

Genetic structure and adaptation of Columbia River Basin steelhead and rainbow trout

Scott M. Blankenship

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Authors

Scott M. Blankenship (WDFW), Matt R. Campbell (IDFG), Jon E. Hess (CRITFC), Maureen A. Hess (CRITFC), Todd W. Kassler (WDFW), Christine C. Kozfkay (IDFG), Andrew P. Matala (CRITFC), Shawn R. Narum (CRITFC), Melanie M. Paquin (NOAA – Montlake), Maureen P. Small (WDFW), Jeff J. Stephenson (CRITFC), Kenneth I. Warheit (WDFW), Paul Moran (NOAA – Montlake)

A special section of TAFS "Genetic adaptation of natural salmonid populations"

<u>Manuscript Title</u>: Major lineages and metapopulations in Columbia River *Oncorhynchus mykiss* are structured by dynamic landscape features and environments

Overview

- Oncorhynchus taxonomy and background
- Primary objectives
 - Examine existing genetic diversity in the context of adaptation and historical contingency
 - Compared observed population structure with that expected under neutrality, and explored correlations between population structure and environmental variables
- Genetic data were SPAN standardized microsatellite suite (13 loci)
- Used F_{ST} outlier tests and regression analysis of genetic differences on landscape features to investigate adaptation

Rainbow Trout

- Genus Oncorhynchus contains a diverse assemblage of species
- The three major evolutionary lineages within Oncorhynchus:

Pacific salmon
 cutthroat trout (O. clarkii)
 rainbow trout (O. mykiss)

- Rainbow trout phylogeny ambiguous, but recognized subspecies
 - Sacramento redband (e.g., *O. m. stonei*)
 - Klamath Lake
 - ➤Columbia redband
 - ➤Coastal rainbow

(O. m. newberrii)

(O. m. gairdneri)

(O. m. irideus)

Rainbow Trout

- Migration differences
 - Anadromous, non-anadromous
 Differences in freshwater residency duration
- Migration timing differences

Summer run return April – March (July peak)
 Winter run return October – July (April peak)

Regulatory Perspective

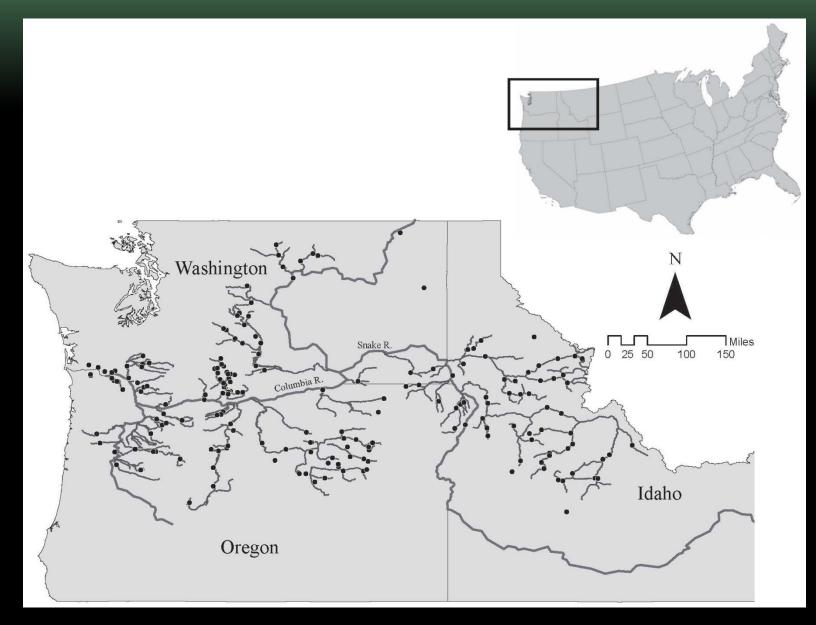
NOAA has jurisdiction of anadromous form
 USFWS has jurisdiction over non-migratory form
 Five ESU from system listed as "threatened" under ESA

Columbia and Snake River Rainbow Trout

- Columbia Basin a dynamic landscape (glacial, volcanic, tectonic)
- As recently as 14,000 yrs. ago glaciers occupied northern Washington and Idaho.
- Some phenotypic and genotypic diversity may have developed through chance extinction-recolonization and periods of localized isolation.
- Interactions between ancestral diversity and dynamic environmental processes likely have contributed to diversifications and provided a mechanism for adaptation

Genetic structure and adaptation

Location of Collections



Collections – General Descriptions

- N =15,658 individuals
- 18 hatchery-origin
- 200 wild-origin

Run type

- 1 early winter
- 1 late winter
- 32 winter
- 142 summer
- 3 non-migratory redband
- 47 unknown run

Collections – General Descriptions

Geographic Groupings	run types
Columbia_R_Lower	winter, summer
Columbia_R_Middle	unknown, summer
Columbia_R_Upper	unknown, summer
Deschutes_R	unknown, summer
Santiam_R	unk, winter, summer
South_Santiam_R_	winter
Snake_Clearwater_R	summer
Snake_Grande_Ronde_R	summer
Snake_Imnaha_R	summer
Snake_Salmon_R	summer
Snake_R	summer
Spokane_R	
Willamette_R	unk, winter, summer

Genetics Metrics - Within Population

223 of 226 collections in Hardy-Weinberg equilibrium.

Elochoman River (winter) Big White Salmon River Okanogan River (summer)

96 of 226 collection had statistically significant linkage disequilibrium

M-ratio test (Mcrit = 0.72)

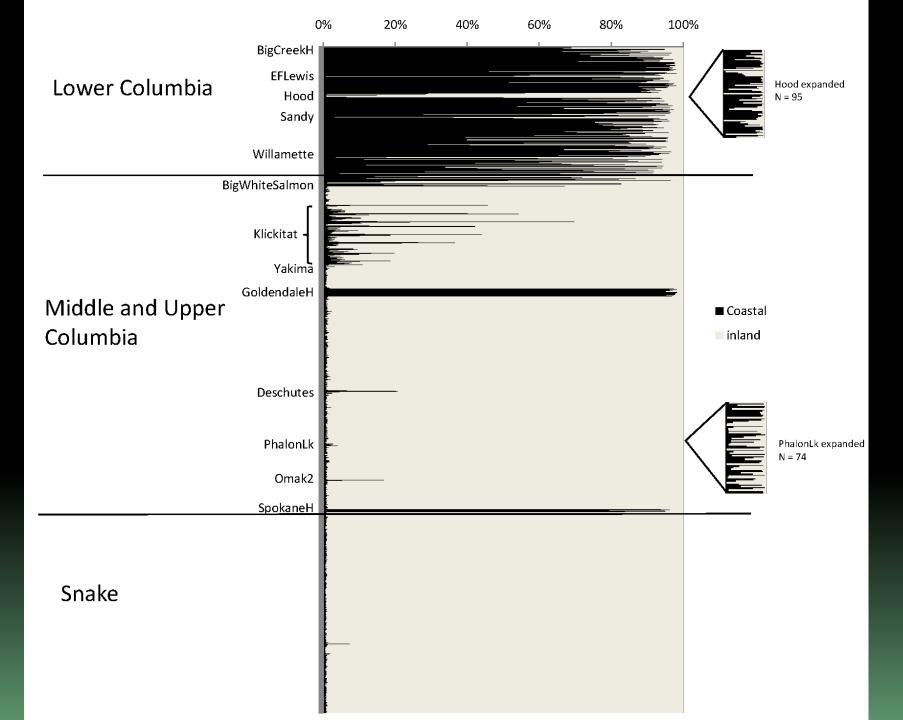
Wild	0.73	Winter	0.70	Columbia_R_Middle	0.69
Hatchery	0.67	Summer	0.74	Spokane_R	0.54
		LateWinter	0.61	Willamette_R	0.66
		EarlyWinter	0.68	Willamette_R_Summer	0.66
		Unknown	0.69		

Genetics Metrics - Among Population

Allele frequency distributions (i.e., genic tests) all statistically different

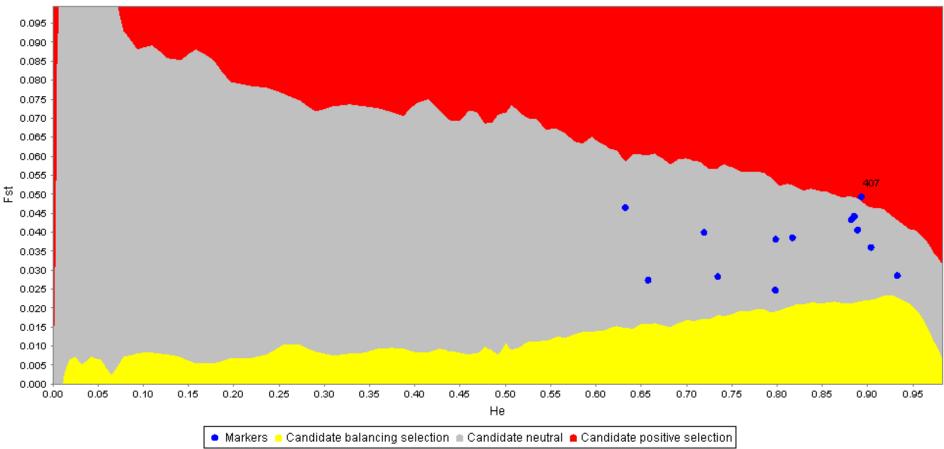
STRUCTURE

- Inclusion of demographically distinct populations can greatly influence F_{ST} outlier tests
- Lineage was one predictor variable in the multivariate multiple regression against pairwise F_{ST} distance measures



F_{ST} Outlier Tests

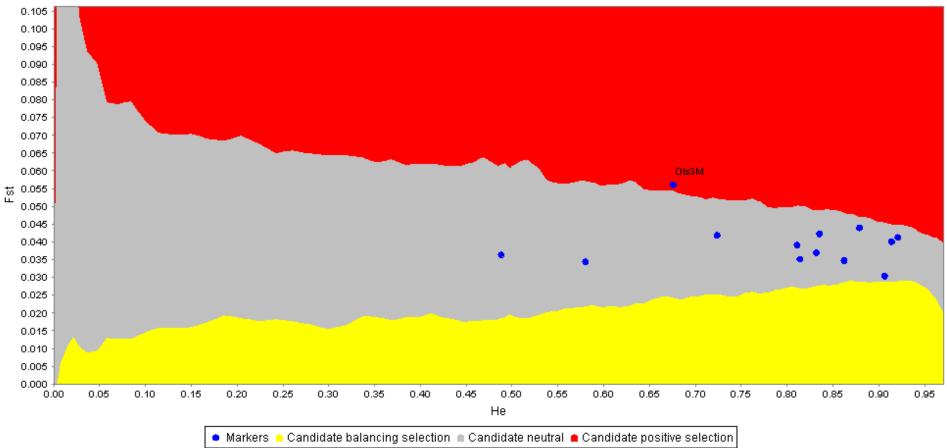




Coastal lineage

F_{ST} Outlier Tests





Inland lineage

Landscape Genetics

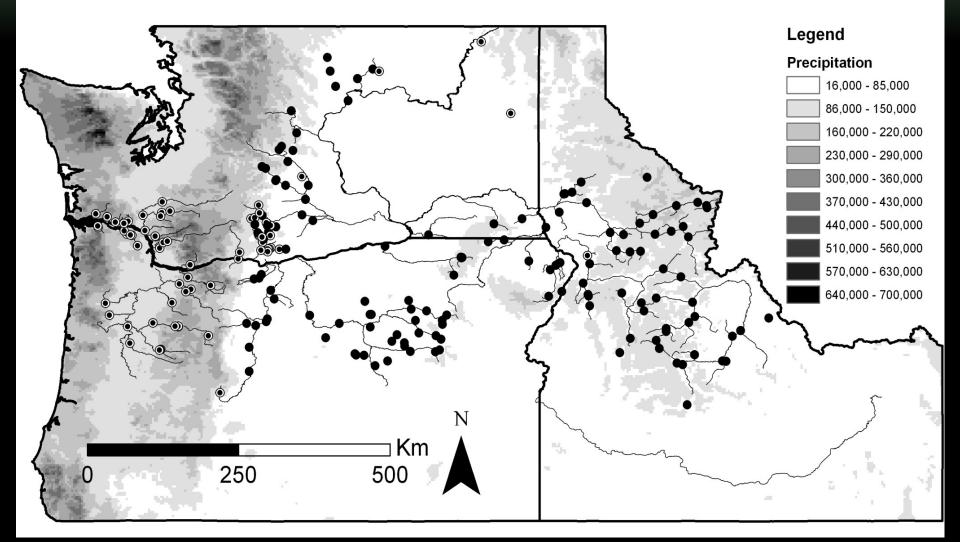
<u>Question</u>: Can some aspect of observed genetic variation be explained by landscape features?

- Generate pairwise F_{ST} matrix and use a metric for genetic differences (i.e., genetic distance)
- Perform regression analysis
 - Marginal (single variable)
 - Conditional (multivariate multiple regression)
- Variables:
 - distance (latitude and longitude)
 - elevation (m)
 - precipitation (total annual accumulation, cm)

Temperature (annual daily means of minimum and maximum °C)

lineage (individual Q values)

Landscape Genetics



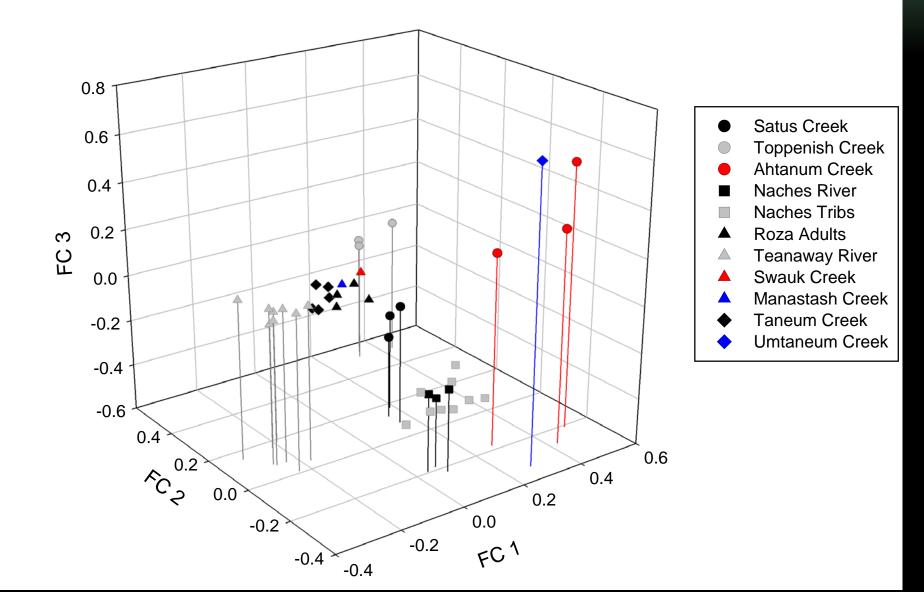
Landscape Genetics

				Cumulative
Variable	F	Р	Proportion	Proportion
Marginal Tests				
Elevation	33.44	0.0001	0.1299	n/a
Precipitation	42.25	0.0001	0.1587	n/a
Temperature	23.81	0.0001	0.1760	n/a
Distance	31.66	0.0001	0.2211	n/a
Lineage	75.61	0.0001	0.2524	n/a

Conclusions

- Ancestral inland (Columbia redband) and coastal lineages are the major genetic variation partition
- Genetic differences observed between all collections within regions
- Two loci were possibly under positive selection, Ssa407 (coastal) and Ots3M (inland)
- Genetic structure primarily influenced by lineage, but also contemporary gene flow related to distance.
- Of variables tested, precipitation appeared to have greatest potential to act as a proxy for habitat characteristics important in local adaptation

Yakima Basin Reference Collections



Unknown-origin adults from Prosser - 2007

Population	Proportion		Aggregates	
Satus	0.07	(0.01, 0.12)	lower	0.38
Toppenish	0.20	(0.12, 0.26)	Naches	0.28
Ahtanum	0.11	(0.03, 0.16)		0.34
Naches	0.28	(0.19, 0.34)	Upper Yakima	0.54
Upper Yakima	0.26	(0.16 <i>,</i> 0.35)		
Teanaway	0.09	(0.04, 0.20)		
Swauk	0.00	(0.00, 0.01)		
Manastash	0.00	(0.00, 0.00)	N=165	
Taneum	0.00	(0.00, 0.03)	11-100	
Umtanum	0.00	(0.00, 0.02)		
Skamania	0.00	(0.00, 0.00)		

Unknown-origin adults from Prosser - 2008

Population	Proportion		Aggregates	
Satus	0.10	(0.03, 0.14)	lower	0.46
Toppenish	0.29	(0.21, 0.34)	Naches	0.29
Ahtanum	0.07	(0.03, 0.13)		
Naches	0.29	(0.21, 0.37)	Upper Yakima	0.24
Upper Yakima	0.17	(0.09, 0.23)		
Teanaway	0.06	(0.03, 0.18)		
Swauk	0.00	(0.00, 0.02)		
Manastash	0.00	(0.00, 0.00)	N=228	
Taneum	0.01	(0.00, 0.03)		
Umtanum	0.00	(0.00, 0.01)		
Skamania	0.00	(0.00, 0.00)		

Questions?

