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

Part 3

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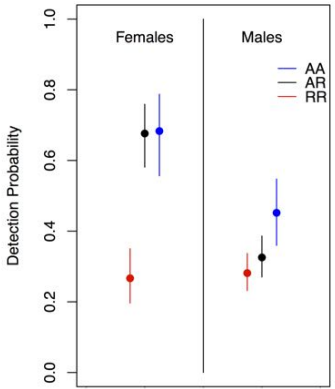
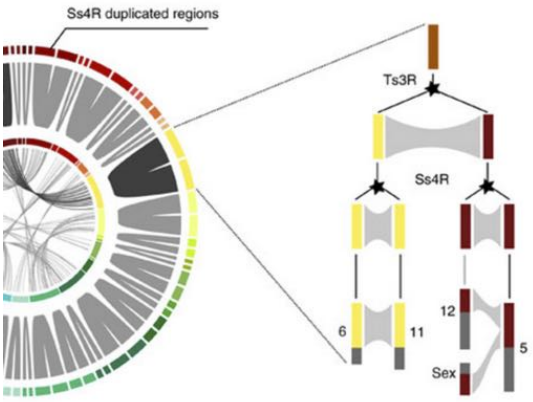
What exactly is the MAR? What are A and R types?



In Prep.

- Migration Associated Region - MAR
- A for Anadromy
- R for Residency

What exactly is the MAR? What are A and R types?



In Prep.

- RT genome is LARGE
- RT genome is DUPLICATED
- RT genome is REPETITIVE (TE)

New Rainbow Trout genome project

Title:
Double inversion mediates selection on sex- and temperature-dependent migration in rainbow trout

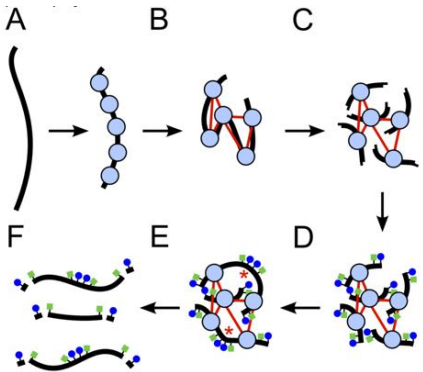
Authors:

Devon E Pearse[1,*], Nicola Barson[2], Torfinn Nome[2], Guangtu Gao[3], Matthew A Campbell[1], Alicia Abadía-Cardoso[1], Eric C Anderson[1], David E. Rundio[1], Thomas H. Williams[1], Kerry A. Naish[4], Thomas Moen[5], Matthew Baranski[6], Sixin Liu[3], Matthew Kent[2], David R. Minkley[7], Marine S. O. Brieuc[4], Simen Rød Sandve[2], Michael R. Miller[8], Kobi Baruch[9], Alvaro G. Hernandez[10], Gil Ben-Zvi[9], Doron Shem-Tov[9], Omer Barad[9], John Carlos Garza[1], Ben Koop[7], Steven T. Lindley[1], Gary H. Thorgaard[11], Yniv Palti[3,*], Sigbjørn Lien[2,*]

- Improve Berthelot et al. (2014)
- Huge project (USDA, CIGENE, Universities)
- I'm somewhere on there!

New Rainbow Trout genome project

Utilized Dovetail technologies



Putnam et al.

- English note: Dovetail
- in-vitro Hi-C???

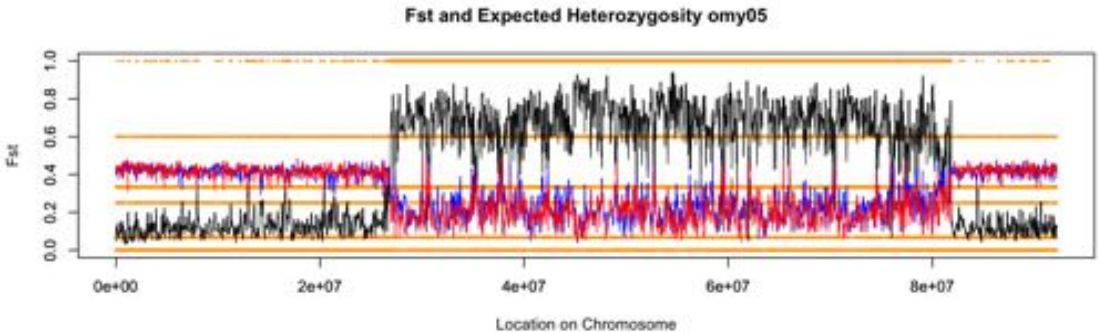
New Rainbow Trout genome project

Assembly specifics

- 29 chromosomes
- 1.92 Gb (88.5% of total assembly)
- Unanchored are repetitive (56% genome is repetitive)
- 50,268 genes

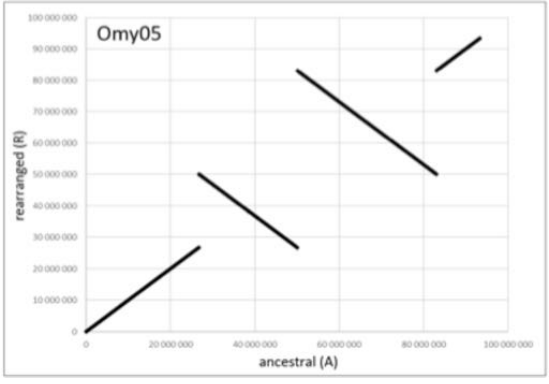
New Rainbow Trout genome project

What is different between A and R types?



New Rainbow Trout genome project

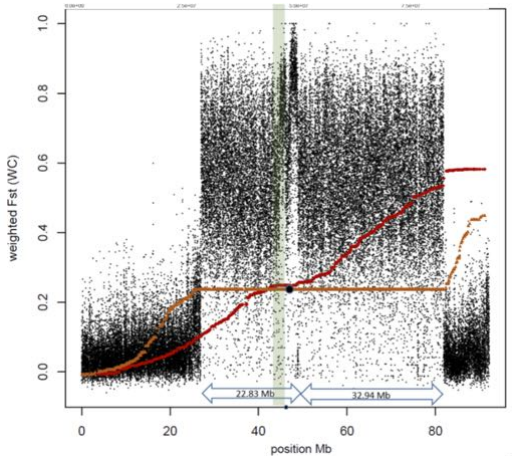
What is different between A and R types?



- Syntenic plot

New Rainbow Trout genome project

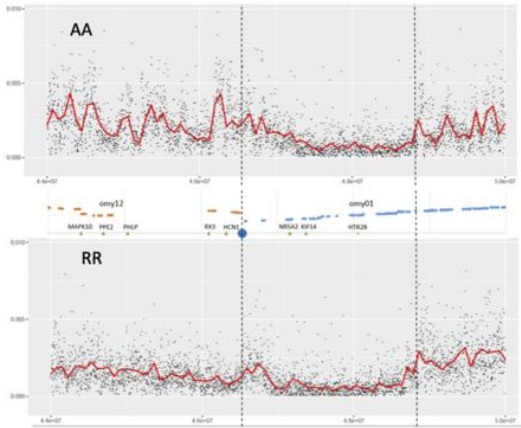
What is different between A and R types?



- Structure is revealed as a doubled inversion
- Non-recombining in heterozygotes, isolating A and R types
- A is ancestral
- R is inverted

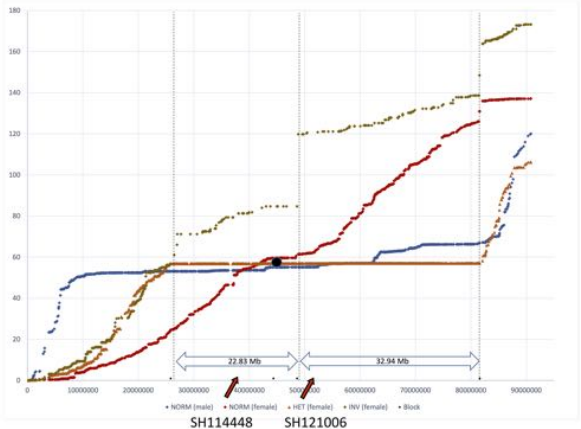
New Rainbow Trout genome project

Area of functional relevance, genes



Placing Known SNPS

SNPs from Pearse et al. (2014) can be placed on genome!!



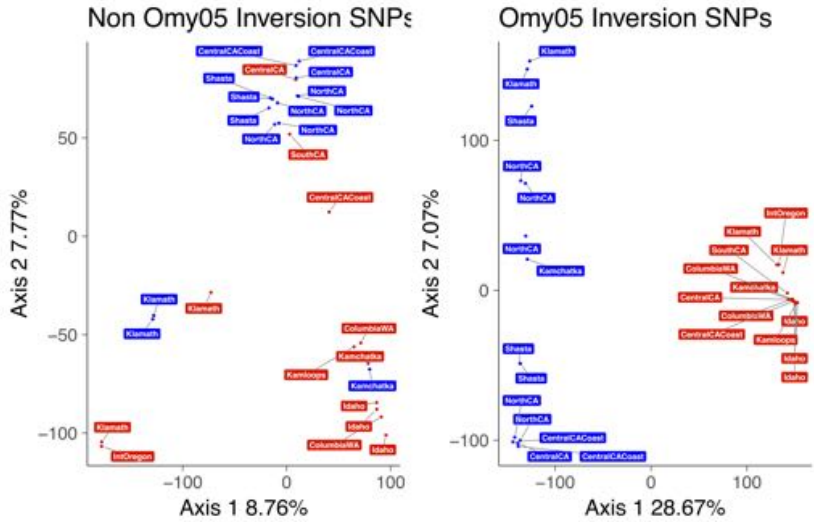
Enough Evidence For You?

- Phenotype - resident or anadromous
- Phenotype - tagging and indirectly evaluated
- Genotype - A or R inversion
- Genomic structure determined
- Candidate genes identified

Enough Evidence For You?

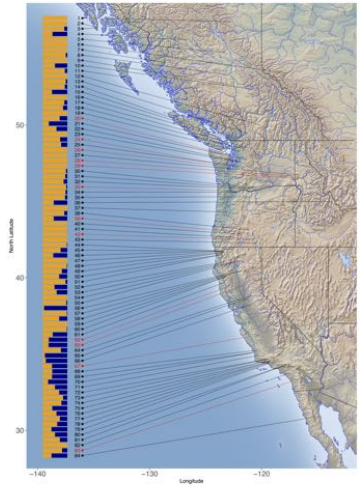
- We have evaluated mostly California fish up to now...
- 10x WGS of 60 fish
- 27 "natural"

Whole-Genome Sequence Data - 32 M SNPS!

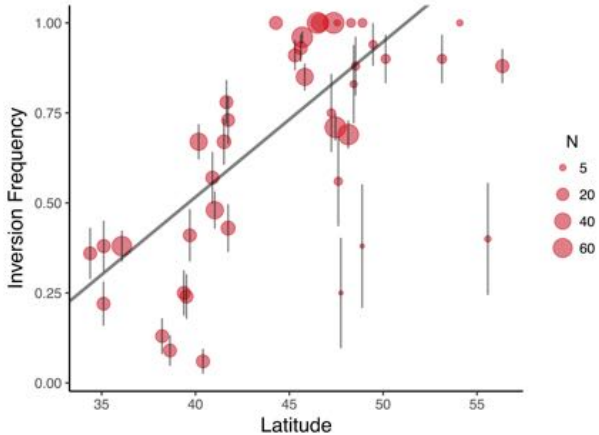


Wide survey of SNP data

Ocean accesible populations shown here

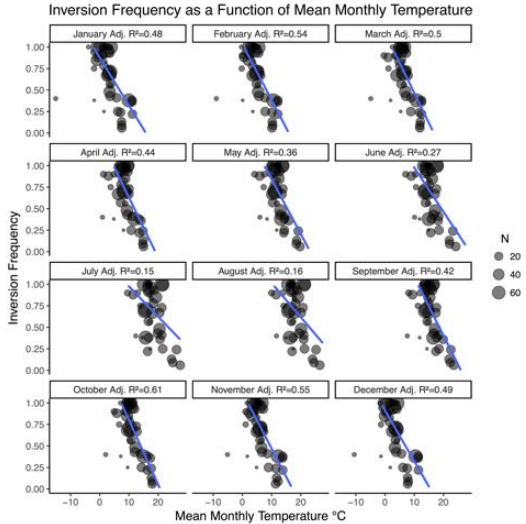


A cline with latitude



Inversion Frequency = 0.04 *x* (*Latitude*) – 1.21, adjusted R^2 of 0.51

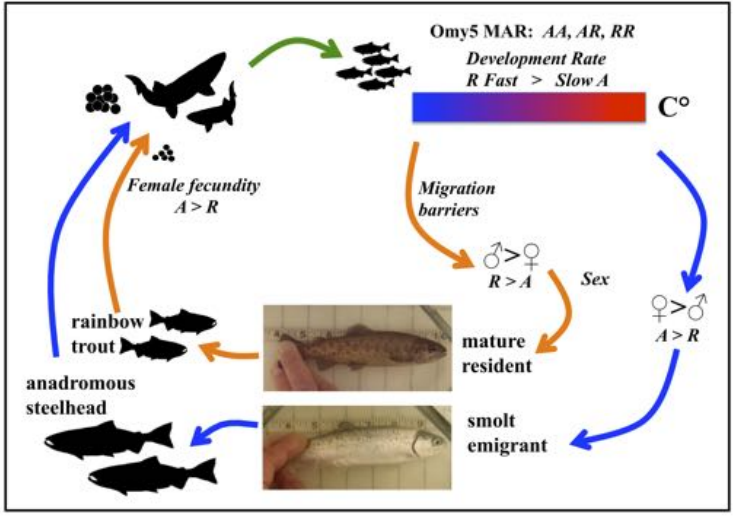
Latitude = Geography + Temperature



Influences on Inversion Frequency

- In Southern part of range, "R" carrying individuals are preferentially residential
- In Northern part of range, the frequency of "R" can be very in anadromous populations
- Inversion frequency relates to both migration and temperature - developmental rate, and exhibits gender differences

It's Complicated!!!



Enough Evidence For You!

Let's examine the Pearse and Campbell (2017) manuscript

November 9, 2017

Final Report

on

Genetic analysis of *Oncorhynchus mykiss* in the Upper Tuolumne and Merced Rivers to evaluate ancestry and adaptive genetic variation

Submitted to:

National Marine Fisheries Service
West Coast Region California Central Valley Office
Federal Energy Regulatory Commission Branch