Genomic Adaptation and Conservation and Management of Life-History Variation

NOAA FISHERIES
Southwest Fisheries Science Center

Devon Pearse

March 8, 2016

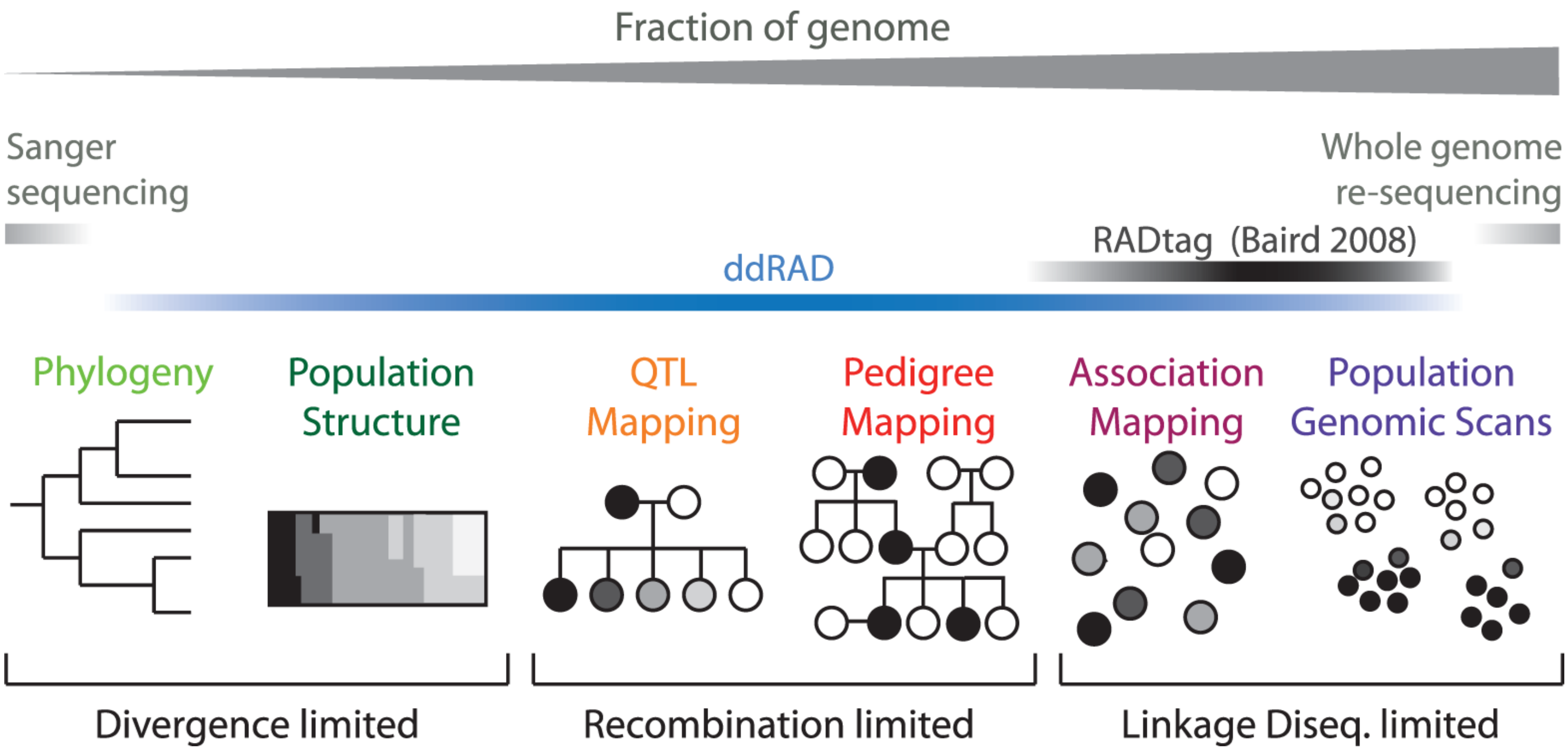
>What is the role of **population genetics** in conservation?

Delineate ESU/DPS boundaries, stock identification (GSI), parentage based tagging, and hatchery broodstock management (e.g. inbreeding avoidance).

>How is the emerging field of **‘adaptation genomics’** different?

>Emerging due to change in our ability to find and quantify the effects of specific genetic elements using genome-wide DNA data:

1996	2006	2016
1 locus	Microsatellites/SNPs	1,000s→1,000,000 of SNPs



Peterson et al. 2012, *PLOS One*

Level of biological question

Higher Level Taxonomy, phylogeny	Species & Sub-species Relationships, phylogeography	Population Structure, Migration, Stock ID)	Relatedness Parentage Pedigrees, Inbreeding	Individual identification, Fitness, Behavior

Scale of genetic data

Single-locus DNA sequences

"Next-generation Sequencing" (NGS)

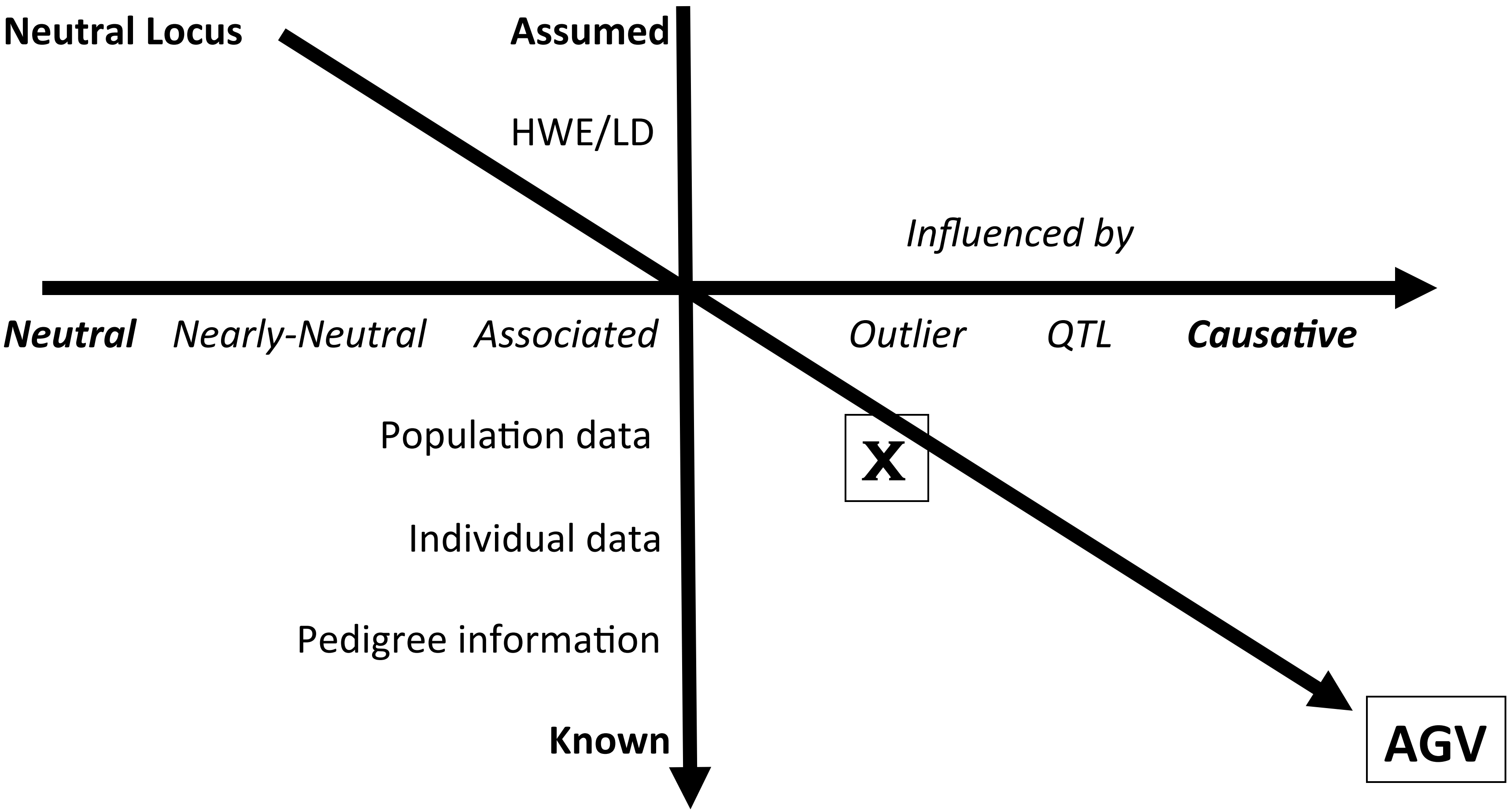
Allozymes, Microsatellites, SNPs

Type of genetic data

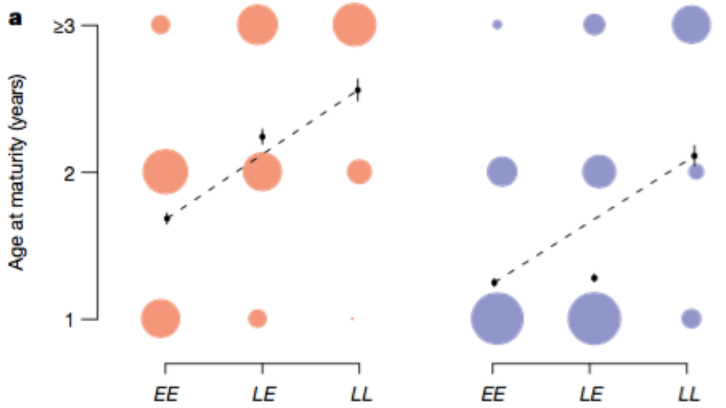
"Neutral" Population Genetic Data

"Adaptive" or "Functional" Genomic Variation

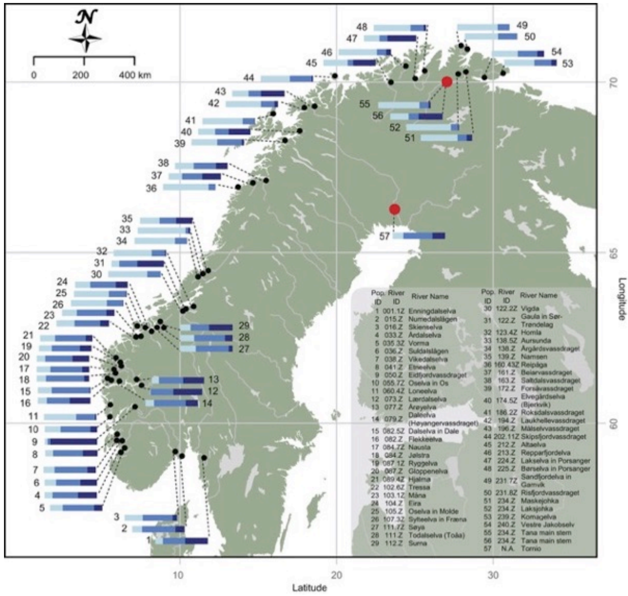
>**Adaptive Genomic Variation (AGV);** Specific SNPs or genomic regions that have been shown to have an adaptive evolutionary effect in wild populations. Almost always uncertain, and likely to have intraspecific variation.



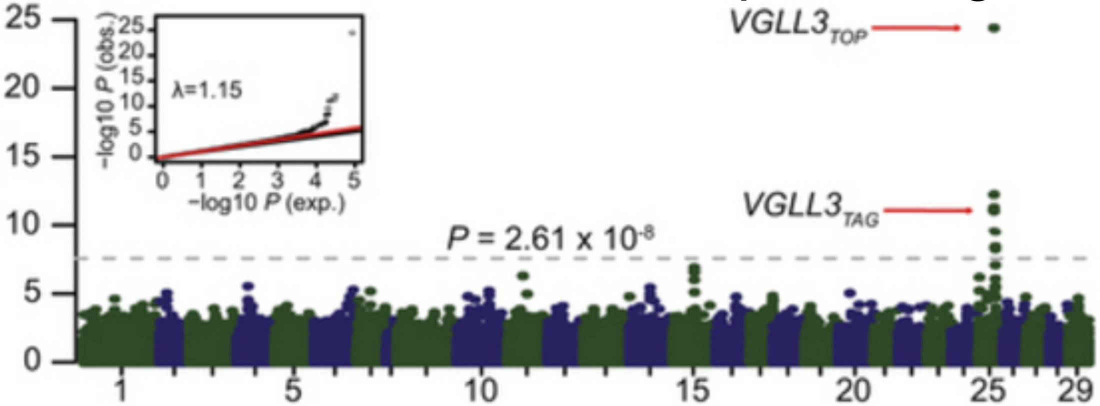
Early vs. Late Age-of-Return in Atlantic Salmon:



EE, EL, LL
2yo, het, 3yo



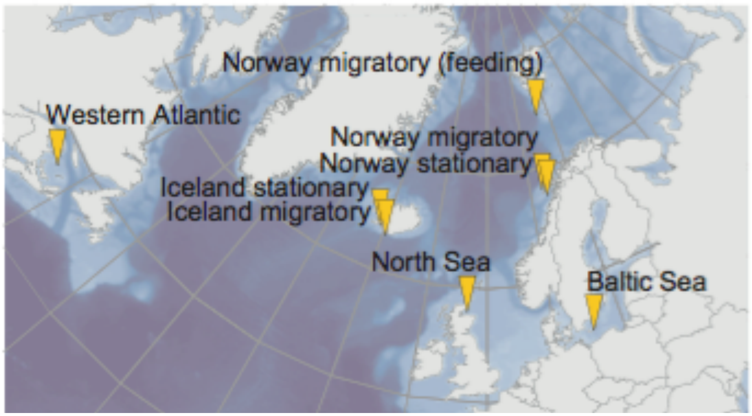
VGLL3 is associated with lipid storage and age of puberty in humans.

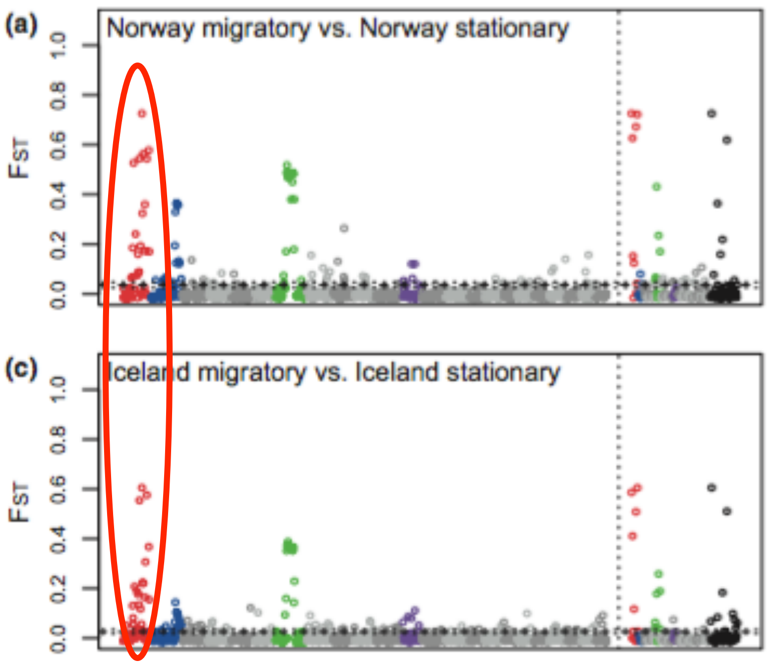


>Sex-dependent dominance reversal.
>Explains 39% of variance.

Barson et al. 2015

Genomic ‘islands of divergence’ in coastal and migratory Cod:

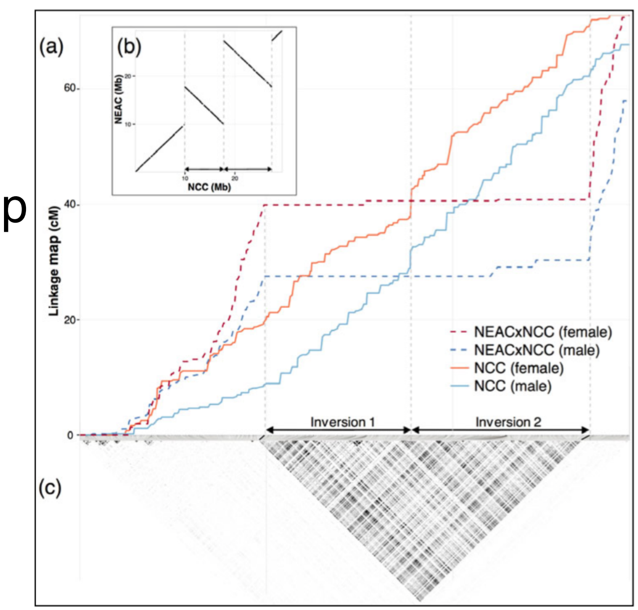




>10,000 SNP loci

-LG1=29,521,491 bp

-1,262 genes



Hemmer-Hansen et al. 2013; Kirubakaran et al. 2016

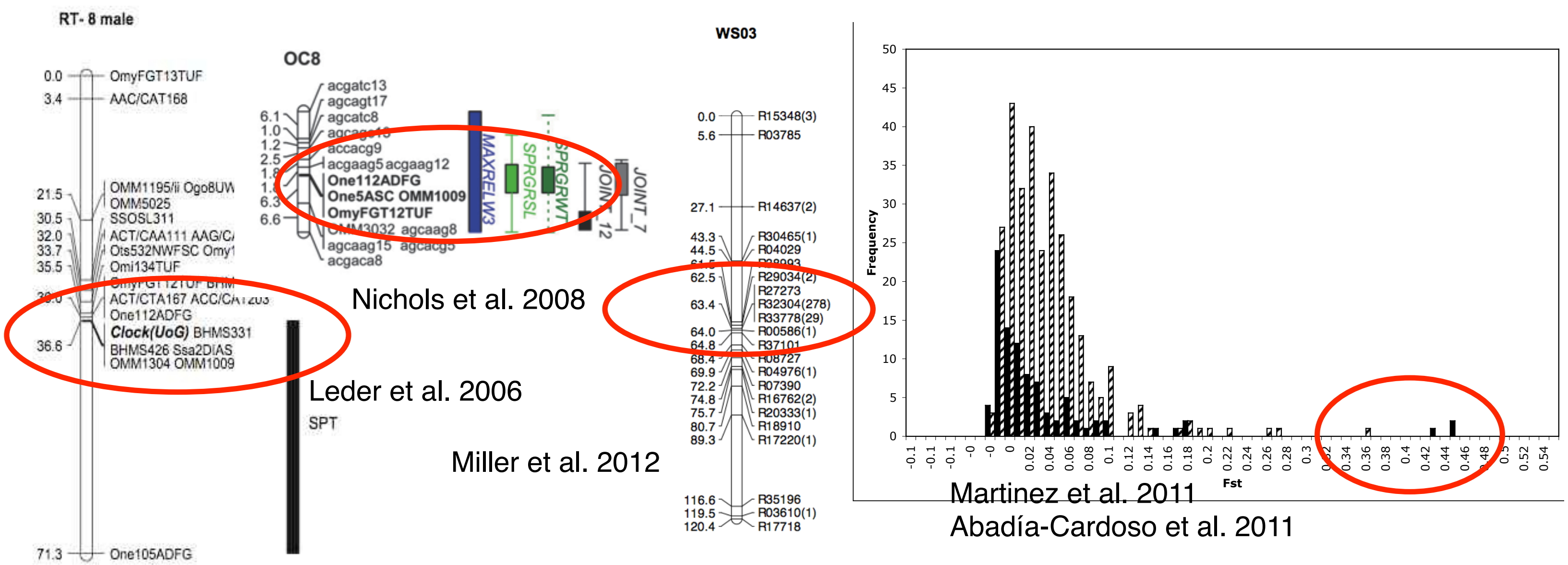
NOAA Fisheries
National Marine Fisheries Service

Smoltification in steelhead/Rainbow Trout:

>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.



Nichols et al. 2008

Leder et al. 2006

Miller et al. 2012

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

NOAA Fisheries
National Marine Fisheries Service

Smoltification in steelhead/Rainbow Trout: **Omy5**.

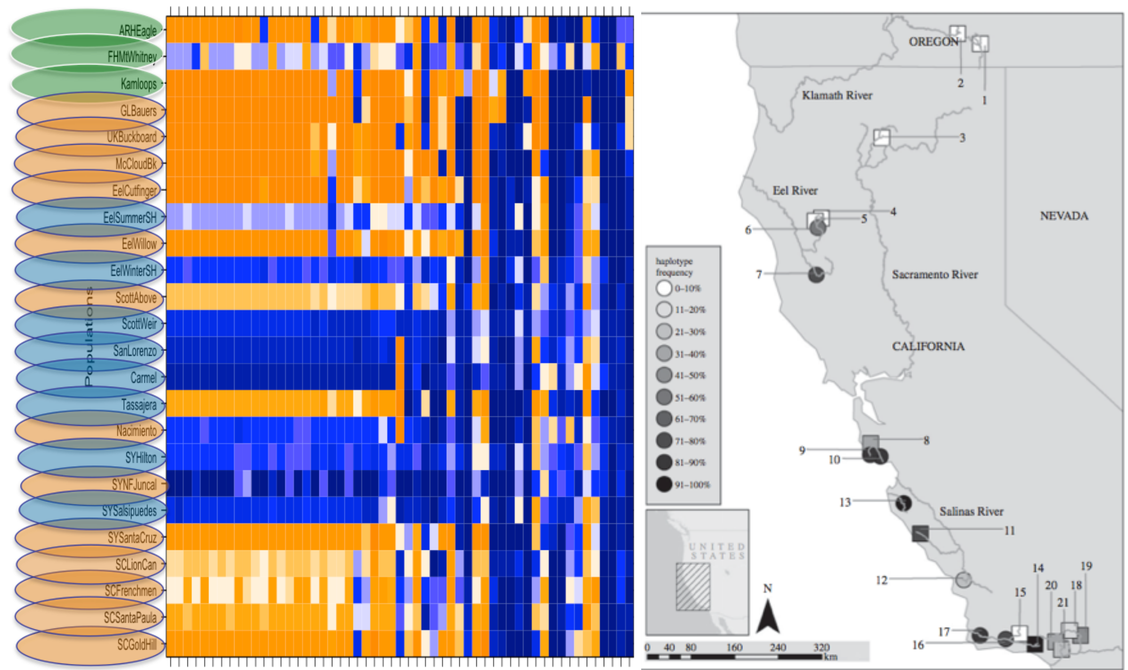
>**Rapid** adaptation of Rainbow Trout above barriers associated with evolution on one genomic region.

>**Repeated parallel evolution** from standing variation.

>Significant effect of above-barrier population **age**. (natural populations fixed)

>**Individual** smoltification effects.

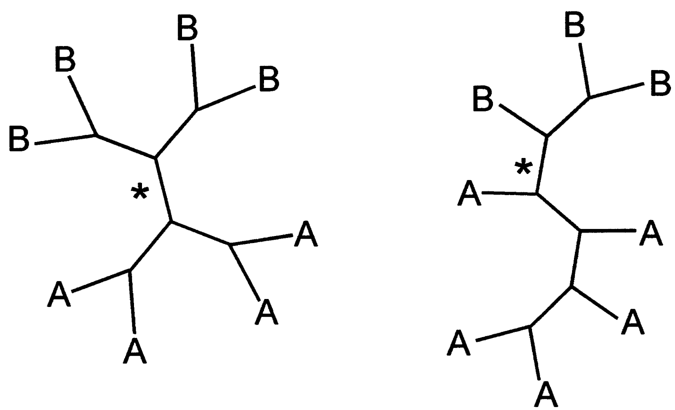
>**Genomic** characterization in progress.



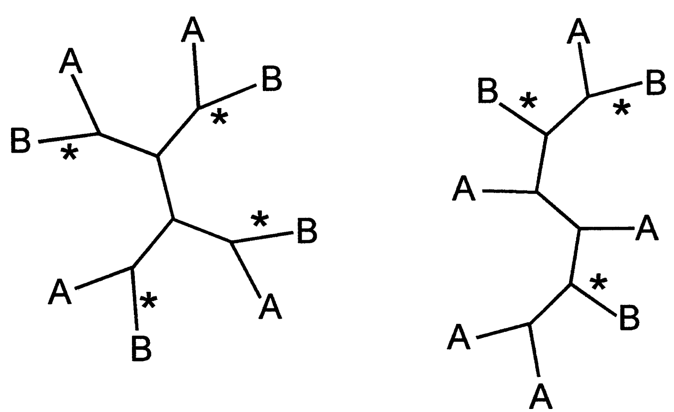
Pearse et al. 2014, *Proc. Roy. Soc. B*

Parallel evolution of residency in *O. mykiss*

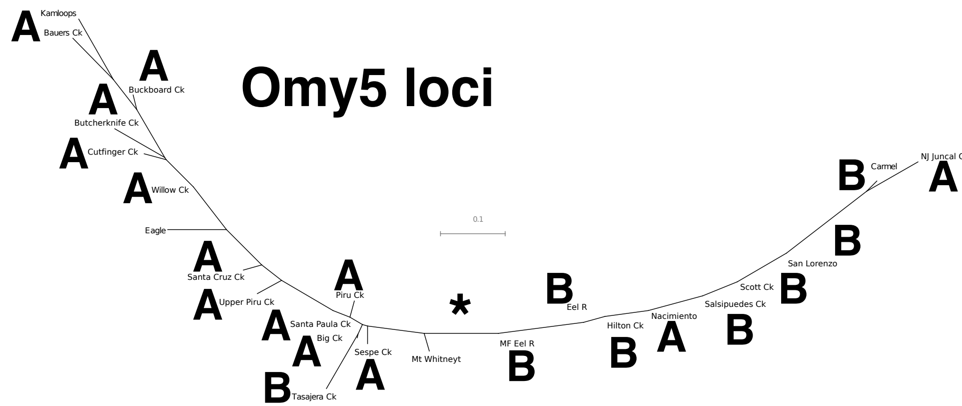
Single evolutionary event

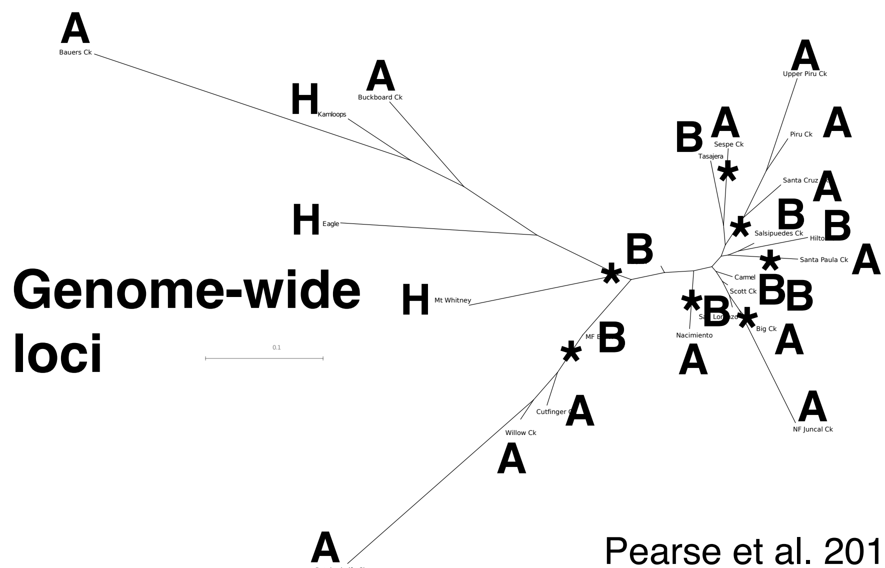


Parallel evolution



Waples et al. 2004



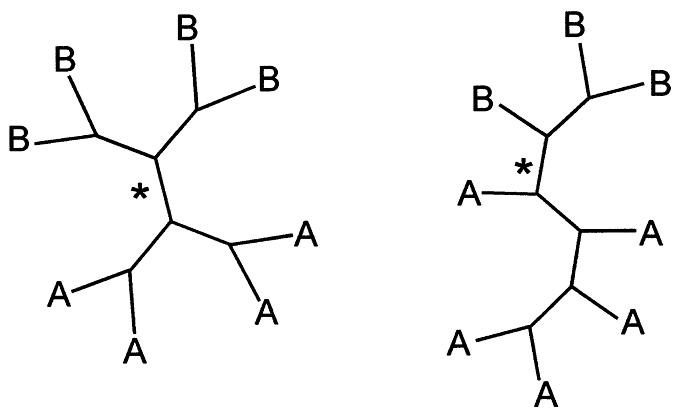


Pearse et al. 2014

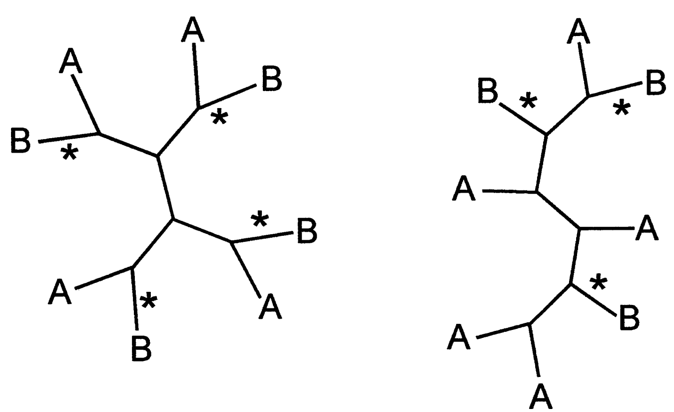
Parallel evolution of residency in *O. mykiss*

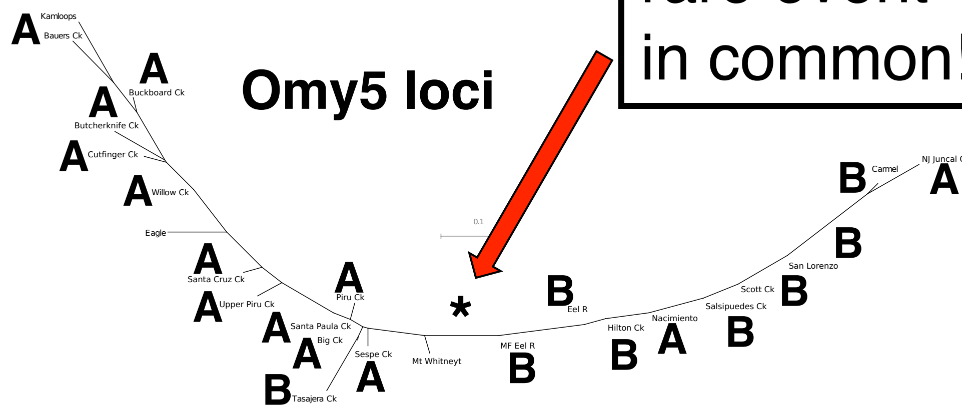
A single rare event in common!

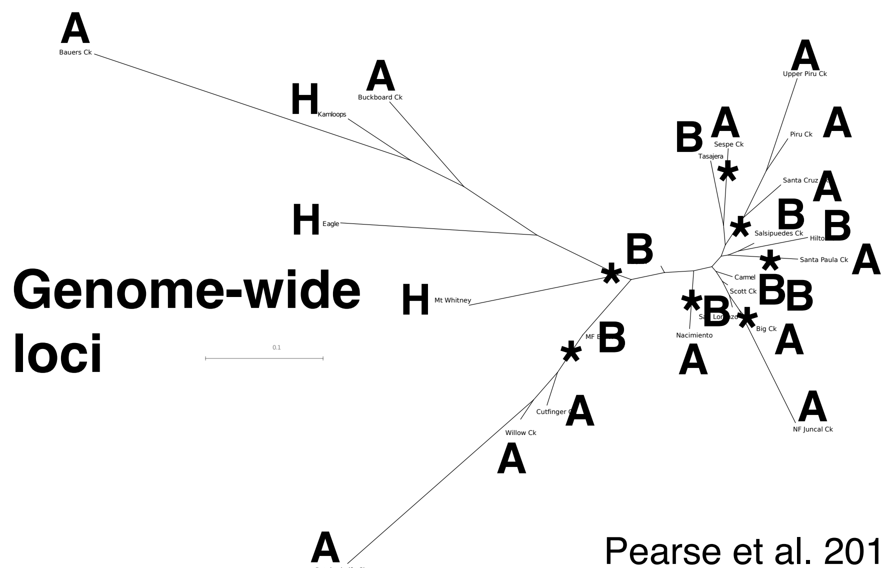
Single evolutionary event



Parallel evolution





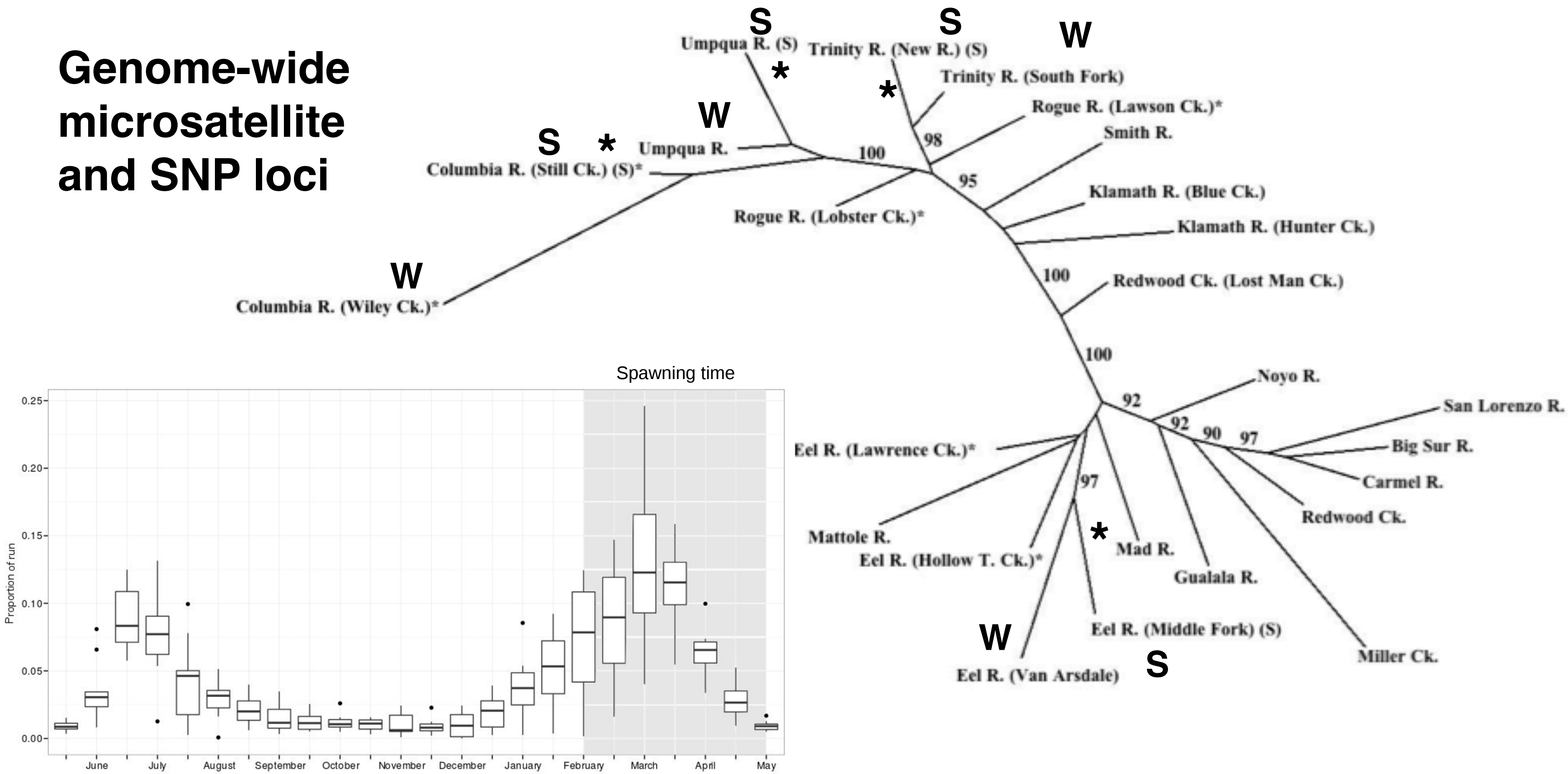


Waples et al. 2004

Pearse et al. 2014

Parallel evolution of Summer/Winter run-timing in steelhead

Genome-wide microsatellite and SNP loci

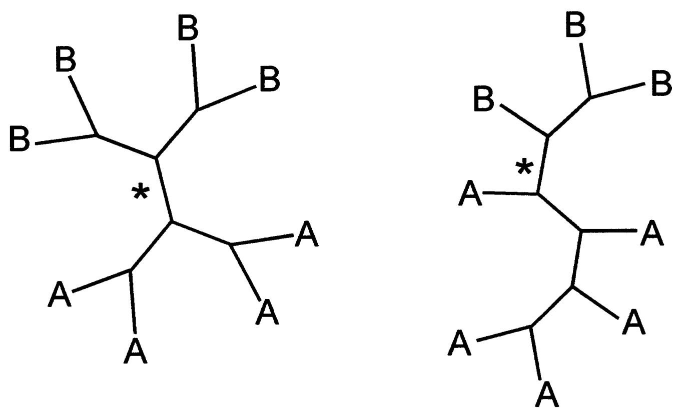


Summer **Winter**

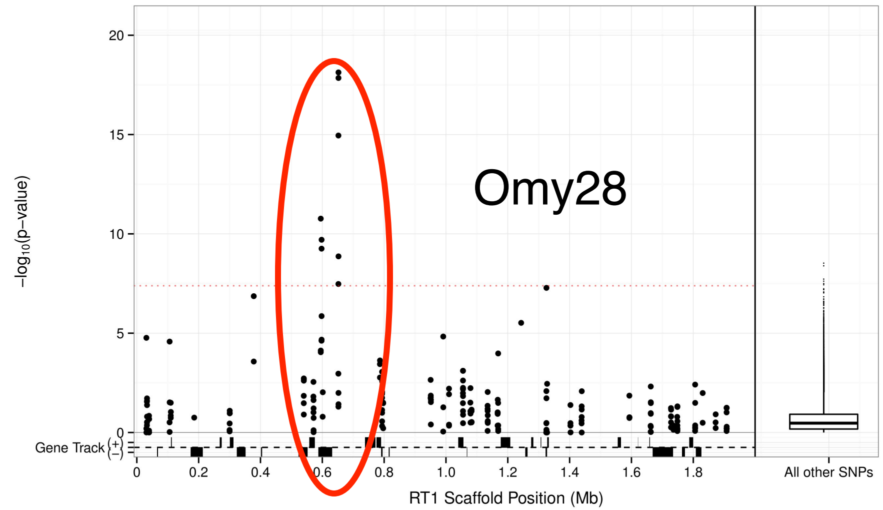
Arciniega et al. 2016, *Conservation Genetics*

Parallel evolution of Summer/Winter run-timing in steelhead

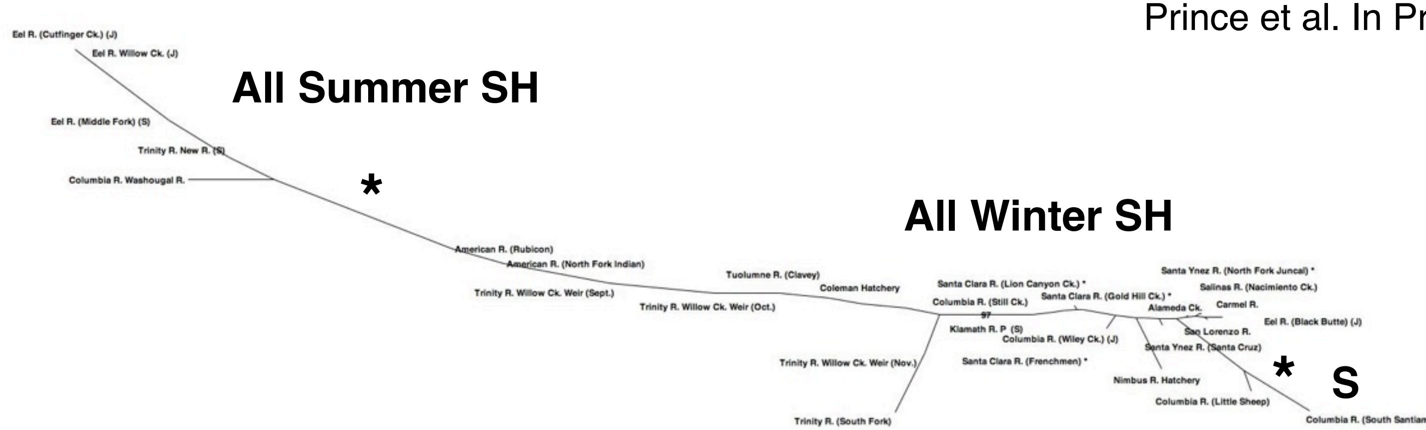
Single evolutionary event



Waples et al. 2004



Prince et al. In Prep



Arciniega et al. In Prep

Applied Conservation & Management:

How should we incorporate Adaptive Genomic Variation into steelhead management?

How is ‘Conservation Genomics’ different?

“all naturally spawned **anadromous** *O. mykiss* (steelhead) populations **below** natural and manmade impassable barriers”

NMFS 2006

Approaches to Adaptive Genomic Variation:

A) Passive Monitoring

B) Active Management

C) Marker Assisted Conservation

Passive Monitoring & Process Management:

AGV is subject to same genome-wide forces as neutral loci

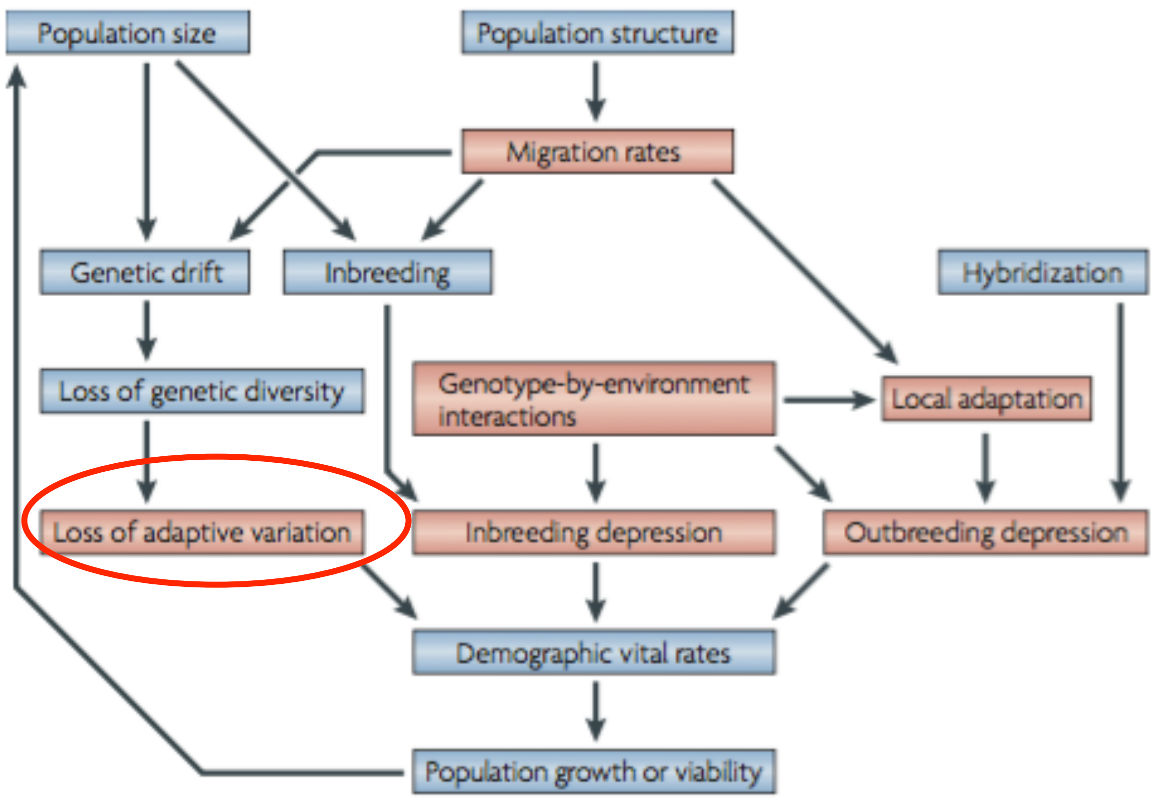


Figure 1 | **Schematic diagram of interacting factors in conservation of natural populations.** Traditional conservation genetics, using neutral markers, provides direct

Allendorf et al. 2010, Nature Reviews Genetics

Active Management:

>Follows existing ESA listing process.

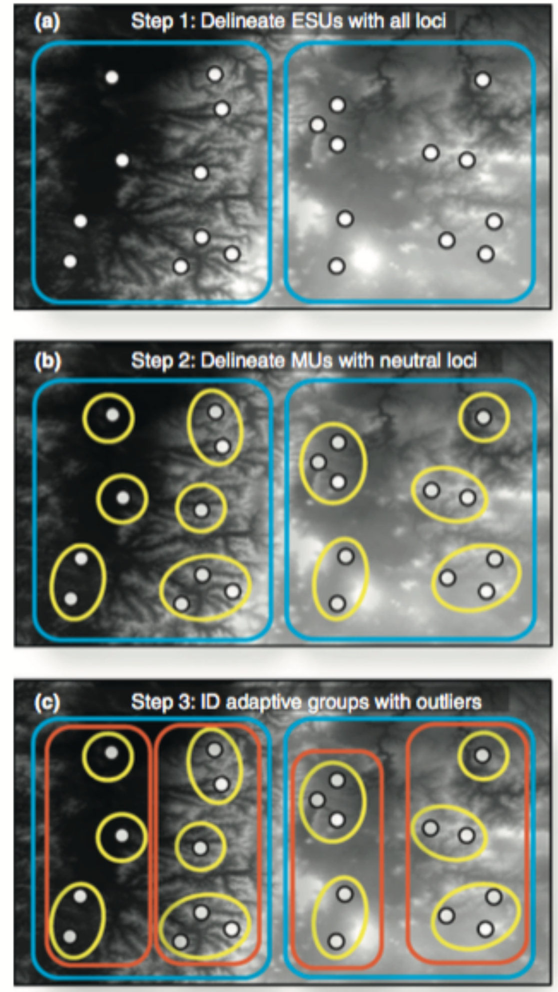
>Additional potential level for Management Unit designation (Adaptive Group).

>Likely only useful for major phenotypes.

>>Will not capture all AGV.

>Identify source populations for re-introductions.

(He et al. 2016 Con Bio)



TRENDS in Ecology & Evolution

Figure I. Proposed steps in using genomic data [e.g. single nucleotide polymorphisms (SNPs)] to define conservation units and test for adaptive differentiation among management units (MUs). White circles represent sampling localities, blue outlines are evolutionarily significant units (ESUs), yellow ellipses are MUs, and orange outlines are adaptively similar groups of MUs. The grayscale background is an elevation layer (white is high elevation, black is low elevation).

Funk et al. 2012, *TREE*

Marker Assisted Conservation:

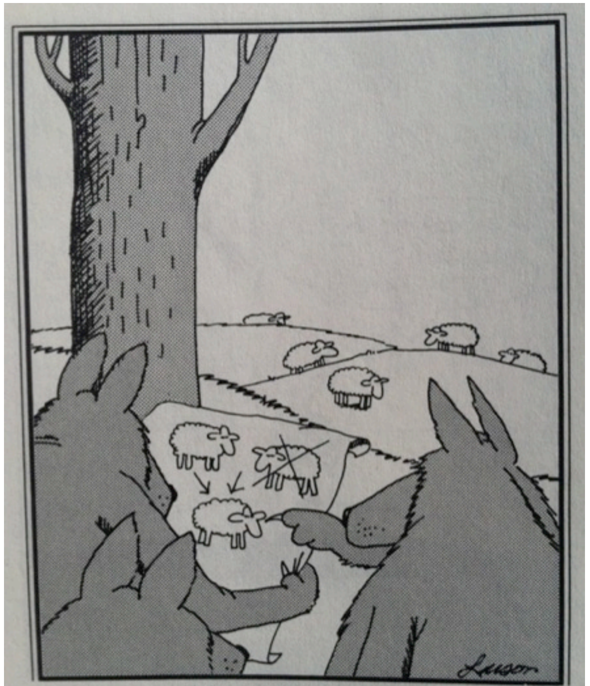
>Use of genotype at specific loci to select individuals for breeding.

>Widely used for livestock and crops.

>Hatchery broodstock selection.

>Released animals must be fit in their environment.

>Habitat is critical.



Natural selection at work

Adaptive variation reflects ecological conditions:

>Relative reproductive success of alternative individuals.

>Balance of selection.

>Non-equilibrium populations.

>River connectivity, geologic time and intermittent fish passage…

>Dynamic equilibrium!

since
1920

Carmel River

today
2016

Summary: What should we do with this information?

- Adaptive genomic variation can be targeted for conservation.

- Even genes of major effect are probabilistic indicators of individual phenotype.
(Major exception; immune system genes)

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

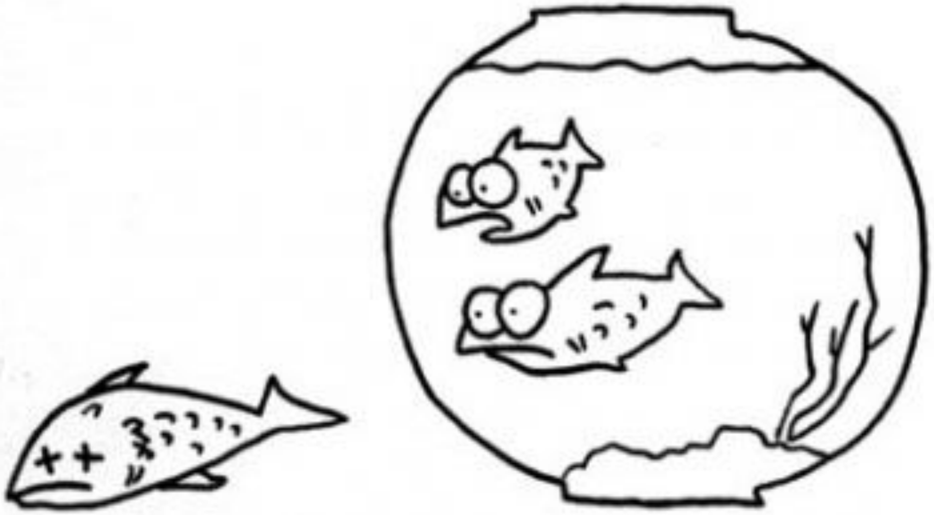
Acknowledgements

Co-Authors (UCSC and/or NMFS/SWFSC except as noted):
Alicia Abadía-Cardoso, Martha Arciniega, Eric Anderson, Anthony Clemento, Carlos Garza, Sean Hayes, Steve Lindley, Jonathan Moore, Matt Petterson (HSU/FishBio), Corey Phillis, Dave Rundio, Tommy Williams, Mathieu Bouro (UC Berkeley), Michael Miller (UC Davis).

Thanks to:
Vanessa Apkenas, Cassie Columbus, Libby Gilbert-Horvath, Kerrie Pipal, Heidi Fish; Mark Readdie and Feynner Arias, Monterey Bay Salmon & Trout Project, Erick Sturm. Robin Waples, Cramer Fish Sciences, and CA Dept. of Fish & Wildlife Tissue Archive.

Funding
NOAA Fisheries
CA Dept. Fish & Game Fisheries Restoration Grant Program
California Bay-Delta joint DOI/DOC Task Force
Bureau of Reclamation

Thank You!



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