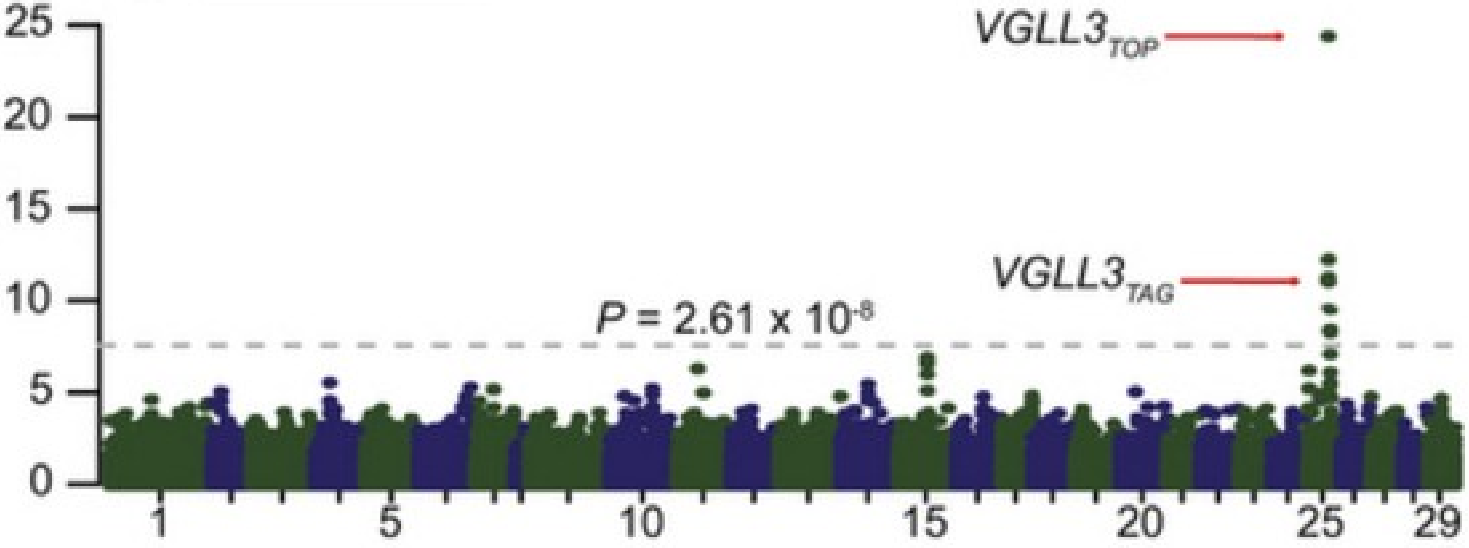
>>Spawn at about the same time!

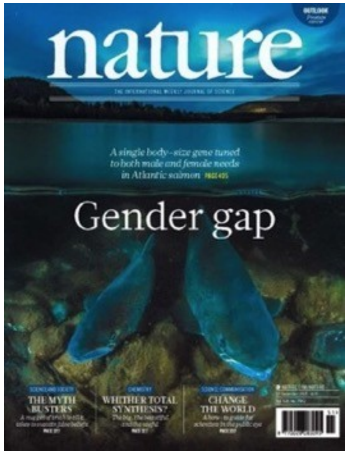
>**Anadromy/Residency**: Migrate to the ocean or not?

Oncorhynchus mykiss: **steelhead** or **Rainbow trout**

>**Many others!!**

Early vs. Late **Age-of-Return** in Atlantic Salmon:





Barson et al. 2015

Early = 1 or 2 years
Late = 2 or 3 years

EE, EL, LL

>Sex-dependent **dominance**
EL male = EE
EL female = LL

>**Single locus of major effect.**

>Explains 39% of variance.

>Not associated with age-of-return in Pacific Salmon. (Waters et al. 2021)

Genomic basis of: Run Timing in Steelhead

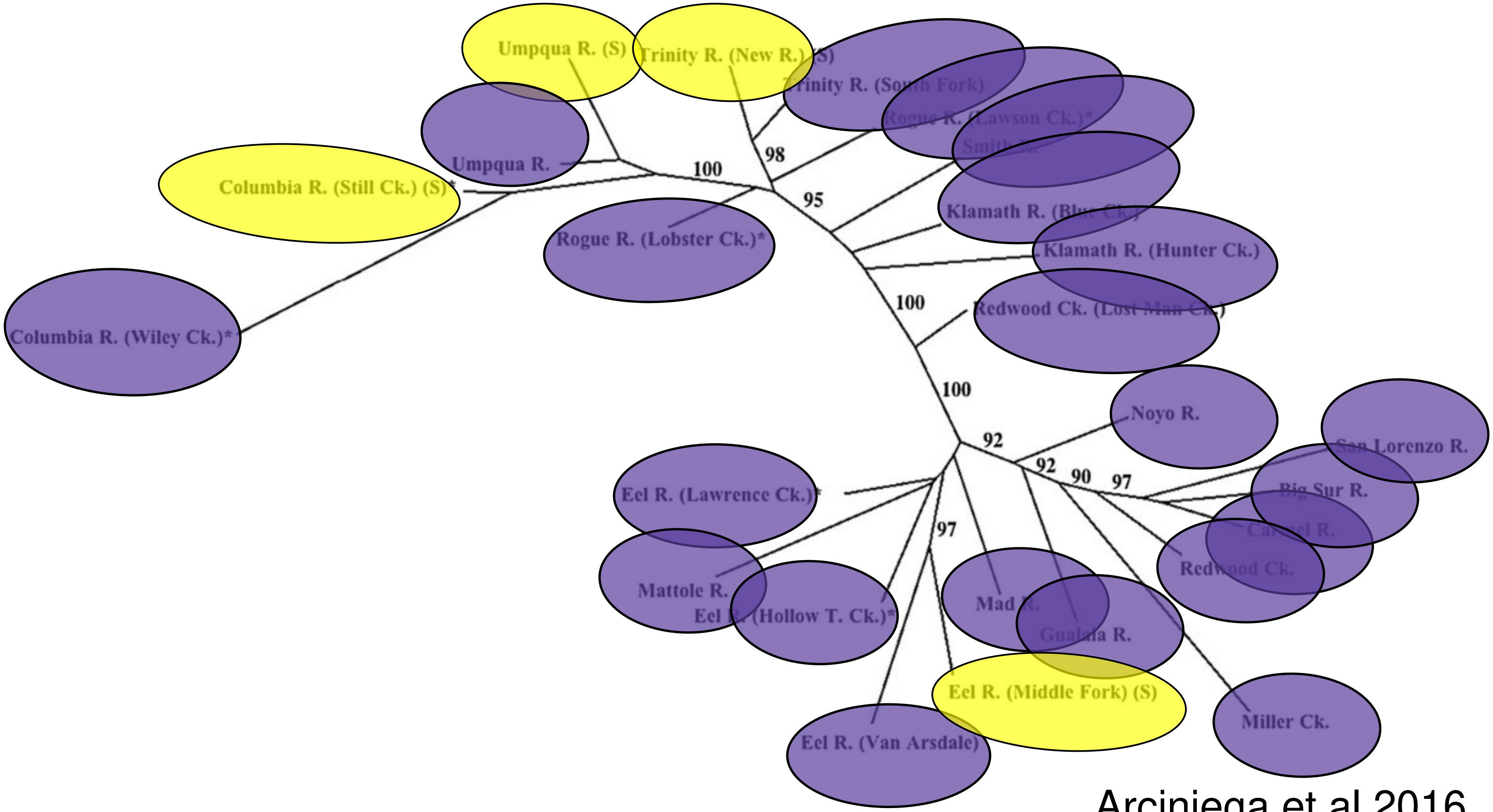
>Multiple studies on genetic basis of run timing:
Hess et al. 2016; Prince et al. 2017; Micheletti et al. 2018; Willis et al. 2020;
Pearse et al. 2019; Ford et al. 2020; Kannry et al. 2020; Fraik et al. 2021

>The ***Greb1L*** region of Chromosome Omy28:
Single locus of major effect strongly associated with variation in the timing of adult return in coastal **Summer** and **Winter** steelhead:
(Early) (Late)

Genotypes: SS, **SW**, and **WW**

>Environmental and/or lineage specific effects, variable penetrance
e.g. Columbia River (Micheletti et al. 2018; Willis et al. 2020; Collins et al. 2020)

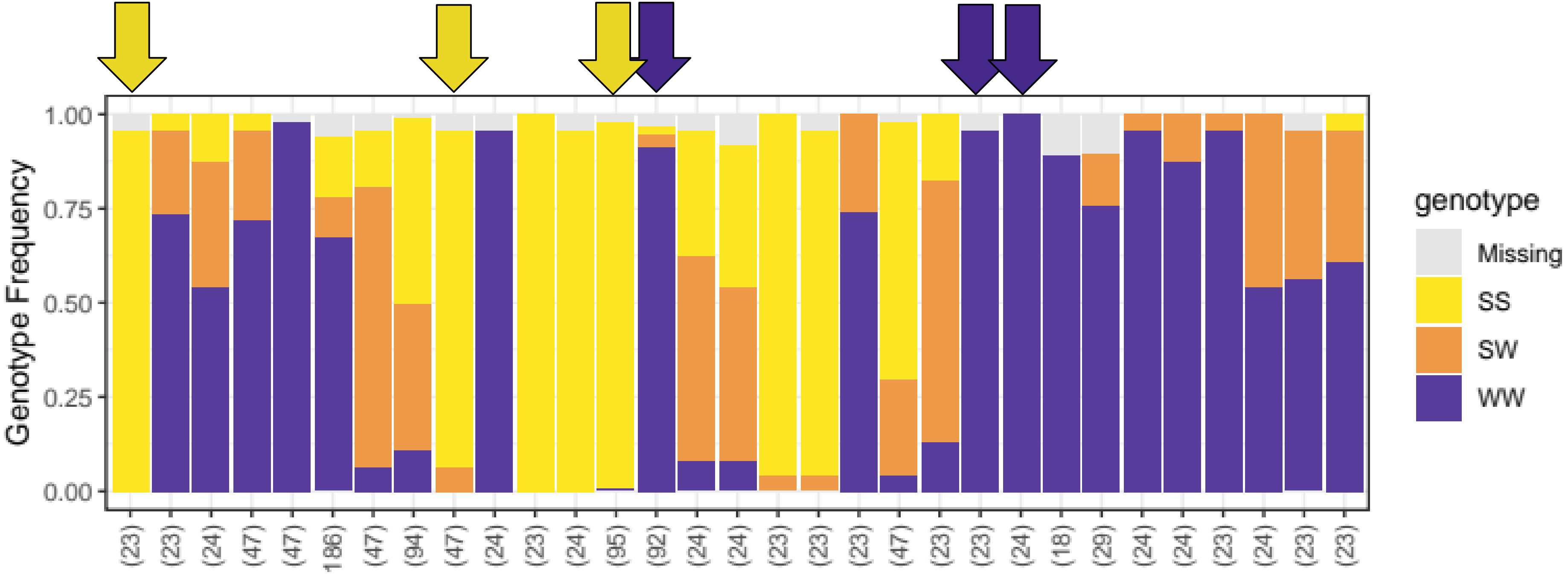
>ANCESTRY and ADAPTATION can be decoupled.



Arciniega et al 2016

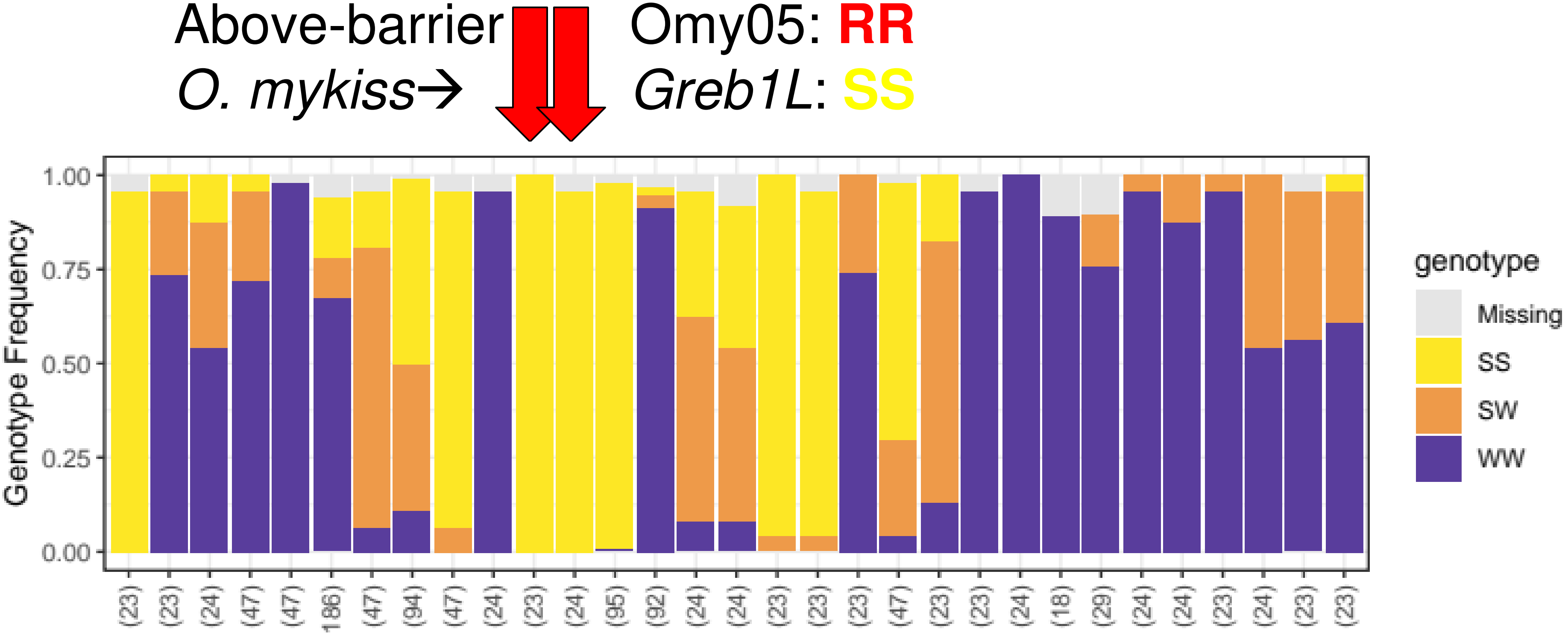
Variation in Omy28 *Greb1L* genomic region:

Phenotypically **Summer** and **Winter** populations



Pearse et al. 2019b

Variation in Omy28 *Greb1L* genomic region:



Above-barrier *O. mykiss*→

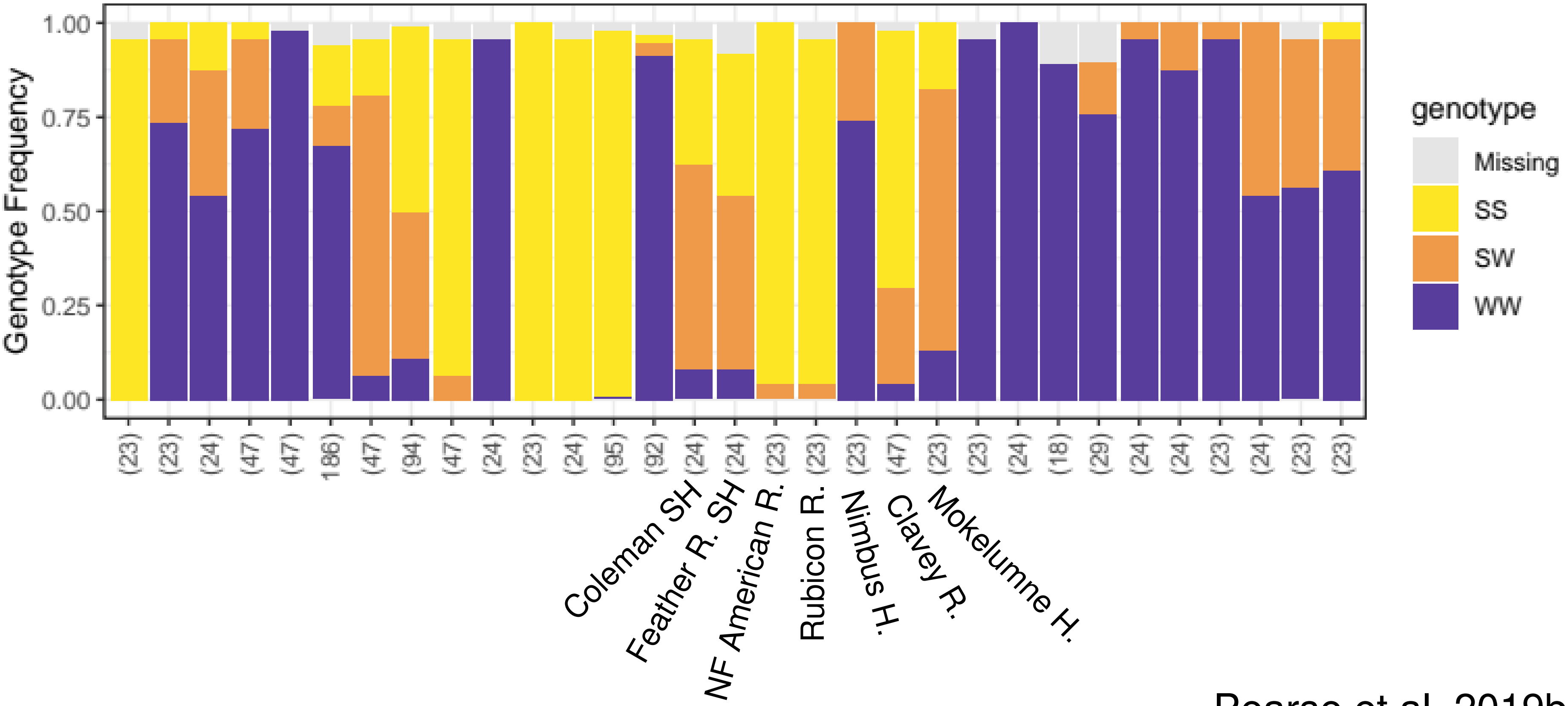
Omy05: **RR**

Greb1L: **SS**

Pearse et al. 2019b

Variation in Omy28 *Greb1L* genomic region:

Central Valley– historical presence of Summer steelhead?



Pearse et al. 2019b

Genomic Basis of Anadromy/Residency

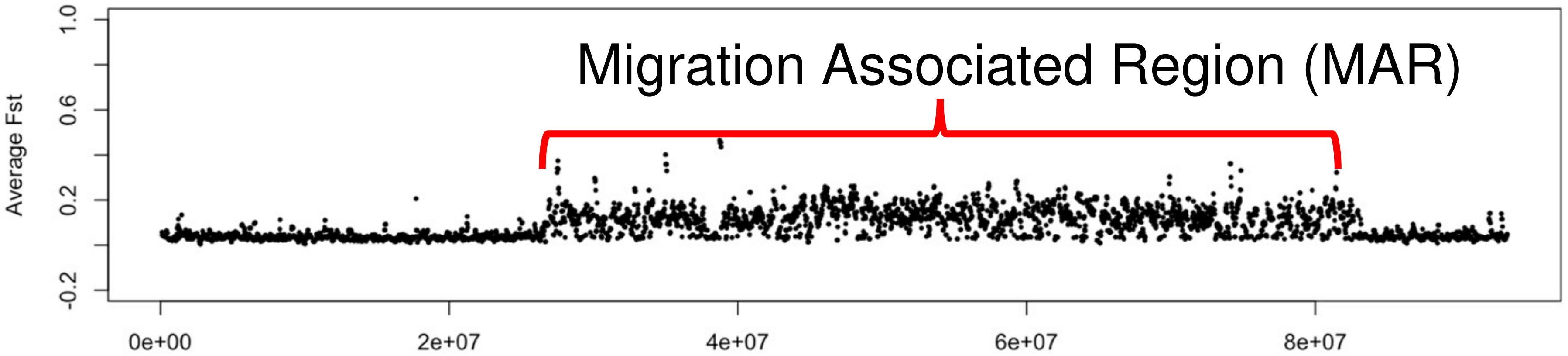
>**Numerous studies on genetic basis of anadromy in *O. mykiss*:**
Robison et al. 2001; O'Malley et al. 2003; Thrower et al. 2004; Leder et al. 2006; Phillips et al. 2006;
Nichols et al. 2007, 2008; Haidle et al. 2008; Colihueque et al. 2010; Paibomesai et al. 2010; Easton et al. 2011;
Le Bras et al. 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; Baerwald et al. 2015; Leitwein et al. 2016; Apgar et al. 2017;
Abadia-Cardoso et al. 2019; Arostegui et al. 2019; Pearse et al. 2019; Kelson et al. 2019a,b, 2020a,b,c; Fraik et al. 2021

>**Polygenic** — multiple loci with environmentally-dependent effects.

>**Chromosome Omy05** contains single locus of major affect for this trait.

Photo: Morgan Bond

Genomic Basis of Anadromy/Residency: Omy05



Massive **double inversion** complex on chromosome Omy05
>50 million DNA base pairs, >1000 genes
>Acts as a **single 'supergene' locus of major effect**.

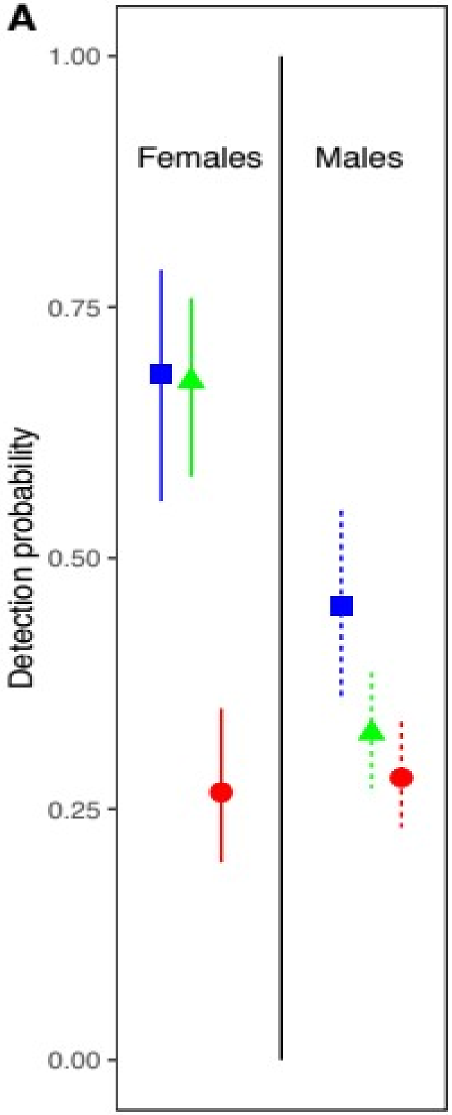
A = ancestral, anadromy **R = rearranged, resident**

Individuals can have genotypes: AA, AR, RR

Pearse et al. 2019,
Nature ecology & evolution

Genomic Basis of Anadromy/Residency: Omy05

Smolt
Migration
Probability



Influences **individual**, **sex-specific** migration:

Model prediction from capture-recapture data:

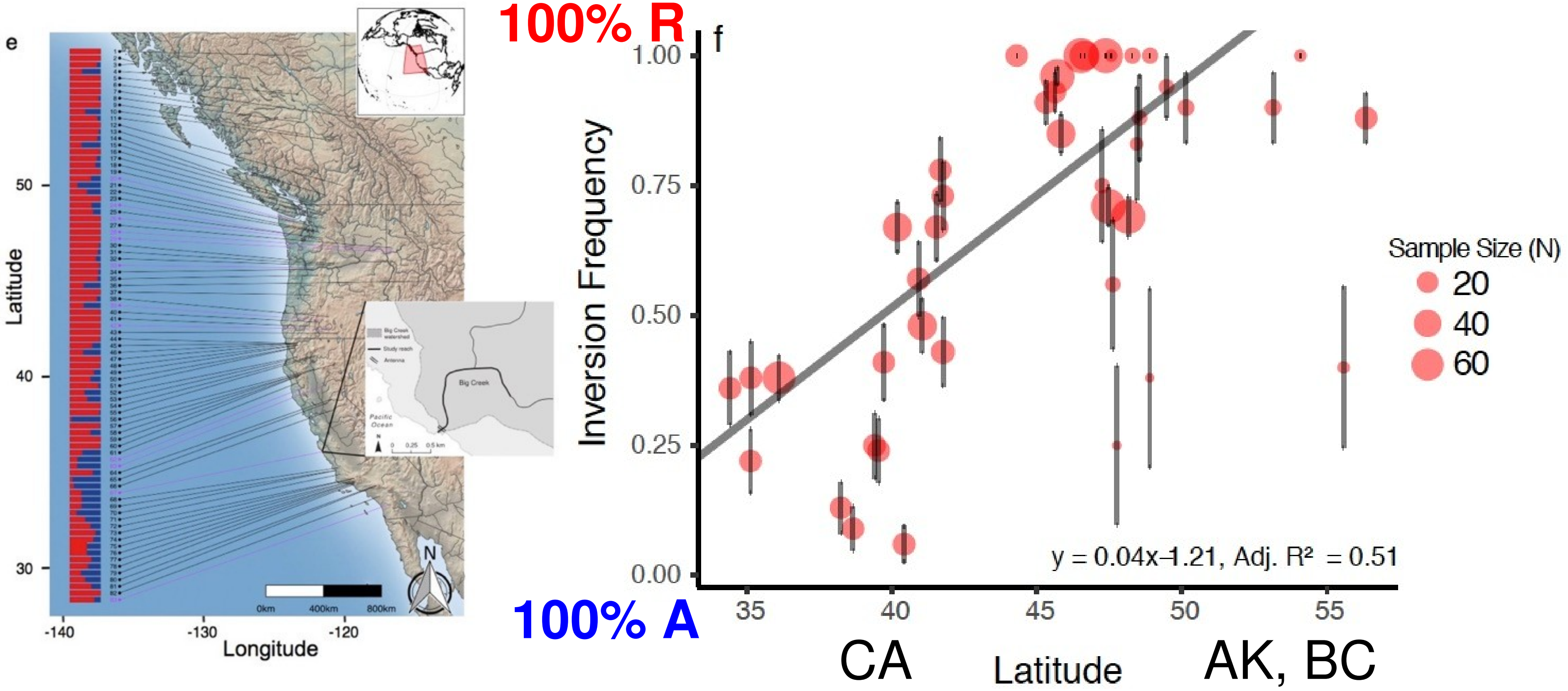
AA, AR, RR

>Sex-dependent dominance

Pearse et al. 2019,
Nature ecology & evolution

Genomic Basis of Anadromy/Residency: Omy05

Strong cline in **steelhead** (below barrier) populations:



Pearse et al. 2019,
Nature ecology & evolution

So what does all this mean for conservation and management?!?

>**Adaptive variants reflect ecological conditions** that favor the phenotypes they are associated with.

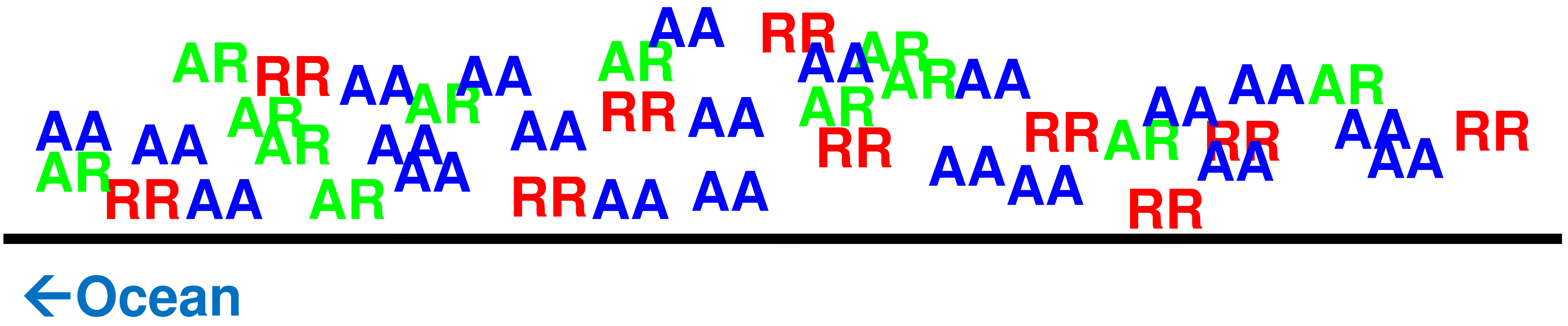
>**Relative success** of individuals with different genotypes/phenotypes.

>**Assortative mating**.

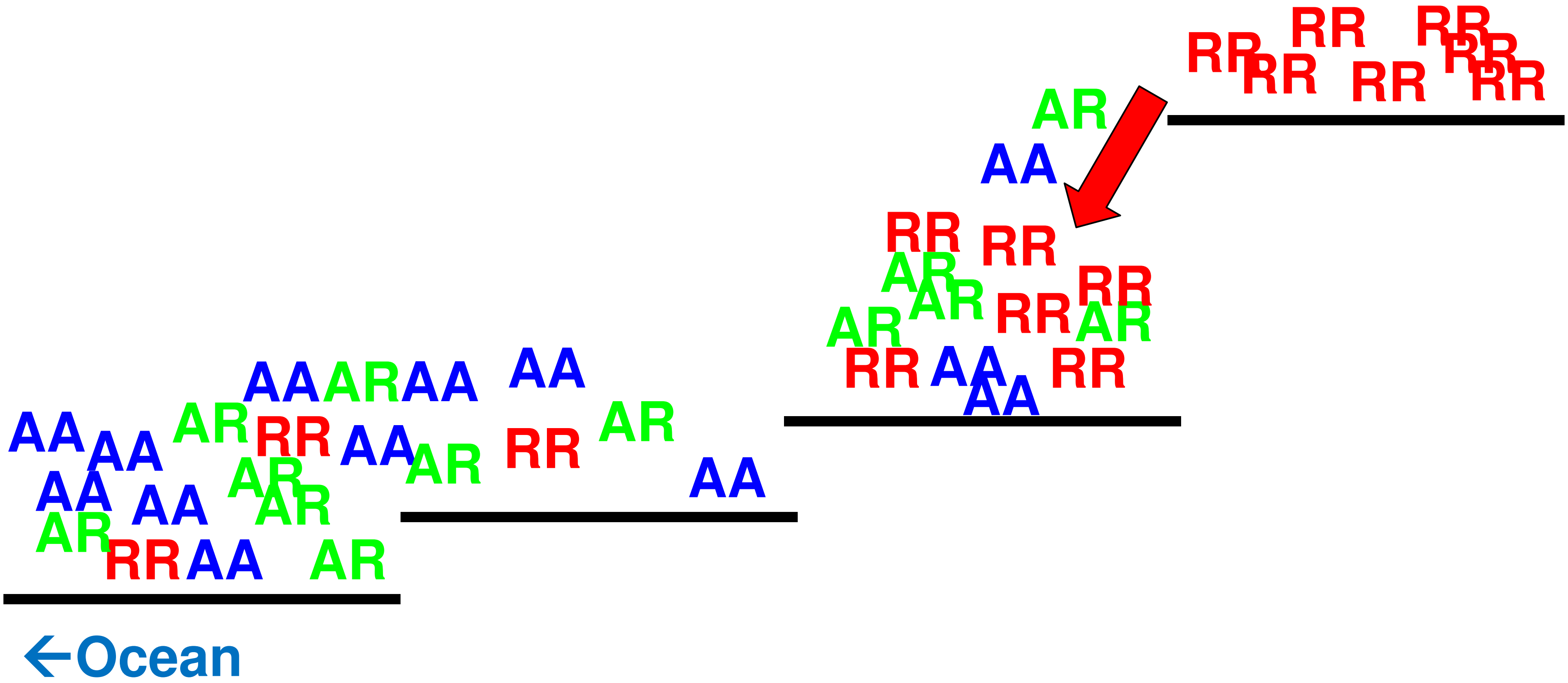
>Distribution of individuals reflects adaptive landscape

>Typical coastal CA below barrier, ~60% **A** and ~40% **R**

(Pearse et al. 2014, 2019)



>Differences among populations reflect adaptive landscape


RR RR RR RR RR RR RR

AR AA RR RR AR AR RR RR AR AR RR AA RR AA

AA AR AA AA AR RR AR AA

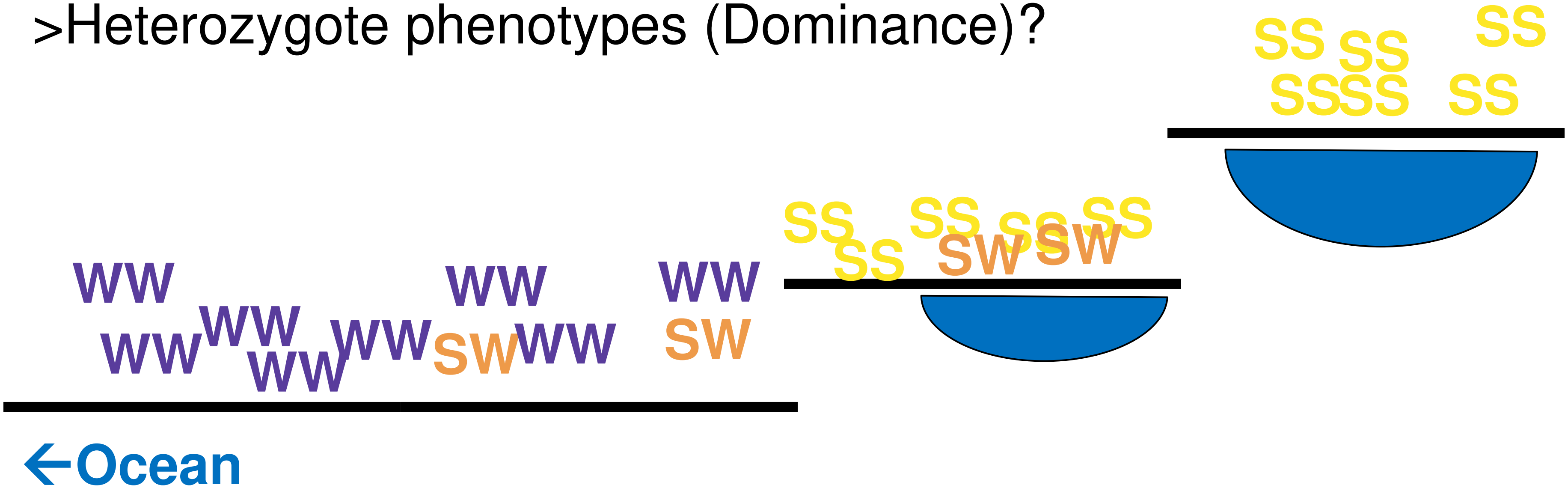
AA AA AR RR AA AA AA AR AR AR RR AA AR

←Ocean

>Distribution of individuals reflects adaptive landscape

>Flow-dependent barriers: **Dynamic over space and time**

>Heterozygote phenotypes (Dominance)?

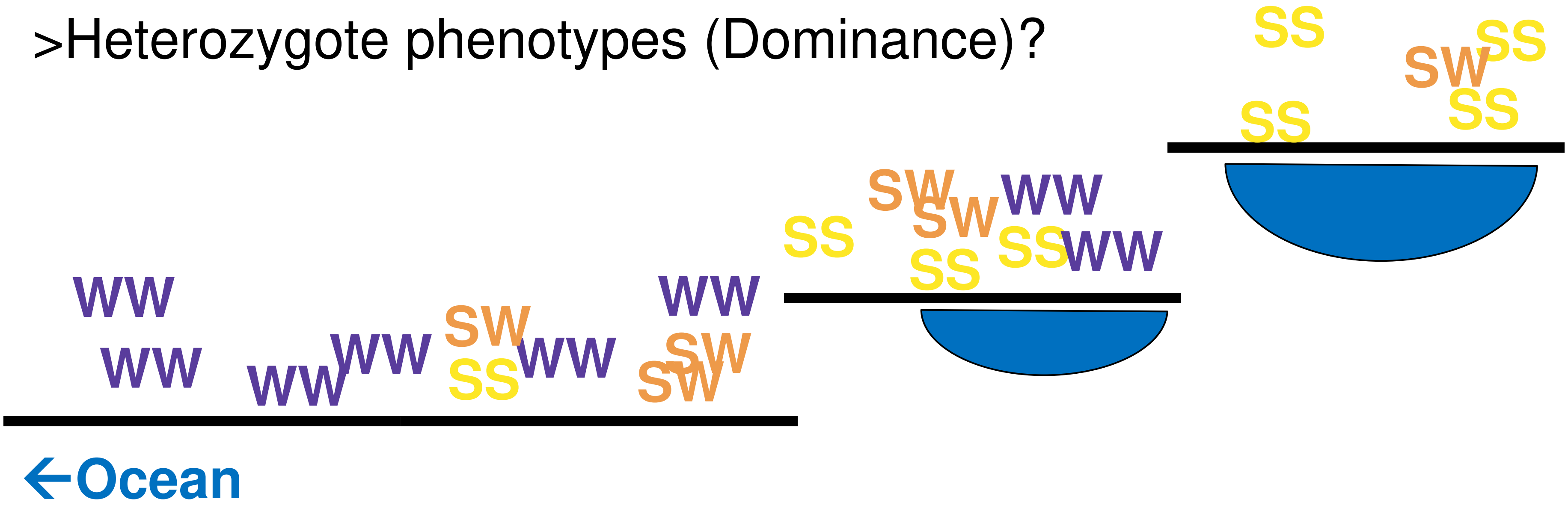


Remember the Omy05 variants are still here too!

>Distribution of individuals reflects adaptive landscape

>Flow-dependent barriers: **Dynamic over space and time**

>Heterozygote phenotypes (Dominance)?



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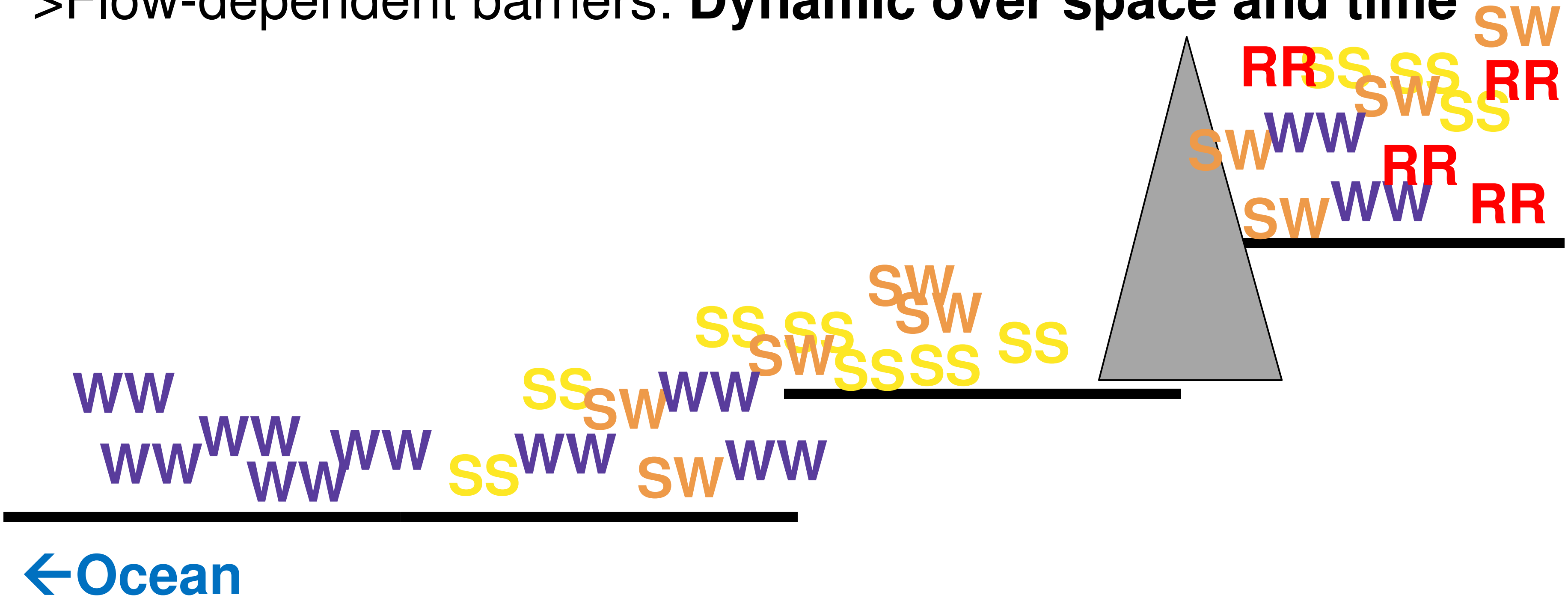
>Flow-dependent barriers: **Dynamic over space and time**



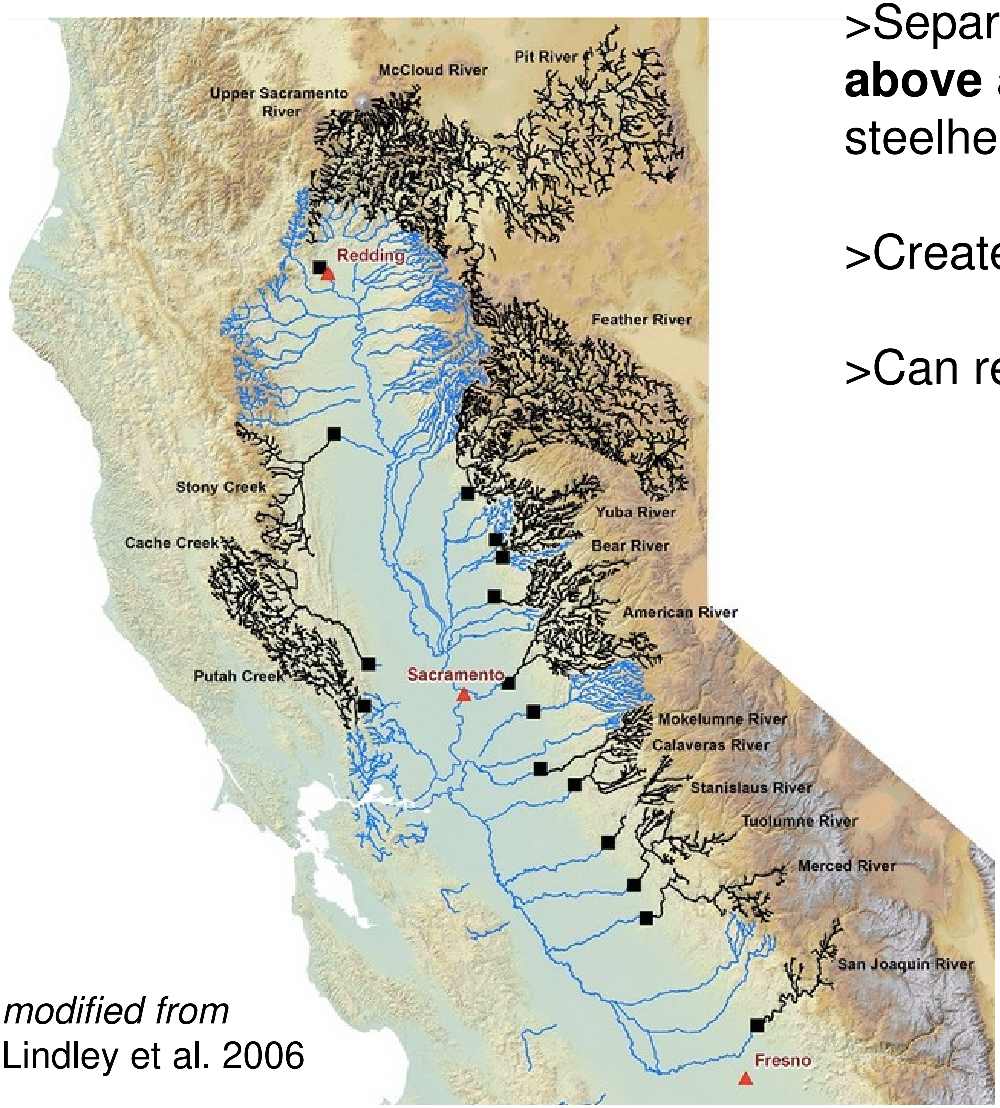
Landslide in lower Eel River ~22k years ago (Mackay et al. 2011)

Dams:

>Separate populations into trapped *O. mykiss* **above** and mixed resident and anadromous steelhead **below**.

>Create reservoirs above them.

>Can retain neutral and adaptive variation.



modified from
Lindley et al. 2006

Matijila Dam, Ventura River

>Dams alter the adaptive landscape

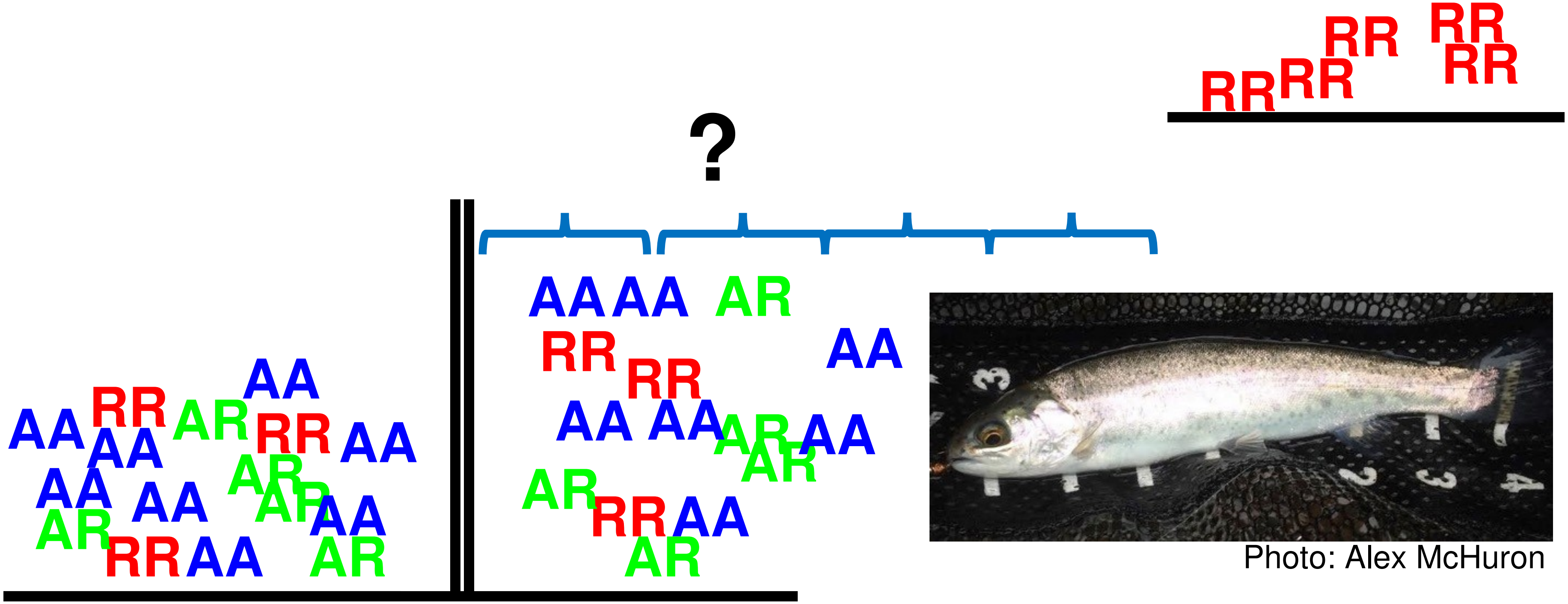


Photo: Alex McHuron

←Ocean

<u>Omy05 A variant present in reservoirs in</u>:

Coastal CA	Pearse et al. 2014, 2019
San Francisco Bay area	Leitwein et al. 2017
Tuolumne and Merced	Pearse & Campbell 2018
American River	Abadía-Cardoso et al. 2019

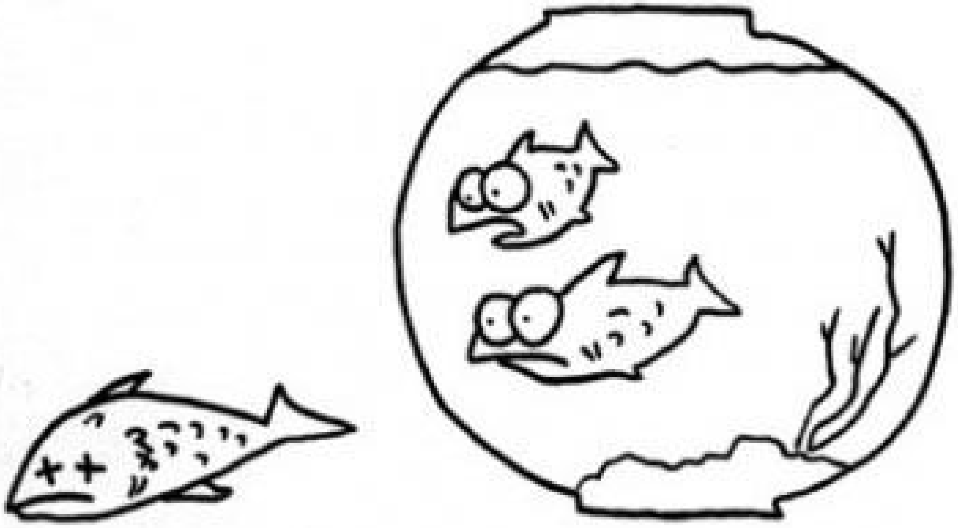
Conclusions

- **How can/Should we incorporate Adaptive Genomic Variation into conservation and management?**

- **Diverse and dynamic habitats and the portfolio effect.**

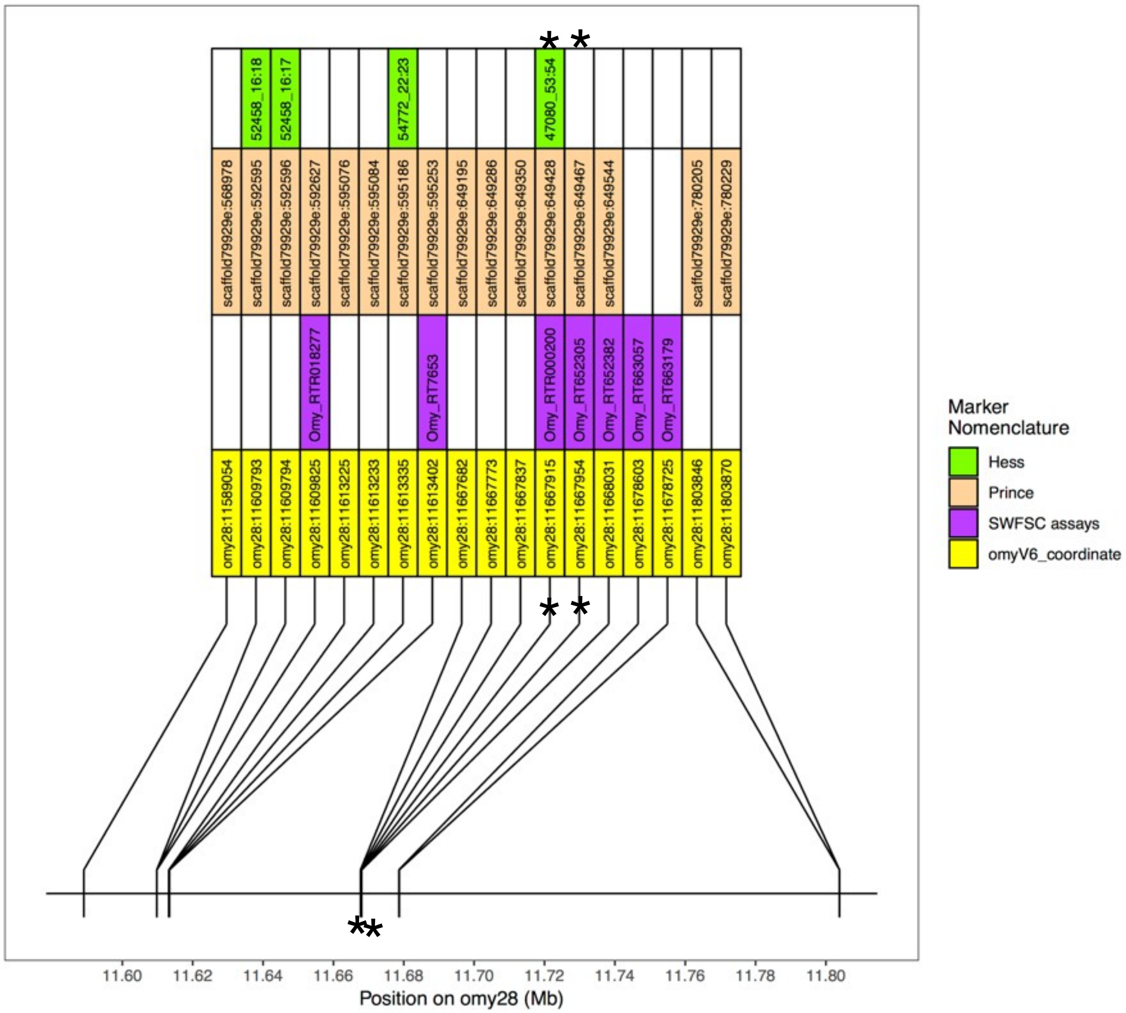
- **Focus on the phenotypes; Adaptive genomic variation provides an additional tool for understand, BUT individual genotypes do not perfectly predict phenotypes, and vice versa.**

Thank you!



... then he yelled "evolution!"
and simply jumped out ...

SWFSC unpublished data, Greb1L genomic region



SWFSC unpublished data, Greb1L genomic region

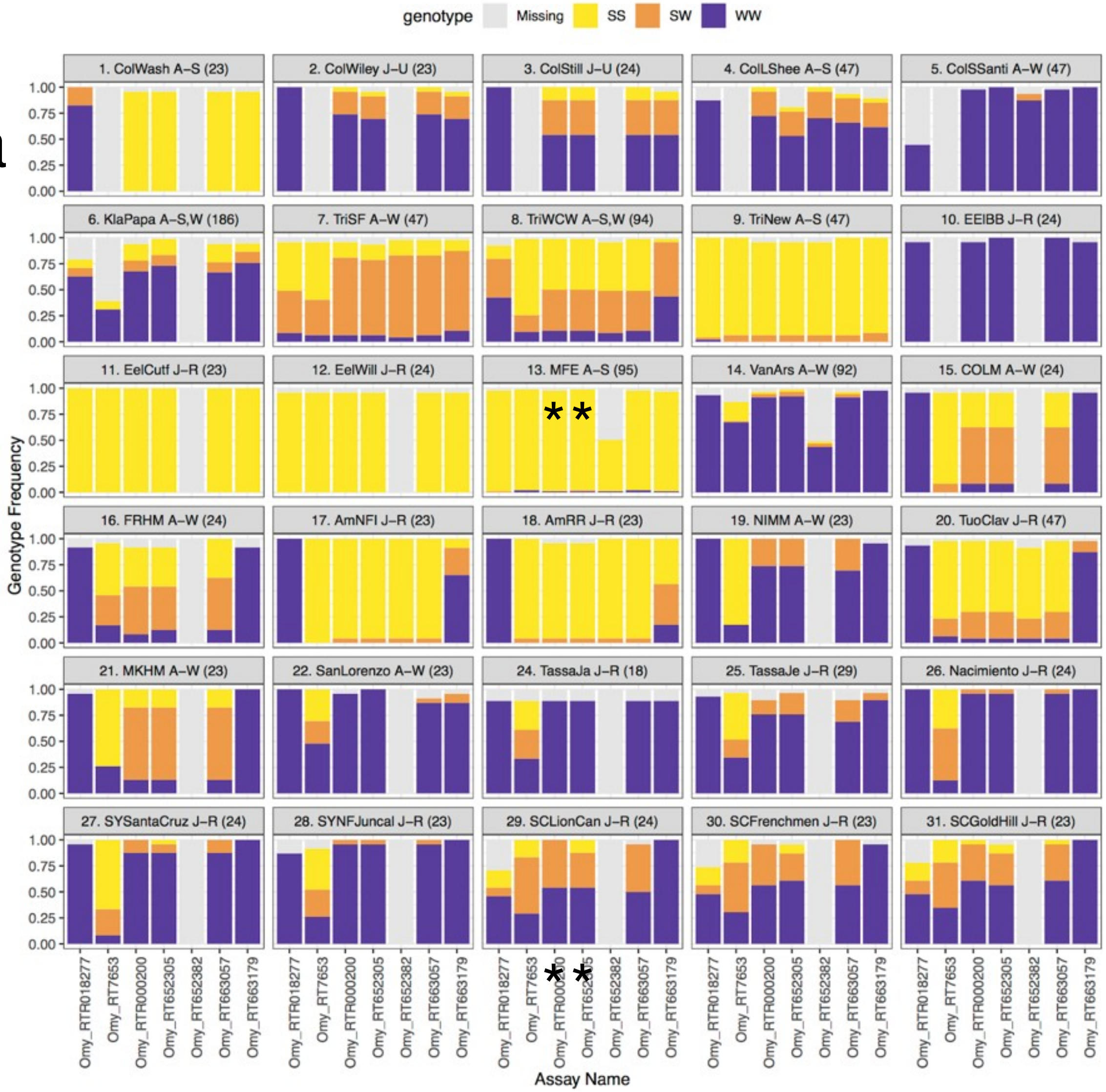
Columbia

Klamath

Eel

Central Valley

Central and Southern Coastal



NOAA Fisheries

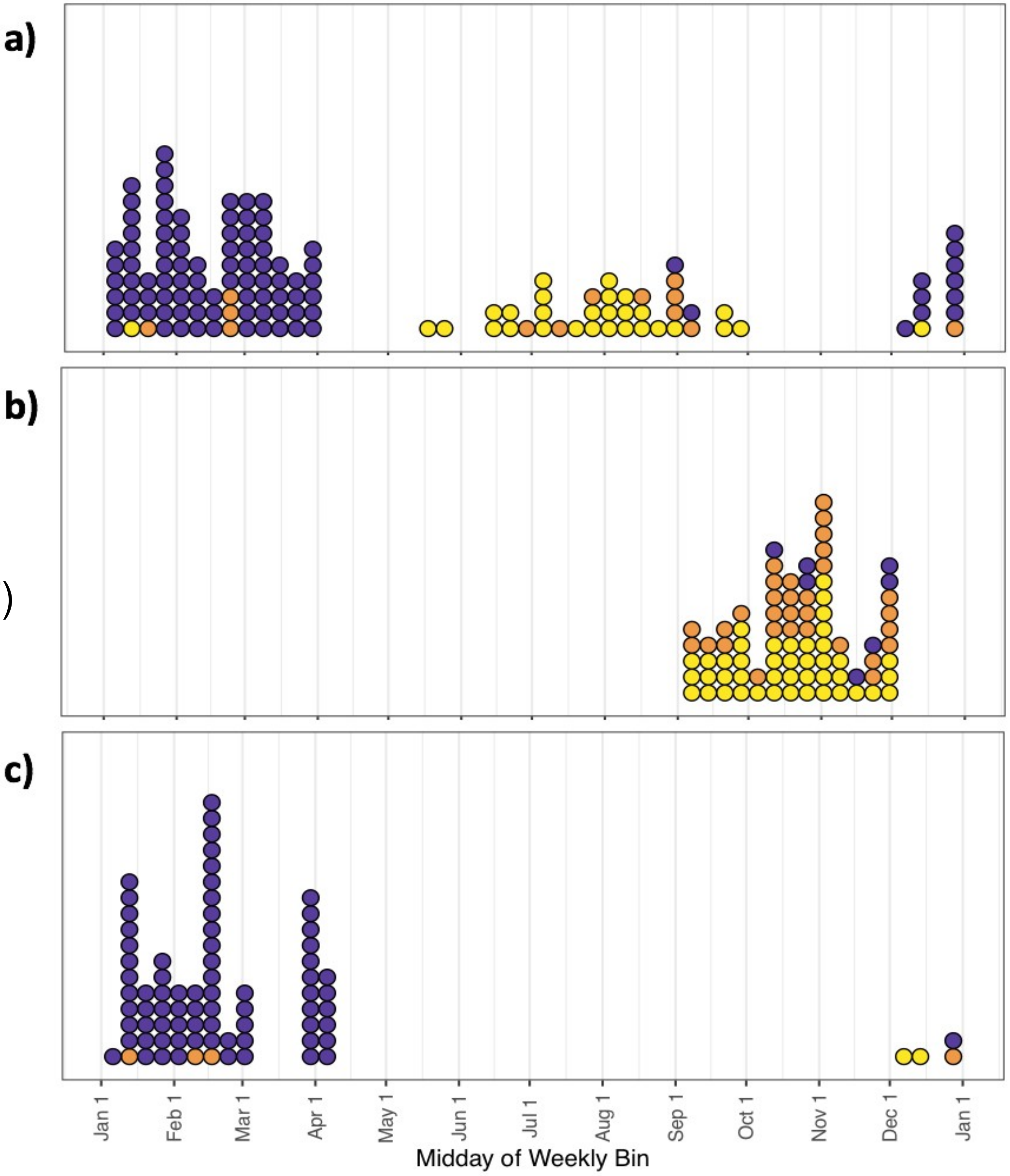
National Marine Fisheries Service

SWFSC unpublished data; Temporal variation

Numbers of Greb1L-region summer-run homozygote (SS, yellow), heterozygote (SW, orange), and winter-run homozygote (WW, purple) individuals among samples from three Sample collections:

a)Lower Klamath River (Papa et al 2007)
b)Willow Creek Weir on the Trinity River
c)Eel River (VAFS)

>This is based on microhaplotype assay data for the two loci identified.



SWFSC unpublished data; Temporal variation

Distribution of dates that steelhead (*O. mykiss* individuals >300mm) for which date information was available ascended the Van Arsdale Fisheries Station fishway between 2009 and 2016, including:
40 summer-run homozygote [yellow],
71 heterozygote [orange], and
1,726 winter-run homozygotes [purple],
(total N=1,837)

>This is based on microhaplotype assay data for the two loci identified.

>Parentage analysis confirms matings between SW hets and WW steelhead.