

Identification of adaptive genetic variation and application to management in rainbow trout/steelhead

Part 5: Coming clean...

Matthew A. Campbell^{1,2*}

¹University of California Santa Cruz, ¹NOAA SWFSC, *Present Address: Hokkaido University

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Alternative genomic adaptations to similar selective environments above barriers to migration in rainbow trout, *Oncorhynchus mykiss*

- ▶ Myself
- ▶ Eric C. Anderson
- ▶ Devon E. Pearse
- ▶ MacCampbell/swainysmoother
- ▶ Identifying outlier loci or genomic regions is a thing...

Migration in Fishes, Rivers in Particular



Catlocarpio siamensis
Photo by I.G. Baird



Psephurus gladius
Muséum d'Histoire Naturelle

Why/How do fish migrate?

- ▶ Environmentally determined?
- ▶ Heritable - non-genetic?
- ▶ Heritable - genetic?
- ▶ Species/populations polymorphic



Oncorhynchus masou
I.-S. Kim

Themes of Current Research

- ▶ Is there a genetic basis to migratory traits?
- ▶ How fast do migratory fish populations adapt to residency?



Photo: US Bureau of Reclamation

Rainbow Trout are Often Migratory

- ▶ Migrate to the ocean, "steelhead"
- ▶ Migrate within drainage basins
- ▶ Residents



Naturally interbreed

Migration Exerts Very Different Pressures Compared to Residency



Emigrant "smolt"

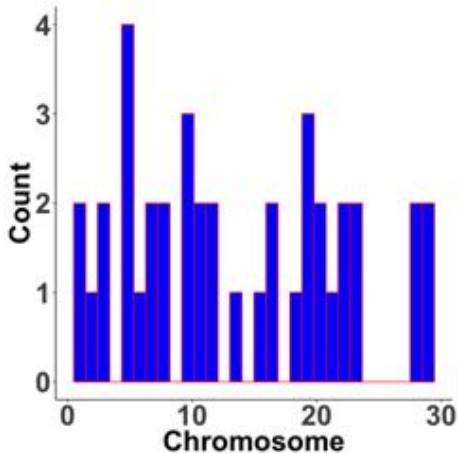


Resident

A Heritable Basis for Migration?

Studies

- ▶ Nichols et al. 2008
- ▶ Martinez et al. 2011
- ▶ Hecht et al. 2012
- ▶ Hecht et al. 2013
- ▶ Hale et al. 2013
- ▶ Pearse et al. 2014
- ▶ Baerwald et al. 2015*



Alternative Selective Forces Maintain Migration-Related and Other Polymorphisms



e.g. ocean versus river

What About When This Happens?



Photo: US Bureau of Reclamation

Or This?



Photo: USDA

What Happens is . . . Adaptation



Anadromous rainbow trout no longer contribute to gene pool

Adaptation

...adaptation is characterized by the movement of a population towards a phenotype that best fits the present environment (Orr 2005)



A common study system

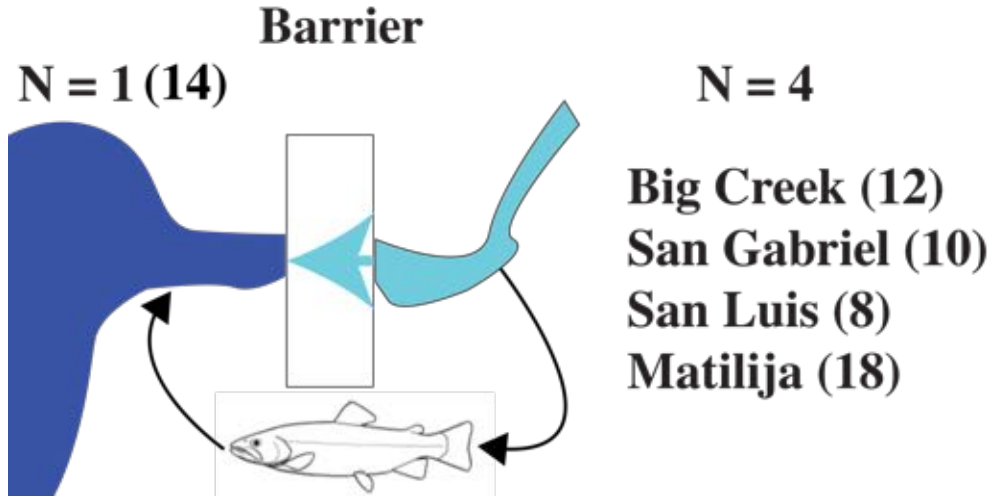
Adaptive Genetic Variation

Big questions about adaptive genetic variation Orr (2005)

1. Does adaptation utilize new or existing variation?
2. Are supergenes players in most adaptations?
3. Does the same phenotypic change occur with the same underlying genetic basis?

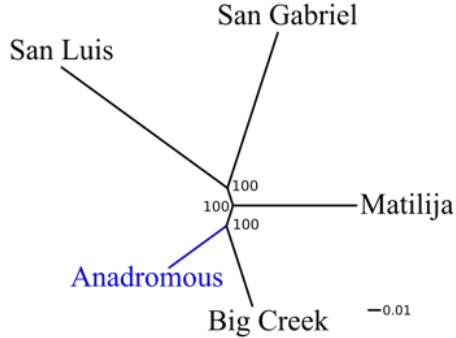
Methodology

Compare anadromous and landlocked *O. mykiss* in a pairwise fashion



Methodology

Compare anadromous and landlocked *O. mykiss* in a pairwise fashion



Population neighbor-joining tree

Methodology

Data type and analysis

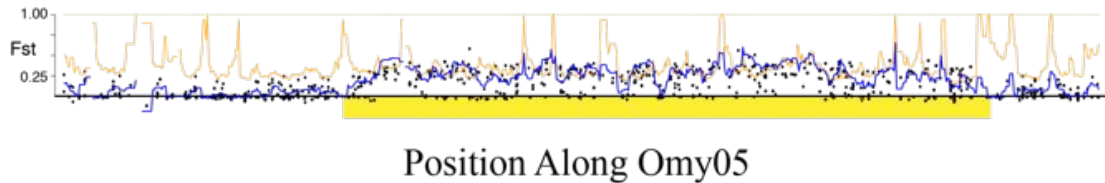
- ▶ "New RAD" Ali et al. (2016)
- ▶ Mapped to *O. mykiss* genome
- ▶ Identified differentiated genomic regions between anadromous and landlocked populations



Ruegg et al. (2014)

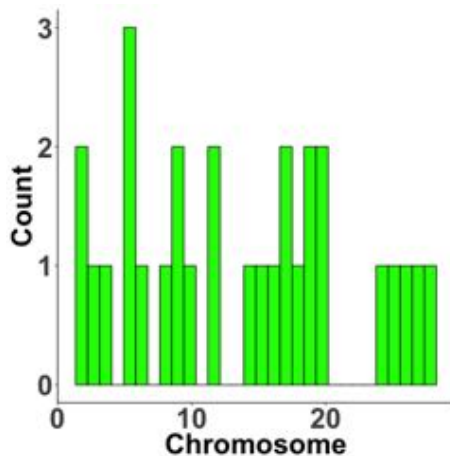
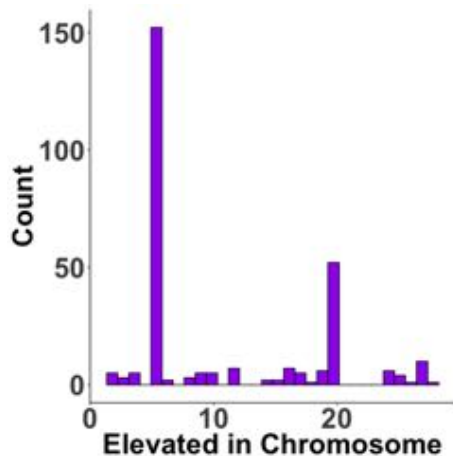
Example Output

Anadromous-Matilija landlocked comparison



Results

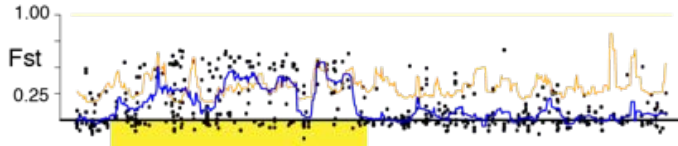
Differentiated genomic regions by chromosome



Results

Altered inversion frequencies in above-barrier pops detected on Omy05 & Omy20

San Gabriel

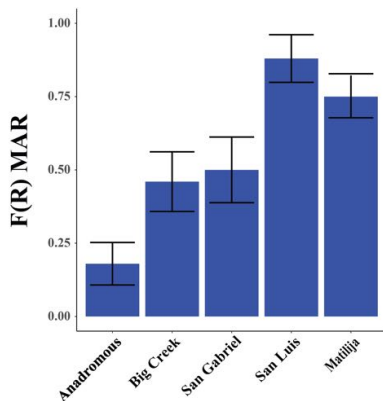


Position Along Omy20

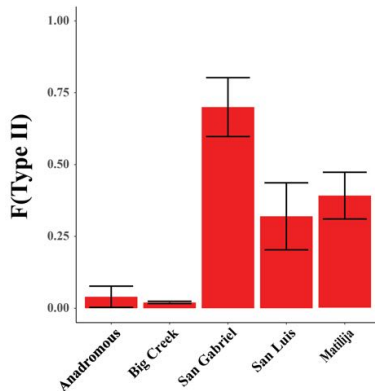
Results

Altered inversion frequencies in above-barrier pops detected on Omy05 & Omy20

Omy05



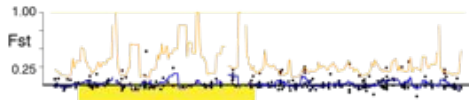
Omy20



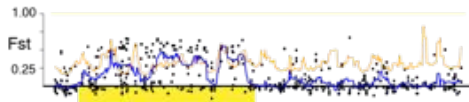
Discussion

Concordance within the study is low, except with inversions

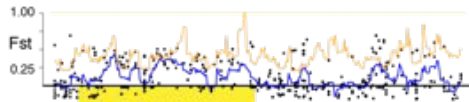
Big Creek



San Gabriel



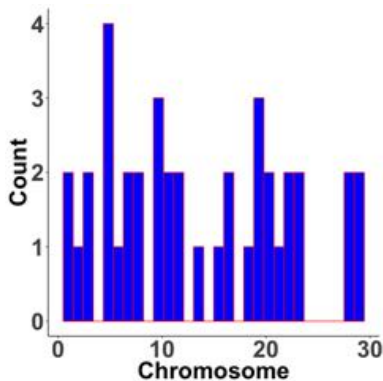
San Luis



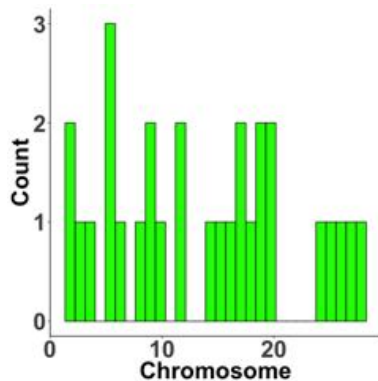
Discussion

Concordance with previous studies at a chromosomal level

Previous Studies



This Study

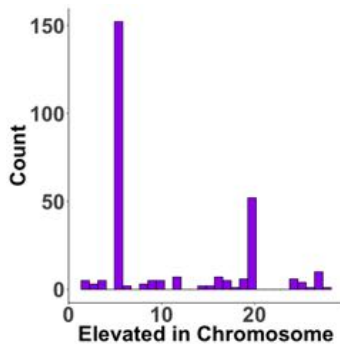


Discussion

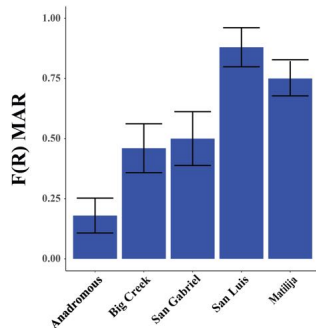
Big questions about adaptive genetic variation

1. Does adaptation utilize new or existing variation?

All Elevated



Frequency of R MAR

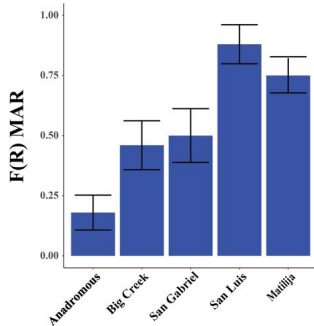


Discussion

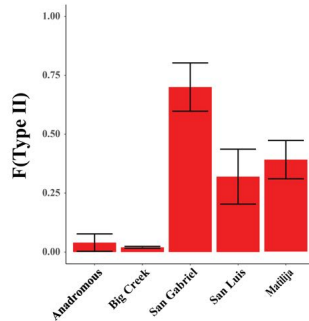
Big questions about adaptive genetic variation

2. Are supergenes players in most adaptations?

Omy05



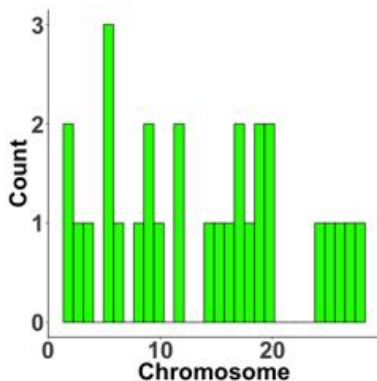
Omy20



Discussion

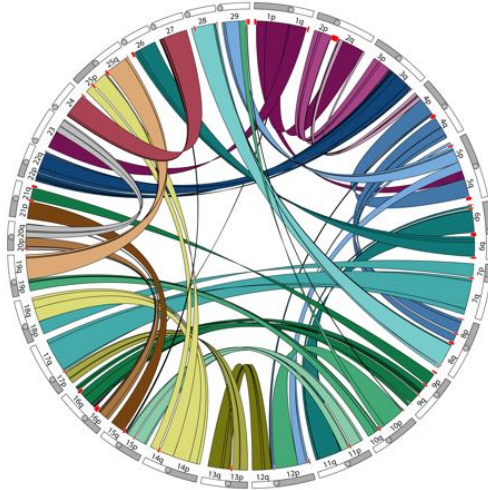
Big questions about adaptive genetic variation

3. Does the same phenotypic change occur with the same underlying genetic basis?



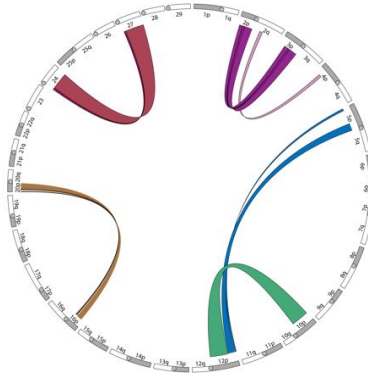
Discussion

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Discussion

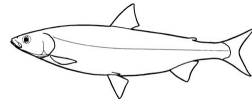
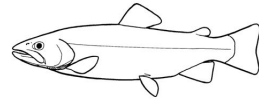
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62% of non-inversion elevated regions

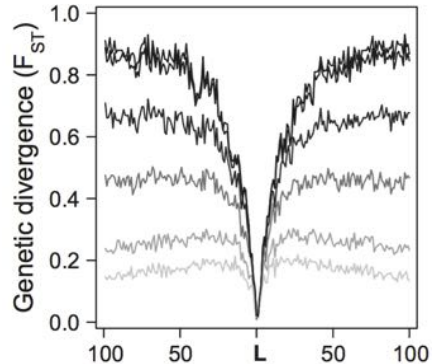
Conclusions

- ▶ Standing genetic variation is important
- ▶ Two chromosomal inversions may be involved
- ▶ Selection often occurs on similar genomic backgrounds
- ▶ Same predictable phenotype, different genetic changes



What about evidence for parallel evolution and function as in MAR?

- ▶ Evidence of parallel adaptation
- ▶ Relating of differentiated regions to known QTL

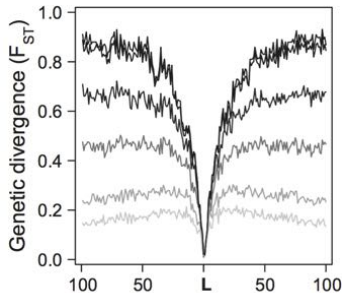


Roesti et al. (2014)

What about evidence for parallel evolution and function as in MAR?

You may have noticed we have some limitations

- ▶ We have few data sets that are suitable
- ▶ RAD data has a lot of holes

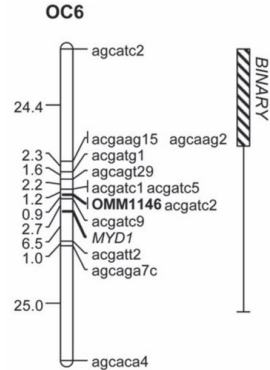


Roesti et al. (2014)
Does seem to work!

What other genomic regions besides Omy05 are involved?

Omy01

- ▶ 46 - 60 Mbp
- ▶ Surrounds a "binary smolt" QTL

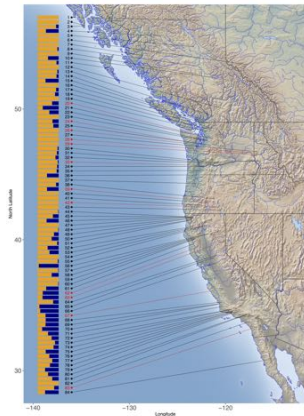


Nichols et al. (2008)

What other genomic regions besides Omy05 are involved?

Numerous uncharacterized, I'm working on it!

- ▶ Main point is, the environmental context is important
- ▶ North versus South of the range
- ▶ Compare an Alaskan population to Big Creek?



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