

2nd Steelhead Summit

October 27 & 28, 2016 in San Luis Obispo, CA



Session Overview



- California Trout
- City of San Luis Obispo
- Sustainable Conservation
- California Conservation Corps
- Cachuma Operation and Maintenance Board
- Wildnote

The year's Summit agenda highlighted adaptive genomic variation, steelhead recovery planning, coastal monitoring status reports, fish passage planning, and water conservation efforts.

The full-day symposium was followed by concurrent field tours to restoration sites that showcase fish passage improvements and water conservation projects.



Presentations

Orientation Presentations

(Slide 4) Saving the Spandrels? Adaptive Genomic Variation in Conservation and Fisheries Management

Devon Pearse, Southwest Fisheries Science Center, NOAA Fisheries

(Slide 31) Steelhead diversity and resilience around the Pacific Rim Dr. Matthew Sloat, Wild Salmon Center

Saving the Spandrels? Adaptive Genomic Variation in Conservation and Fisheries Management

Devon Pearse

Molecular Ecology and Genetic Analysis Team
Fisheries Ecology Division/Southwest Fisheries Science Center
National Marine Fisheries Service
and
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University of California, Santa Cruz



Salmonid Restoration Federation Steelhead Summit San Luis Obispo, CA October 27, 2016





>Population Genetics has many roles in conservation:

>Delineate ESU/DPS boundaries, stock identification (GSI), parentage based tagging, effective population size (Ne), and hatchery broodstock management, etc.

- >Historically "data limited".
- >Theory dating back to modern synthesis (Wright-Haldane-Fisher).
- >Based on the 'neutral theory' (Kimura 1968).

>What is 'Conservation Genomics' and is it different?

Short answer is NO. But see....

(Primmer, 2009; Allendorf *et al.*, 2010; Ouborg *et al.*, 2010; Funk *et al.*, 2012; Shafer *et al.*, 2015, 2016; Benestan *et al.*, 2016; Prince et al. 2016; Garner *et al.*, 2016; Pearse 2016)





Fraction of genome

1 locus mtDNA Microsatellites/SNPs 1,000s→1,000,000s of

SarSNPs
sequencing

RADtag (Baird 2008)



"Neutral" Population Genetic Data Analysis



"Adaptive" or "Functional" Adaptive Genomic Variation (AGV)

- >Genomic data is now almost limitless.
- >Neutral vs Adaptive is a fundamental dichotomy.

 But, it is really a continuum!







Which pieces of grain are 'neutral', and which ones affect the character of the beer?



Fraction of genome

1 locus mtDNA

Microsatellites/SNPs

 $1,000s \rightarrow 1,000,000s of$

Whole genome re-sequencing

RADtag (Baird 2008)

sequencing

ddRAD



"Neutral" Population **Genetic Data Analysis**



"Adaptive" or "Functional" **Adaptive Genomic Variation** (AGV)



SarSINPs

"Under the influence" of selection





Oncorhynchus mykiss

- ➤ Steelhead: Anadromous, spend 1-2 years in freshwater and 1-4 years in salt water prior to spawning. Iteroparous.
- ➤ Rainbow Trout: Stay in stream entire life as Residents. Populations may exisit in isolated freshwater systems.

Determined by some combination of genetics (heritable) and response to environmental effects (phenotypic placticity).





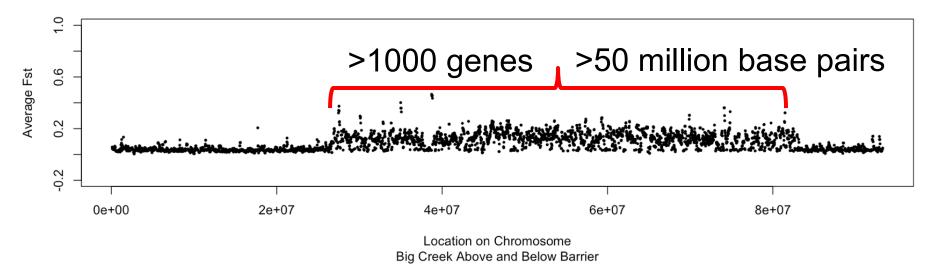
Genomic basis of anadromy

>Numerous studies on genetic basis 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; 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 part of chromosome Omy5 with correlated life-history traits.

Sliding Window of Fst over omy05

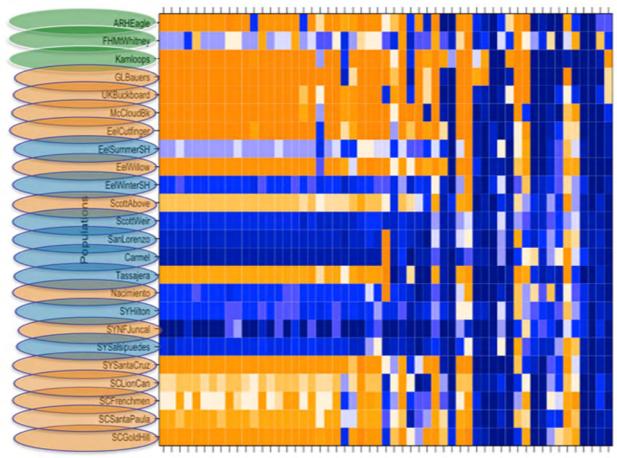


Lein et al. In Prep; Campbell et al. In Prep.



Genomic basis of anadromy

Rapid, repeated, parallel evolution of residency associated with the large Migration Associated Region (MAR) on chromosome Omy5.

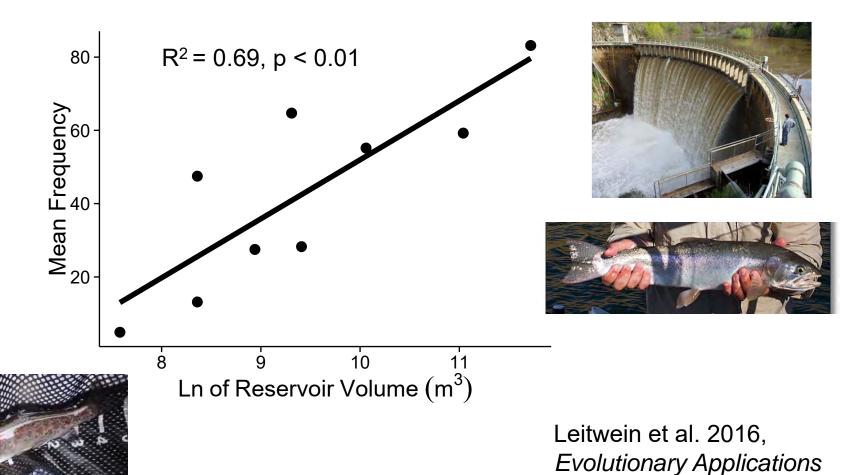


Pearse et al. 2014, Proc. Roy. Soc. B



Genomic basis of anadromy

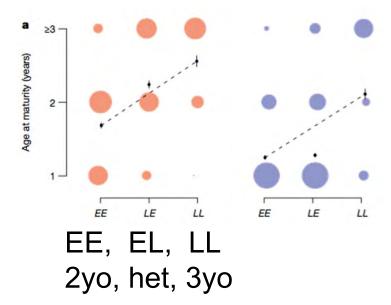
>Omy5 MAR also associated with adfluvial populations above reservoirs.

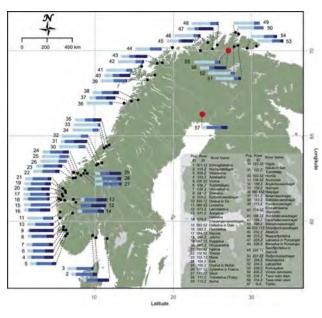




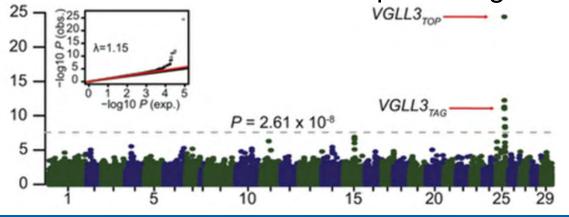
Early vs. Late Age-of-Return in Atlantic Salmon:







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

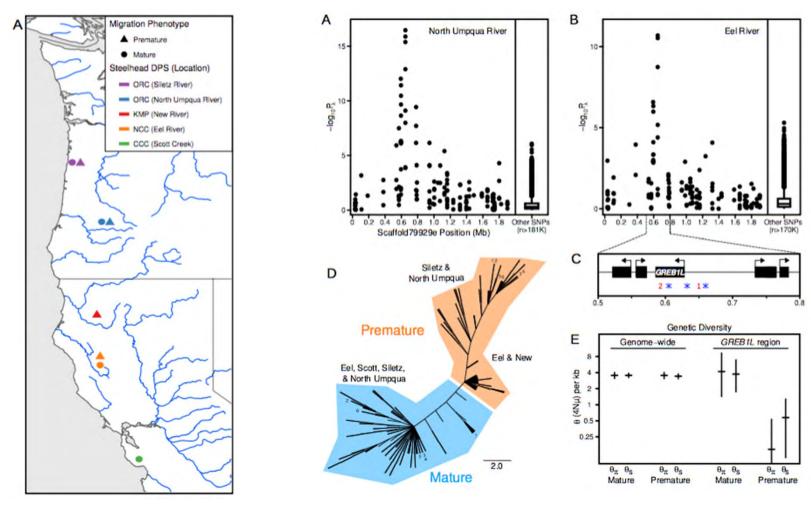


- >Sex-dependent dominance reversal.
- >Explains 39% of variance.

Barson et al. 2015



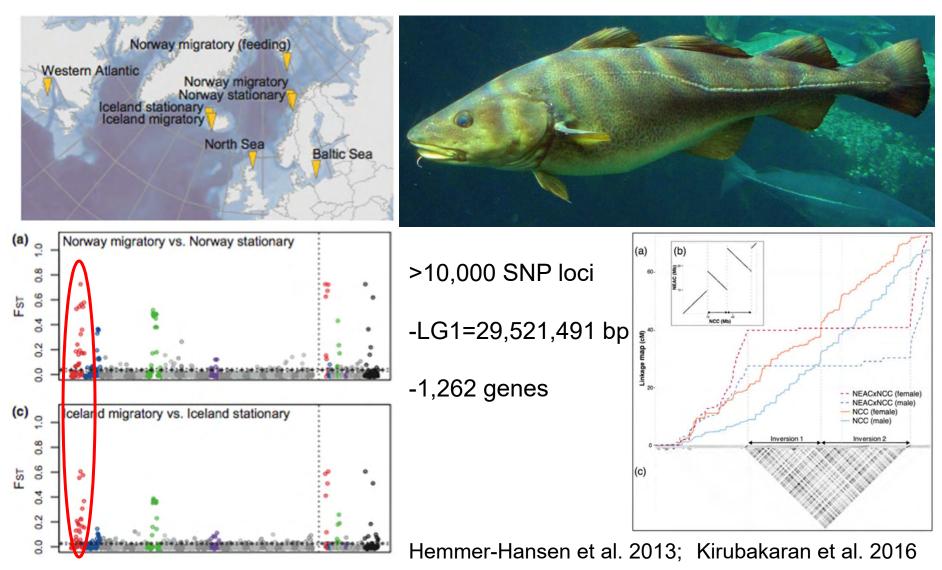
Premature vs. Mature Run-Timing in Steelhead:



Prince et al., In Review

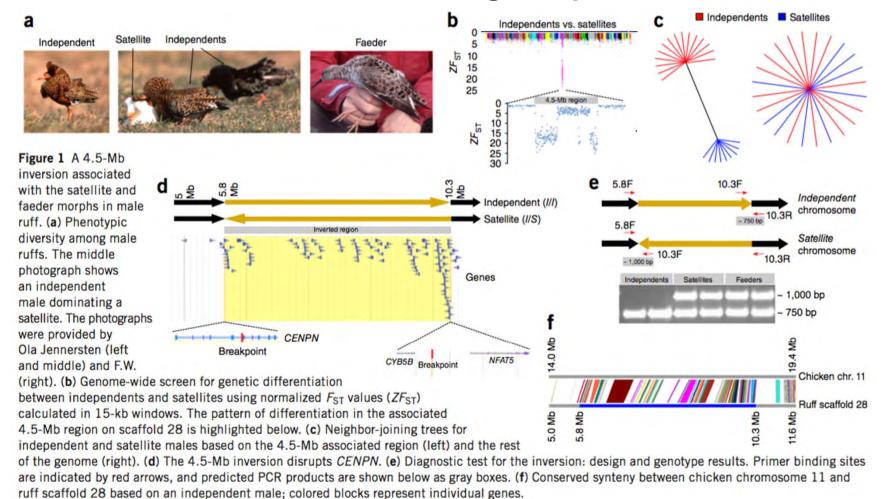


Genomic divergence in coastal and migratory Cod:





Genomic Basis of Male Mating Morphs in Ruff



Lamichhaney et al. 2016 *Nature Genetics* Kupper et al. 2016 *Nature Genetics*



SO, what does all this mean for conservation?





Journal of Fish Biology (2016) doi:10.1111/jfb.13168, available online at wileyonlinelibrary.com

Saving the spandrels? Adaptive genomic variation in conservation and fisheries management

D. E. Pearse*

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Saving the Spandrels?

Proc. R. Soc. Lond. B 205, 581-598 (1979) Printed in Great Britain 581

The spandrels of San Marco and the Panglossian paradigm: a critique of the adaptationist programme

By S. J. Gould and R. C. Lewontin

Museum of Comparative Zoology, Harvard University,

Cambridge, Massachusetts 02138, U.S.A.





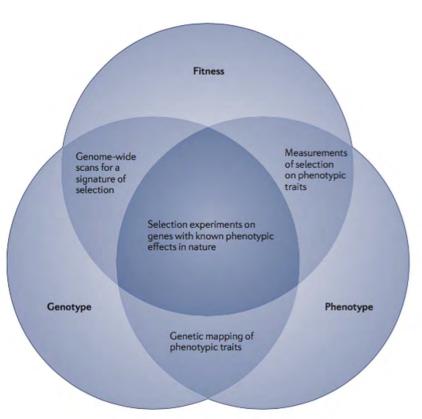
- 1) Don't assume selection.
- 2) Traits are not independent; consider the whole.



Molecular spandrels: tests of adaptation at the genetic level

Rowan D. H. Barrett and Hopi E. Hoekstra

Nature Reviews Genetics, 2011



Genomics gives us the tools to:

>Identify adaptive genomic variants.

>Connect to phenotypes and environmental variables

Stapely et al. 2010, TREE
Narum & Hess 2011, Mol Ecol Res
Vincent et al. 2013, Evolution
Poh et al. 2014, Plos One;
Springer et al. 2016, BioRxiv



Applied Conservation Genomics & Management:

How should we incorporate Adaptive Genomic Variation into steelhead conservation management?

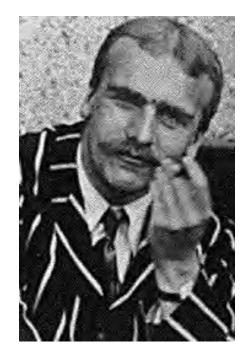
"all naturally spawned **anadromous** *O. mykiss* (steelhead) populations **below** natural and manmade impassable barriers"





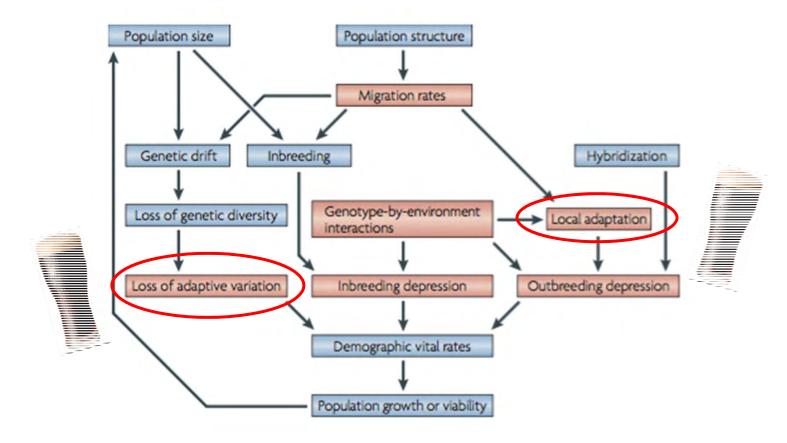
>We can now detect adaptive genomic variation, but the existence of such variation has long been recognized (J. B. S. Haldane, 1932).

>Ecotypic 'proxies' for phenotypes with unknown AGV (e.g. run-timing) have been Incorporated into conservation plans. (Dizon et al. 1992; Waples 2006)





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



Allendorf et al. 2010, Nature Reviews Genetics



Good news!

- >This means that for the most part we are already doing what we need to do from an evolutionary genetic perspective to protect genetic diversity.
- >Continued action is needed.

 (better tools serve to improve efficiency)
- >Protection of ancestral diversity plus recognition of ecotypic variants, regardless of underlying AGV.

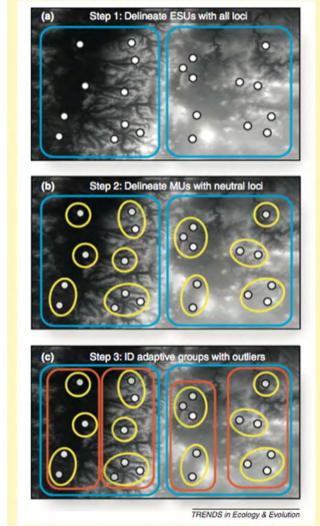


Conservation unit delineation

>Follows from existing ESA listing process.

>Additional potential levels for Management Unit designations and Adaptive Groups.

>Identify source populations for re-introductions. (He et al. 2016 Con Bio; Pearse 2016)



Funk et al. 2012, TREE



Technical Limitations

False Positives and Negatives.

-Polygenic traits, Pleiotropy, Epistasis,

Penetrance

- -Bias in detecting strong signals.
- -Will not capture all AGV.

>AGV associated with unclear phenotypes?



Levels of management: population vs. individual effects

- Unit of concern for conservation is population, not individual.In contrast, medical genomics is individual-based.
- >Marker-Assisted Selection in conservation?
 -Hatchery broodstock selection?
- -Use of genotype at specific loci to select individuals for breeding.
- -Widely used for livestock and crops.
- -Released animals must be fit in the environment.





Adaptive variation reflects ecological conditions:

Not vice versa.

since 1920

>Relative reproductive success of alternative individuals.



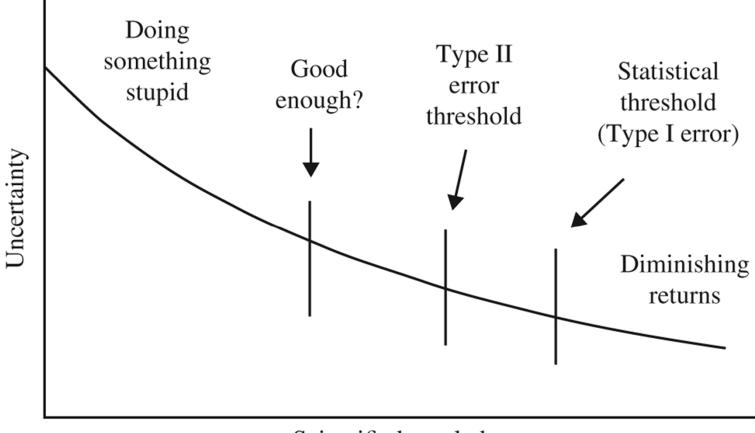
- >Balance of selection.
- >Non-equilibrium populations.
- >River connectivity, geologic time and intermittent fish passage...
- >Dynamic equilibrium!



today 2016



Conservation genomics: coming to a salmonid near you?



Scientific knowledge

No Data???

Population Genetics??

Individual Genetics?

Complete Genomes of all individuals?????

Piccolo 2016; Journal of Fish Biology

11 OCT 2016 DOI: 10.1111/jfb.13172

http://onlinelibrary.wiley.com/doi/10.1111/jfb.13172/full#jfb13172-fig-0001

Conclusions

- ➤ Adaptive genomic variation can be targeted for conservation. Evaluate diversity using neutral and adaptive loci.
- Even genes of major effect are probabilistic indicators of individual phenotype, and can't capture the full extent of phenotypic variation related to fitness.

(Major exception; immune system genes)

Focus on evolutionary processes that promote diversity. This is consistant with 'evolutionarily enlightened management' or 'prescriptive evolution'

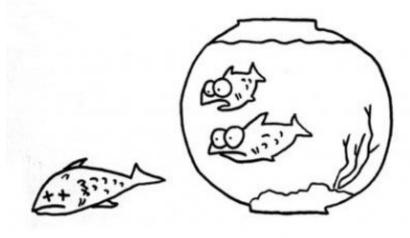
(Ashley *et al.*, 2003; Smith *et al.*, 2014; Pearse 2016).

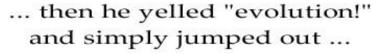


Thank you!

Thanks to past and present members of the NMFS SWFSC Molecular Ecology and Genetic Analysis team, particularly A Abadía-Cardoso, E Anderson, D Baetscher, A Clemento, and C Garza, as well as R Waples from the NWFSC, for many excellent discussions from which I developed the ideas presented here.

I thank F Allendorf, D Baetscher, M Capelli, K Naish, T Quinn, K Ruegg, and R Waples for commenting on the manuscript that led to this presentation.







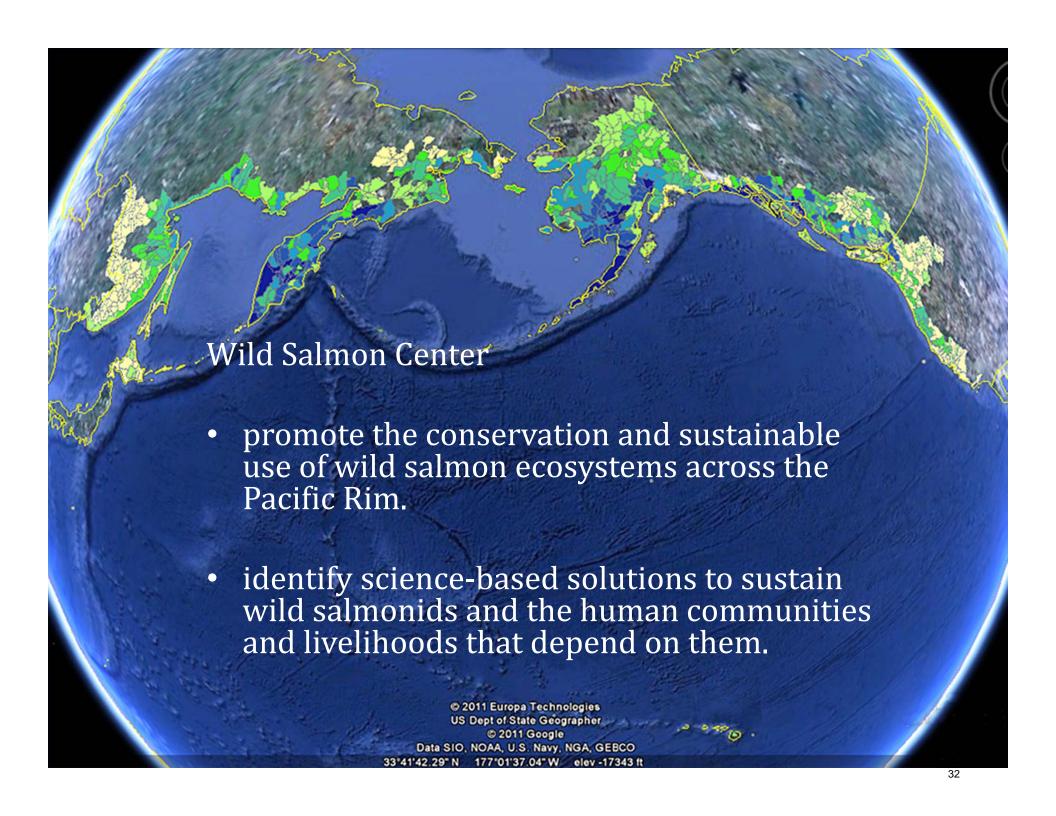


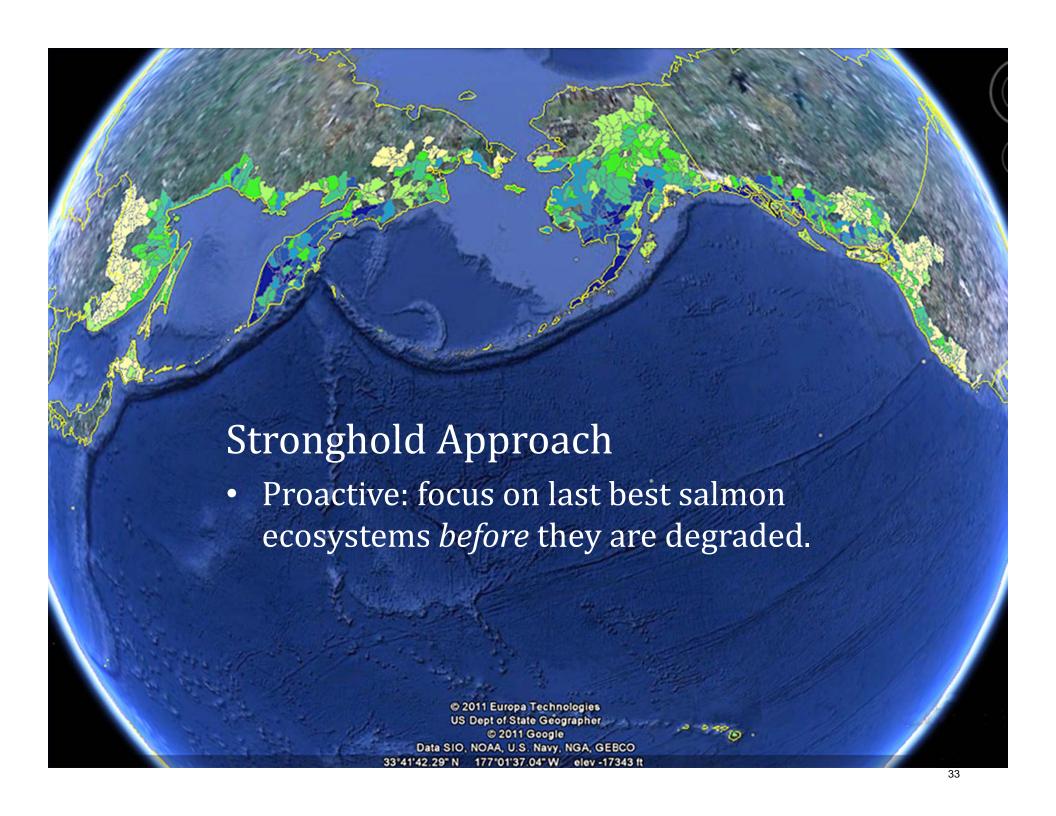
Steelhead diversity and resilience around the Pacific Rim

SRF Steelhead Summit

October 27, 2016

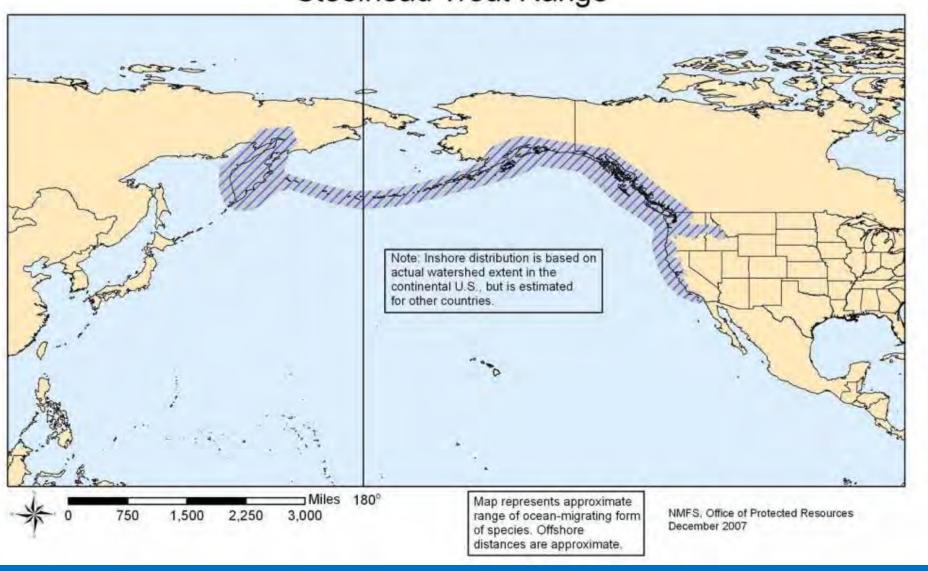
Dr. Matthew Sloat, Director of Science, Wild Salmon Center







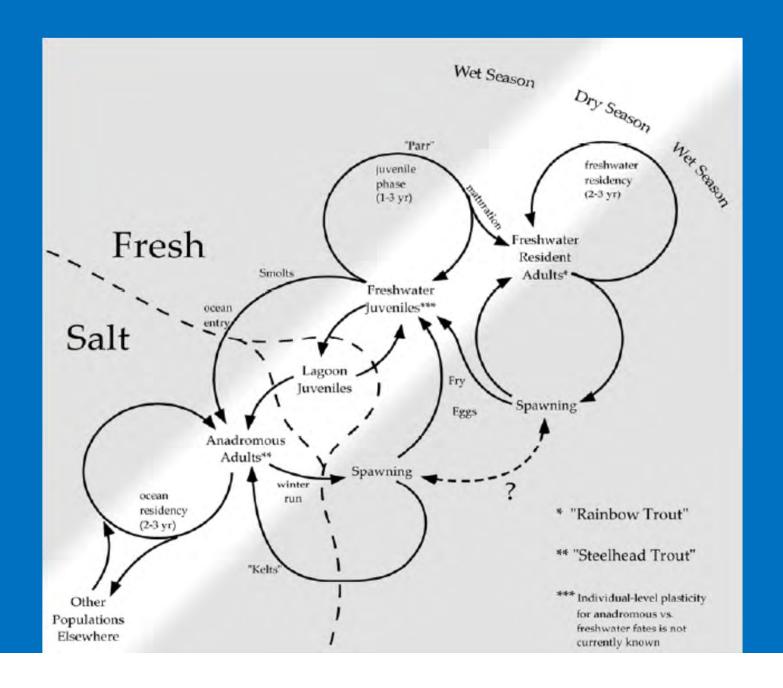
Steelhead Trout Range

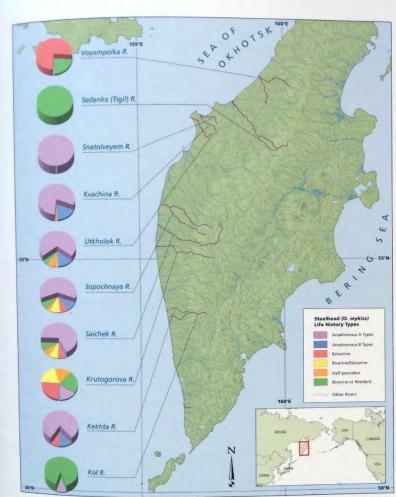






The Steelhead/Rainbow Trout Life Cycle





KAMCHATKA RAINBOW-STEELHEAD LIFE HISTORIES The rivers along the Kamchatka peninsula feature rich life history diversity within the genus Oncorhynchus, particularly within O. mykiss. Water temperature, channel morphology, as well as riverbed composition (e.g., volcanic or tundra) may contribute to the differences in life history types from river to river, ranging from the Kol in the south, where mykiss are largely resident, to the Snatolyweight. Snatokeyem in the rorth, where nearly all are anadromous steelhead. Russian scientists are the first to document this degree of life history variation within one species of *Oncorhynchus*.

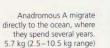
ONCORHYNCHUS MYKISS (PARASALMO MYKISS)

Siblings from the same redd may later exhibit six distinct life history types, from resident (rainbow) to anadromous (steelhead).

> Riverine/Estuarine 1.3 kg (0.4-2.5 kg range)



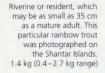
Estuarine, which may grow to around 90 cm. 2.1 kg (0.6–3.2 kg range)



Anadromous B spend a summer at sea, return to freshwater for overwintering, and migrate back to the ocean for several years. 4.9 kg (1.0-9.3 kg range)



Anadromous B-half-pounders, immature entering migration. 0.2 kg (0.1-0.31 kg range)









Key steelhead traits

Anadromy and residency.

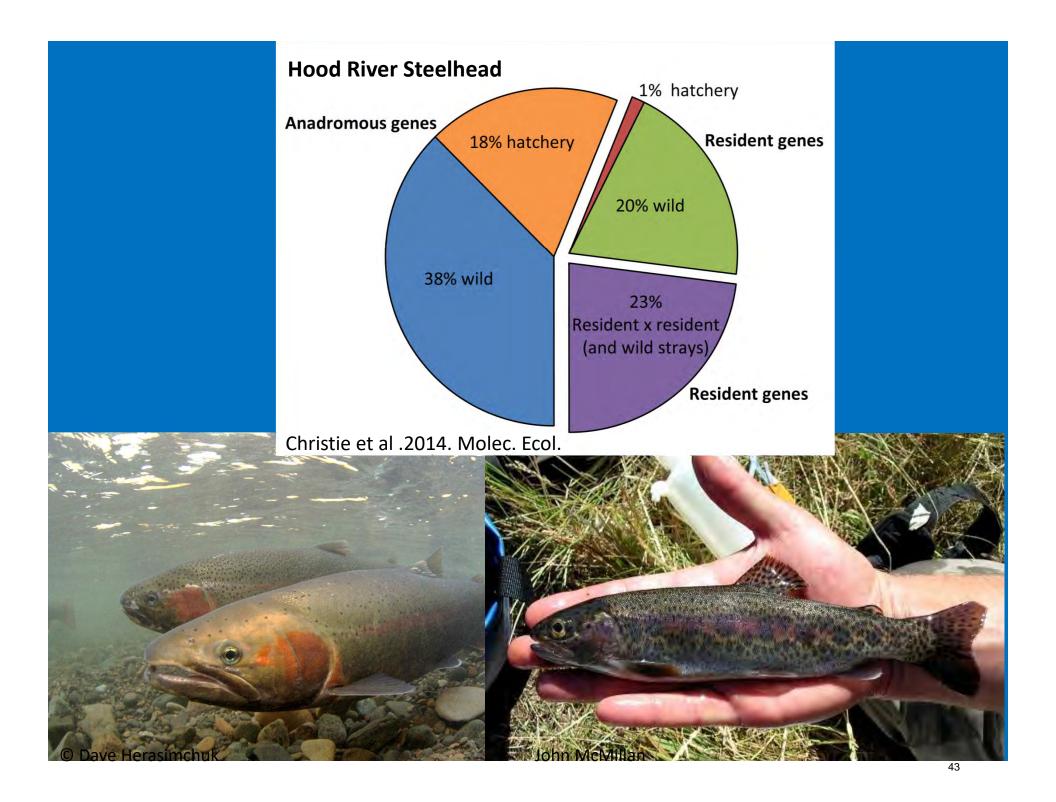
Age structured life histories.

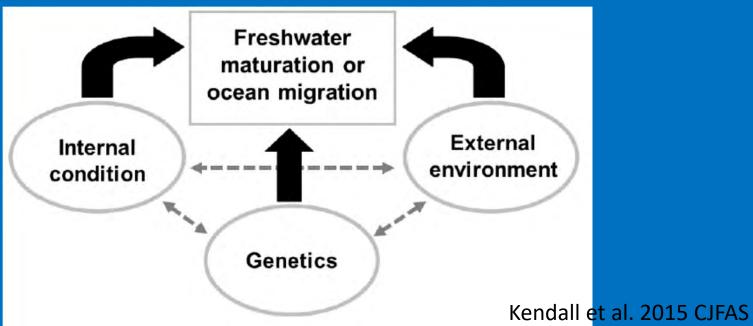
Fine-scale temporal/spatial patterns.

Anadromy and residency

Anadromy and residency





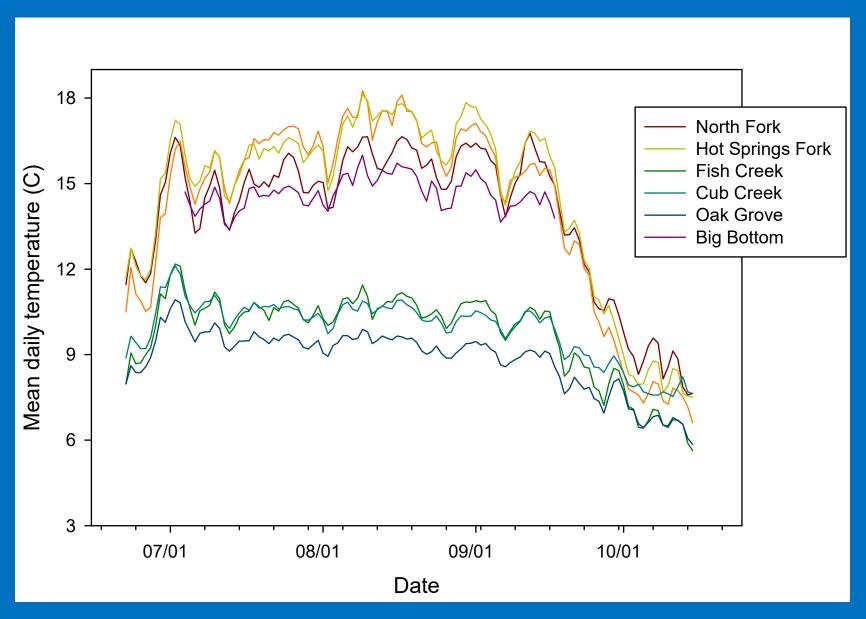




Basin-scale habitat heterogeneity and *O. mykiss* anadromy/residency

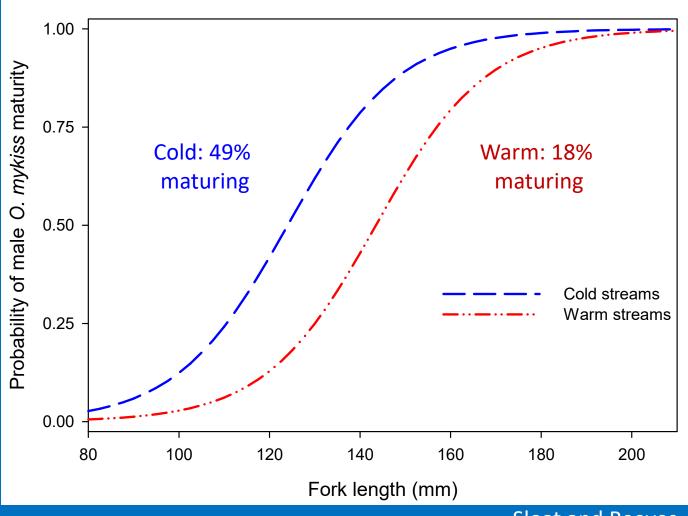


Clackamas Stream Temperatures

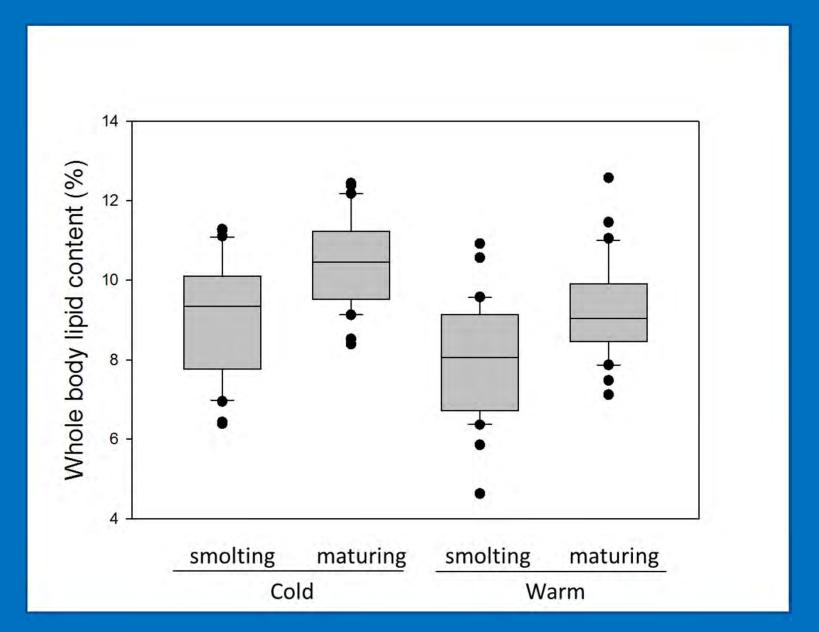


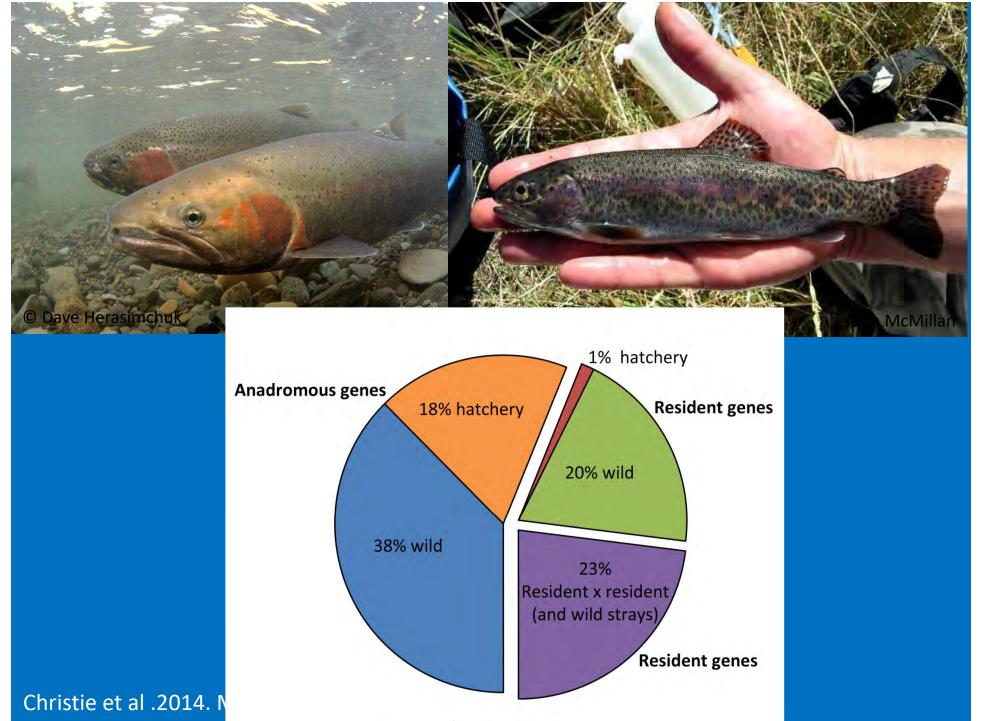
Temperature changes body size thresholds for O. mykiss maturation: Clackamas River

Maturation reaction norms for *O. mykiss* males reared in cold and warm tributaries to the Clackamas River, OR



Is fat where it's at?

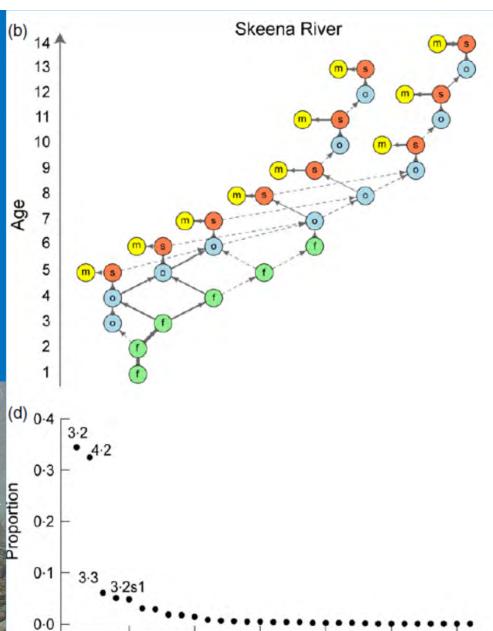




Age-structured Life Histories

Age-structured life histories.



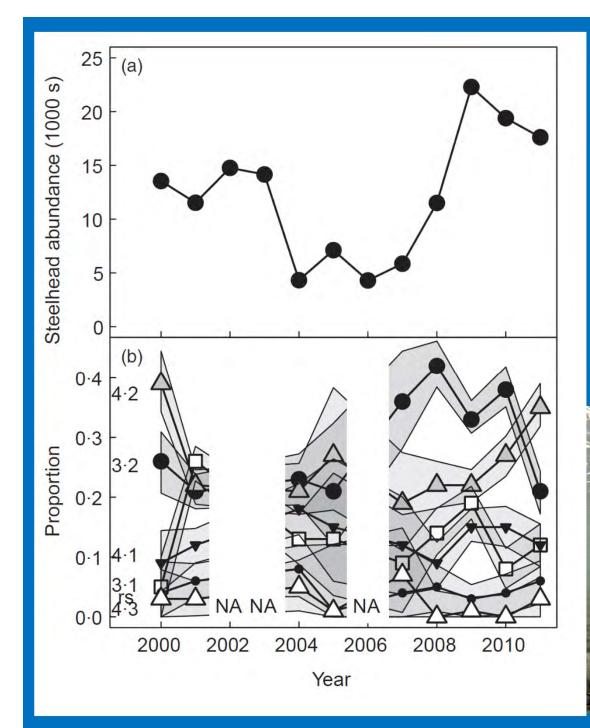


Moore et al. 2014. J. App. Ecol.

Life-history trajectory

25

30

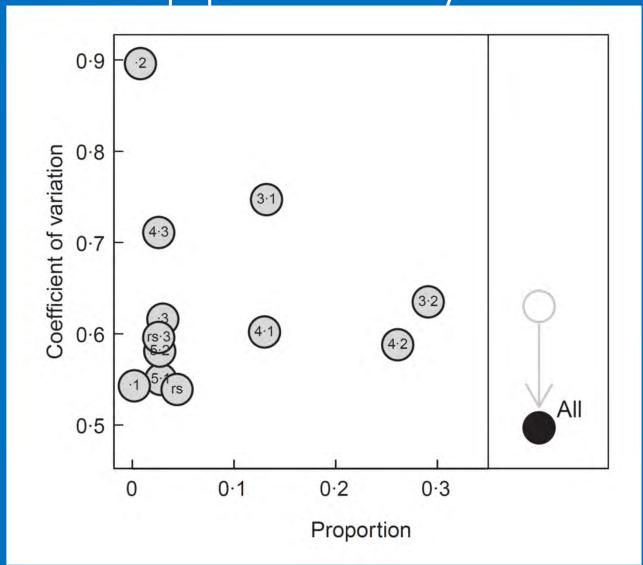


Steelhead populations are comprised of life history classes with asynchronous variation in relative abundance over time

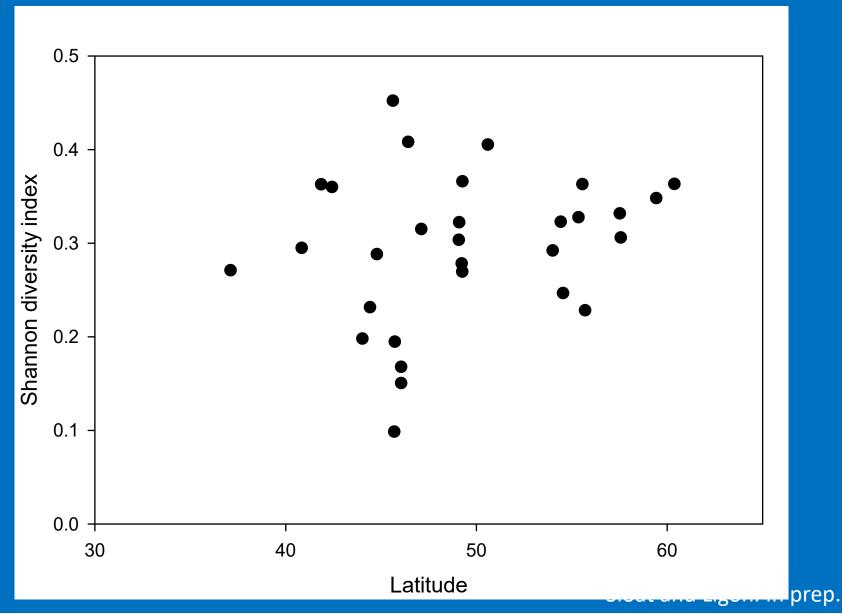
Moore et al. 2014. J. App. Ecol.



Asynchrony in life history components increases population stability



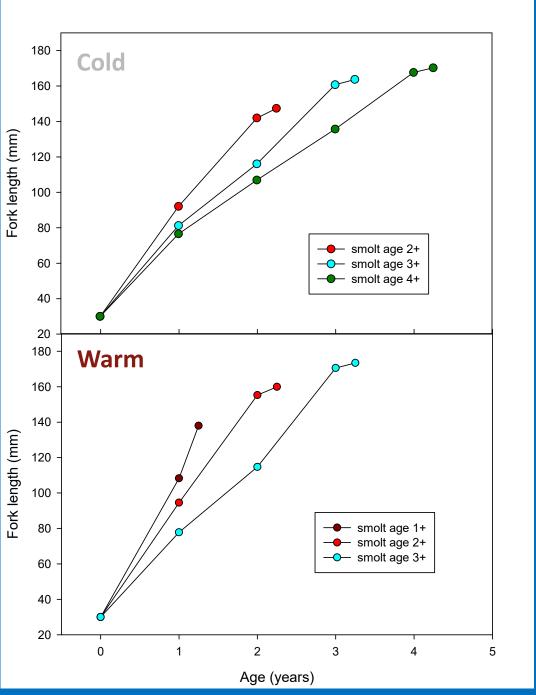
Basin-scale Smolt Age Diversity



Basin-scale habitat heterogeneity and *O. mykiss* life history

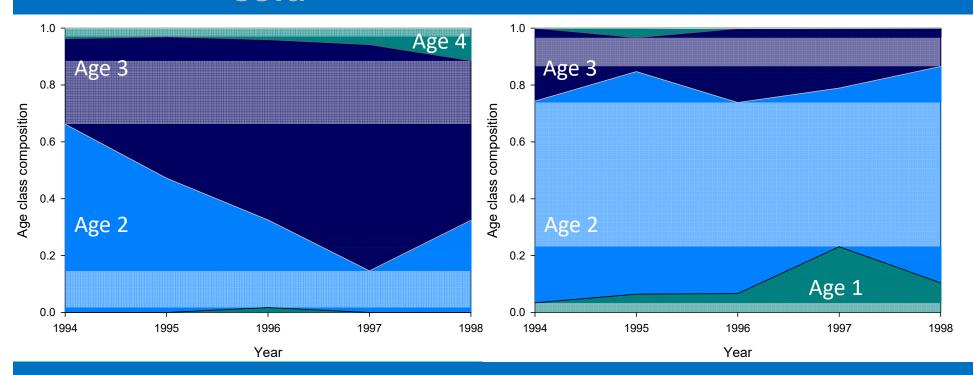


Clackamas basin thermal heterogeneity, fish growth, and smolt age



Clackamas River tributary thermal regimes and smolt age composition

Cold Warm



Mean age: 2.63 yrs

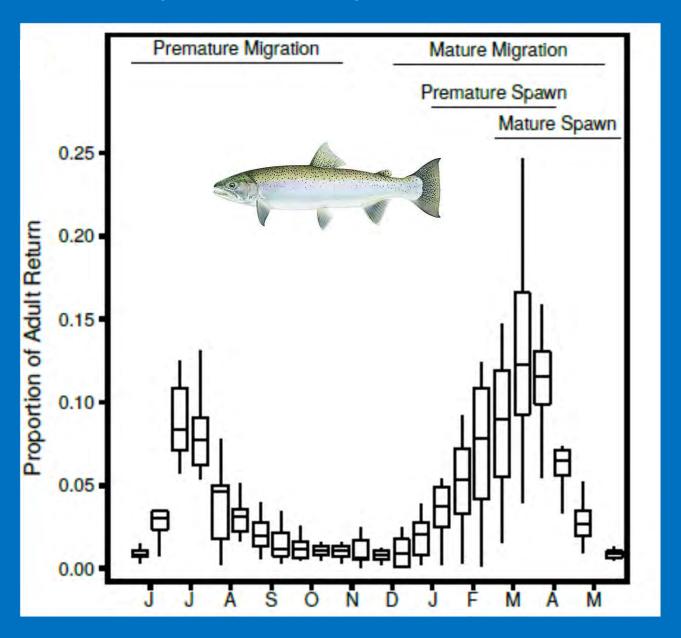
Mean length: 161 mm

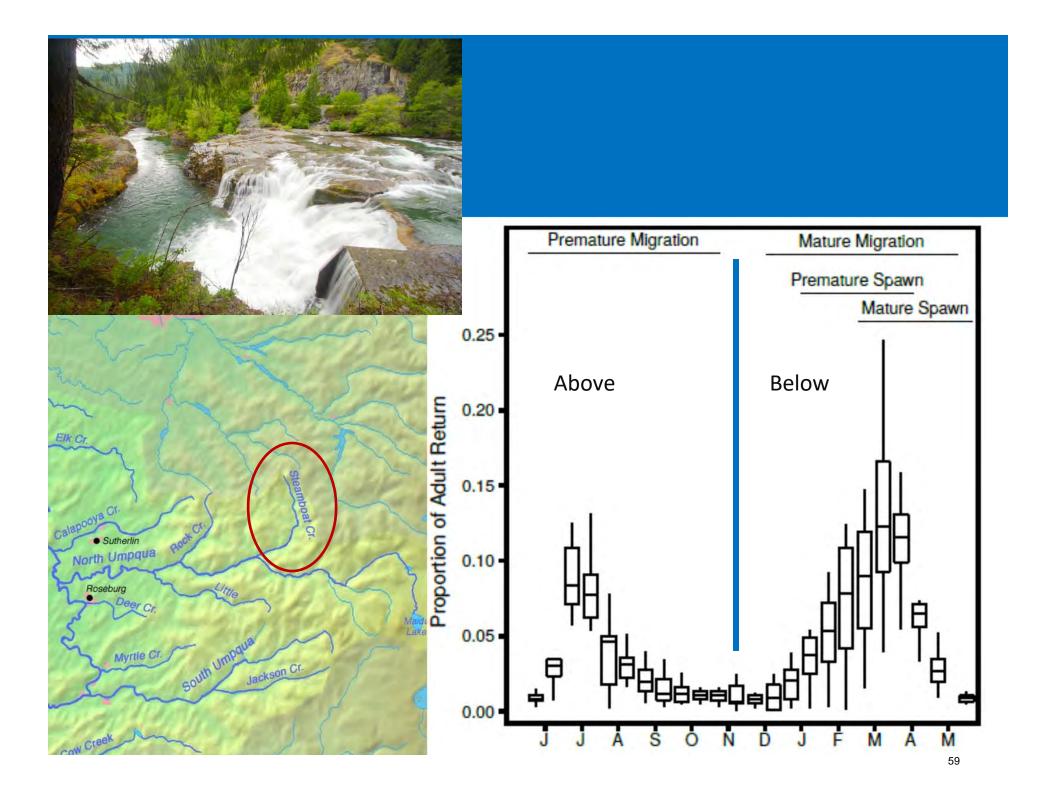
Mean age: 2.11 yrs

Mean length: 163 mm

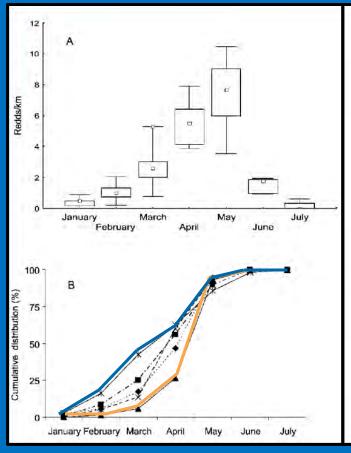
Sloat, Reeves, and Hansen. In prep.

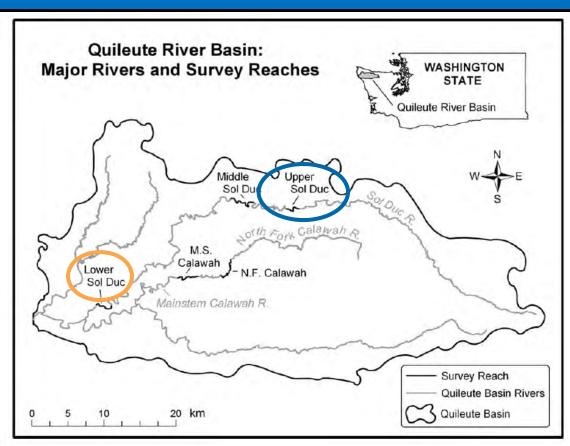
Temporal and Spatial Structure



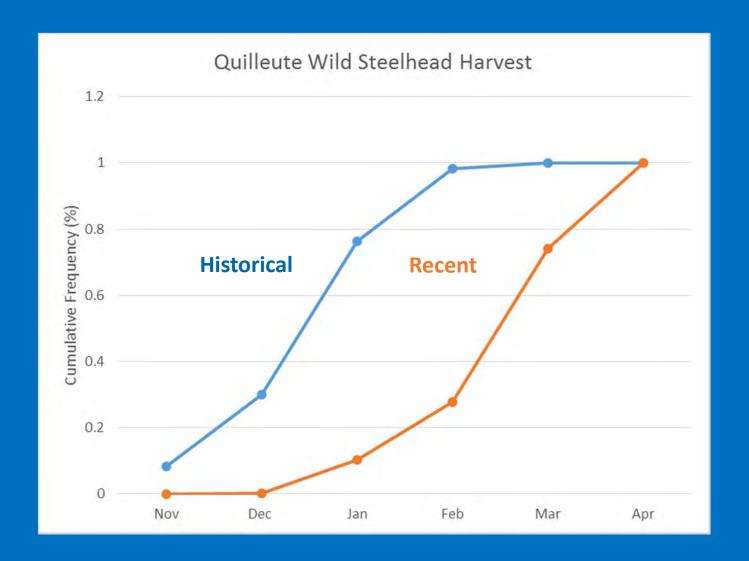


Fine Scale Temporal and Spatial Structure





McMillan et al. 2007 TAFS



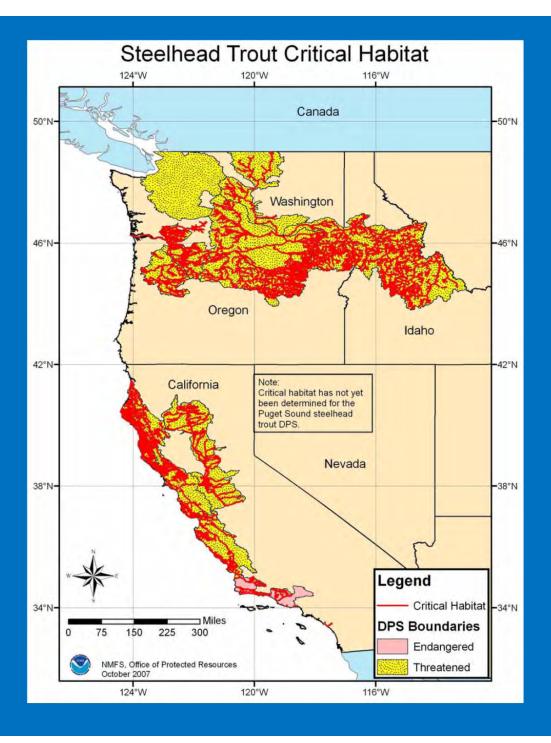
What about the future?

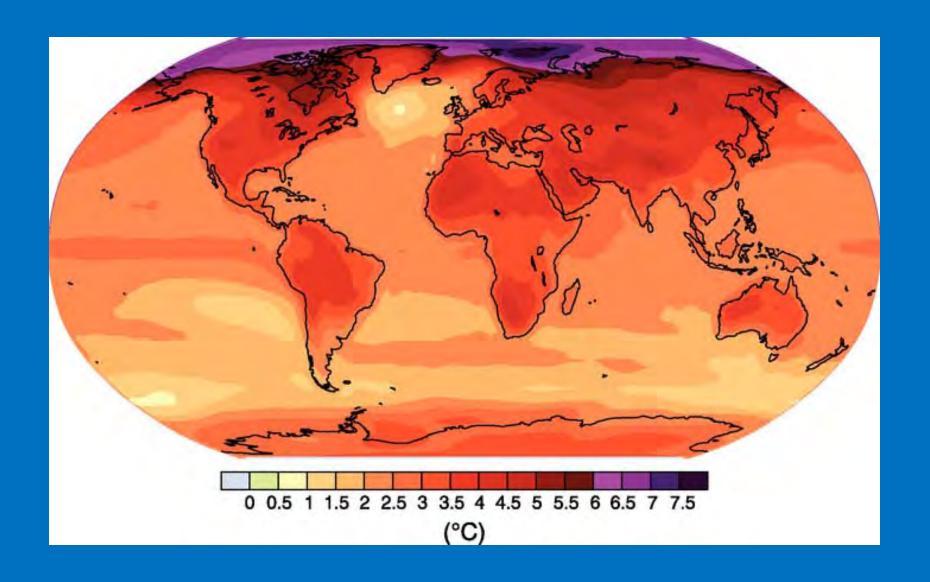


"Худшее Впереди"

Khoodshee vperedy

"the worst is ahead"





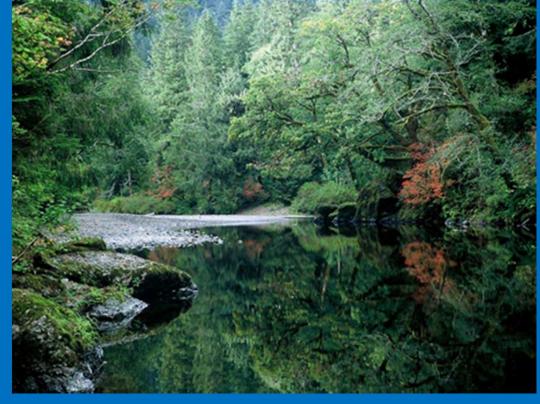
"The last word in ignorance is the man who says of an animal or plant, "What good is it?" If the land mechanism as a whole is good, then every part is good, whether we understand it or not. If the biota, in the course of aeons, has built something we like but do not understand, then **who but a fool would discard seemingly useless parts**? To keep every cog and wheel is the first precaution of intelligent tinkering."

— Aldo Leopold, Round River: From the Journals of Aldo Leopold



Restoring our Future

Protect and restore processes that generate diversity







Restoring our Future

Building resilience:

- Biologically
- Politically
- Socially



