

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

Part 4

Matthew A. Campbell^{1,2*}

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

November 19, 2017

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

Motivation

- ▶ The Western US used to have many salmon
- ▶ Human development has reduced productivity
- ▶ Now, effort to re-establish migratory fish
- ▶ Study commissioned by National Marine Fisheries Service

Motivation

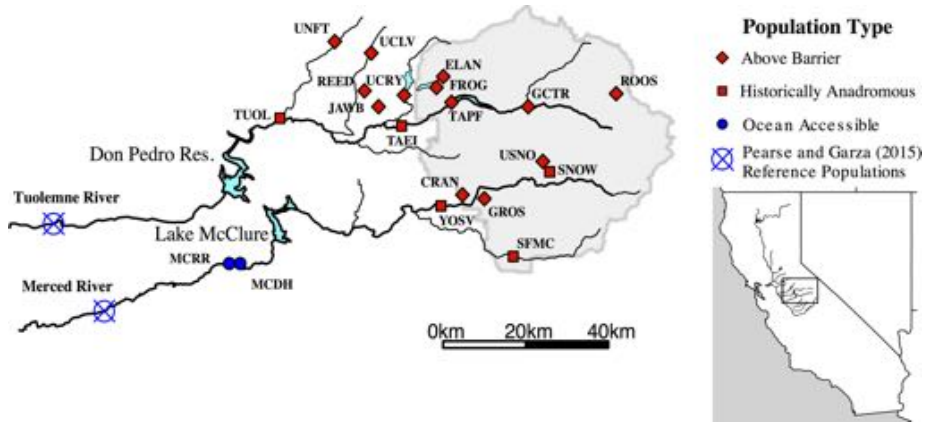


Hetch Hetchy 1914



Hetch Hetchy Now

Pearse and Campbell (2017)



Focus Upper Tuolumne and Upper Merced Rivers in YNP

Objectives

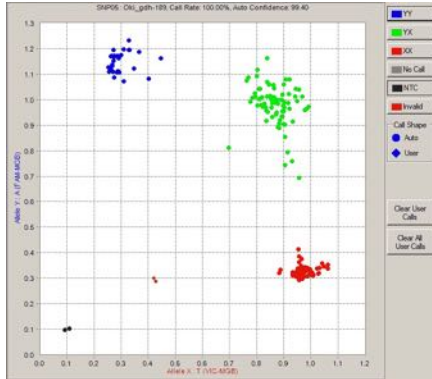
- ▶ Due to extensive stocking, what is the ancestry of RT?
- ▶ How have dams affected genetic make up?
- ▶ What is the predilection of fish in the study area to exhibit migratory behavior?
- ▶ Can above-barrier fish be used in the future to re-establish anadromous populations?

Sampling Methods



- ▶ Low conductivity of streams...
- ▶ Collected various tissues by fishing

Genotyping Methods



- ▶ SNP Genotyping (Are you familiar, do you use?)
- ▶ Allowed integration with numerous other data sets
- ▶ Included 3 SNPs inside Omy5 inversion

Analysis Methods

Individual approach

- ▶ Do not use prior population assignment
- ▶ Test for hatchery influence
- ▶ Detect if geography is meaningful
- ▶ Who is previously familiar with DAPC?
- ▶ Who is previously familiar with STRUCTURE?

Analysis Methods

Population approach

- ▶ Use prior population assignment
- ▶ Evaluate population level relationships
- ▶ Who is previously familiar with Neighbor-Joining as shown in MS?

Results

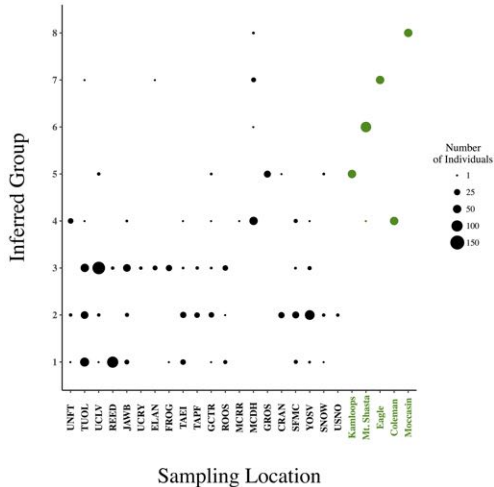
Data composition

- ▶ 20 sampling locations
- ▶ 29 reference populations
- ▶ 2,370 individuals
- ▶ 88 bi-allelic SNPs



Results

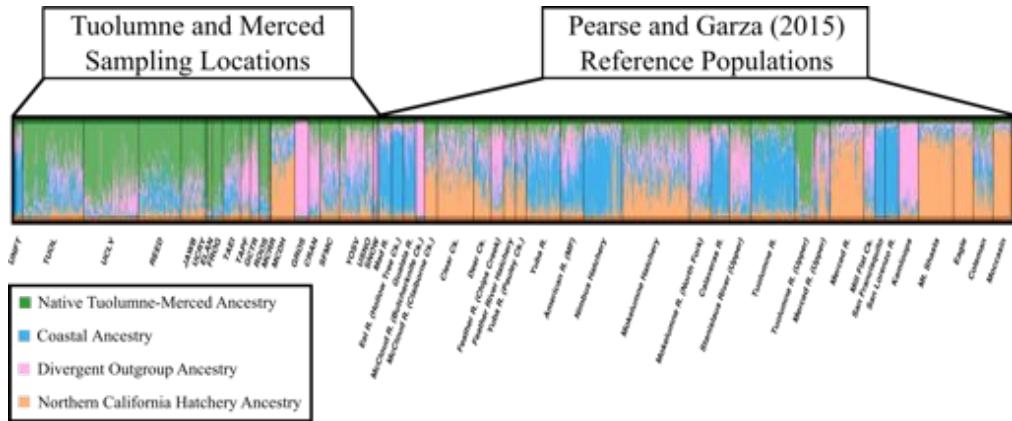
Individual Assignment



- ▶ DAPC assignment plot
- ▶ 20 sampling locations
- ▶ 5 hatchery reference pops

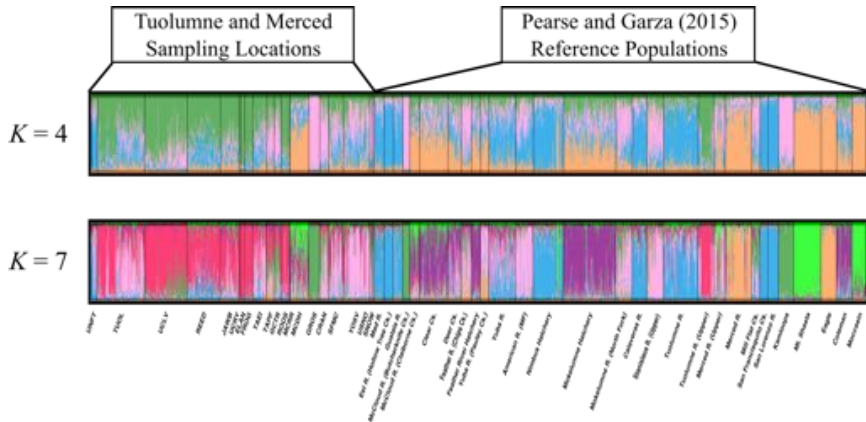
Results

Individual Assignment, STRUCTURE K=4



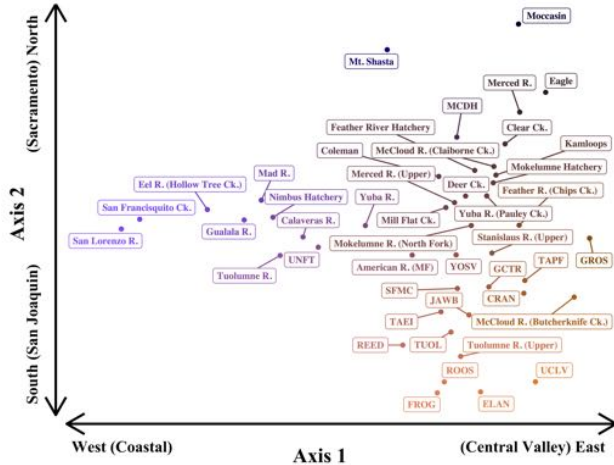
Results

Individual Assignment, STRUCTURE K=4, K=7



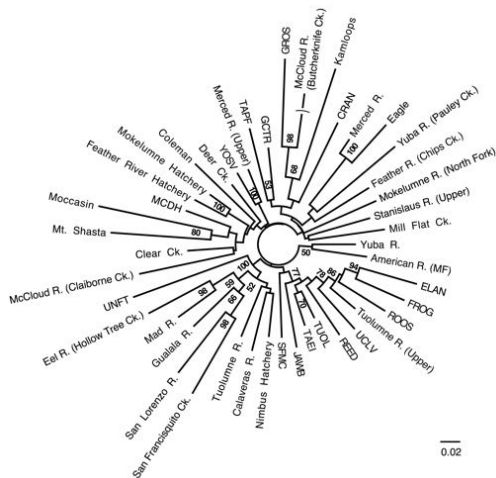
Results

Population Relationships



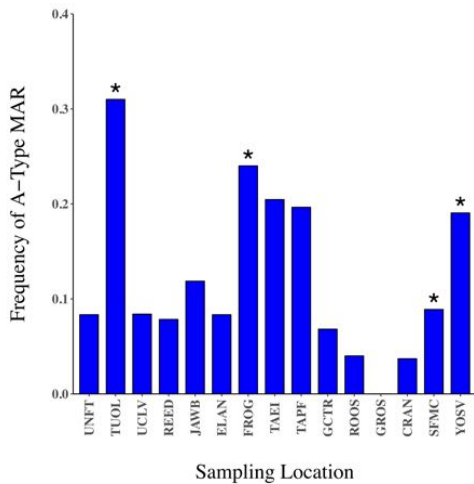
Results

Population Relationships

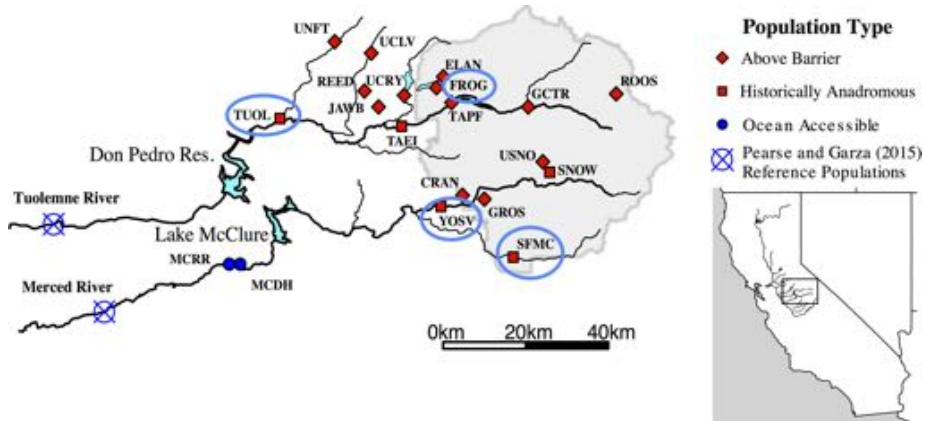


Results

Frequency of A-type MAR



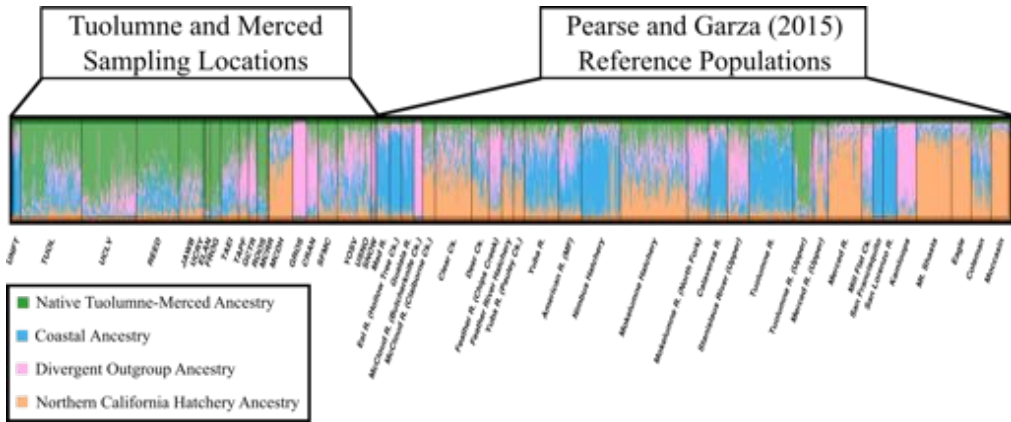
Pearse and Campbell (2017)



Elevated type-A found in historically anadromous pops with access to lakes

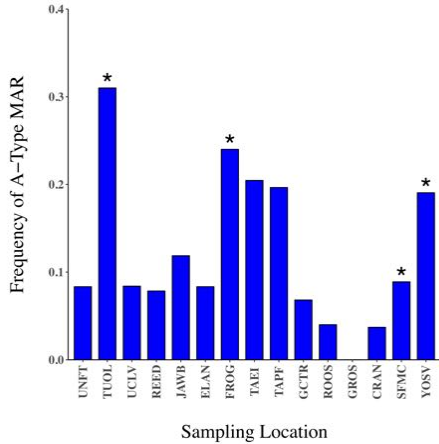
Discussion Points

Ancestry is largely native



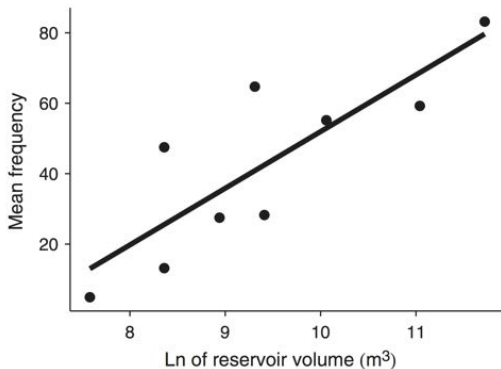
Discussion

Frequency of A-type MAR in potentially adfluvial pops



Discussion

Frequency of A-type MAR in potentially adfluvial pops



Leitwein et al. (2016)

- Previously in California, relationship between the MAR and reservoir volume demonstrated

Conclusion

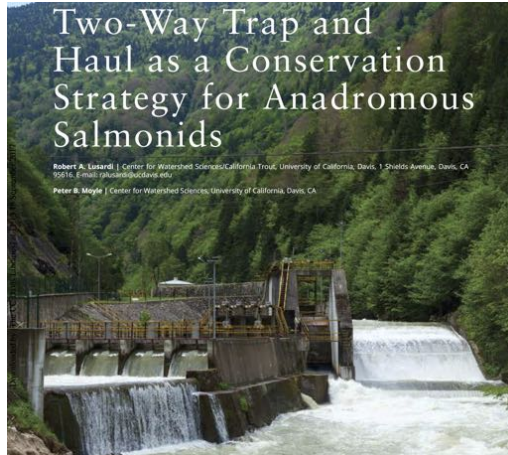
Ancestry is largely native



Large enough reservoirs support adfluvial fish and retain A-type MAR

Conclusion

Native ancestry could be used to re-establish anadromy



Questions?