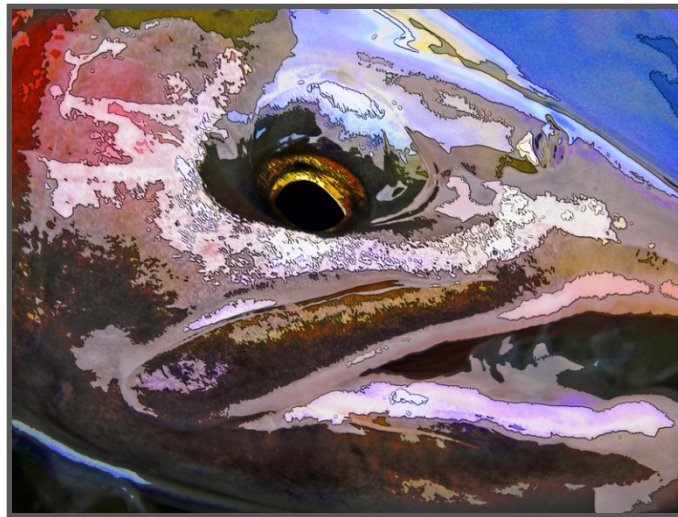


The Genetic Basis for the Propensity to Migrate in a Sequestered Population of Rainbow and Steelhead Trout



Ben Hecht

Columbia River Inter-Tribal Fish Commission

March 19, 2013

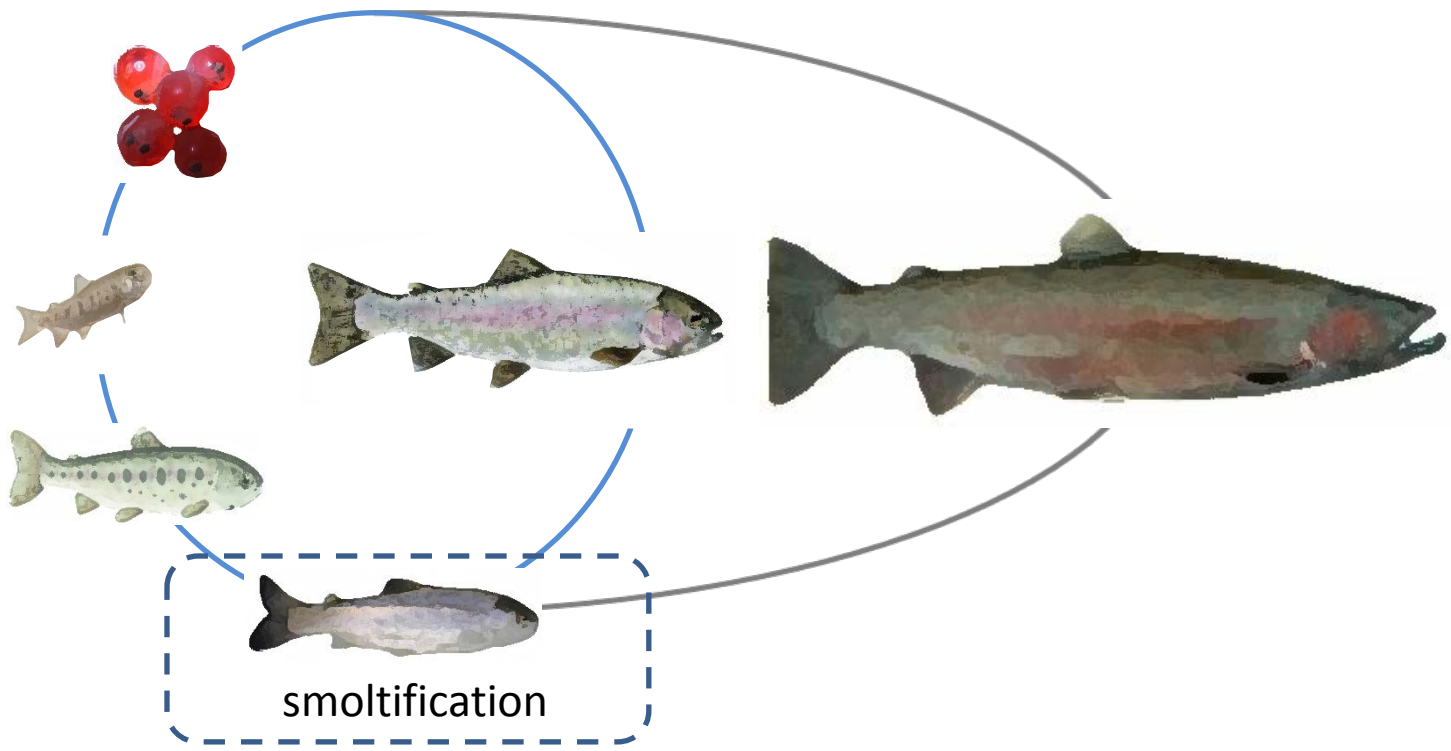
Migration

- Cultural, ecological, and economic benefits and services
- Migratory species declining globally
- Migratory species purported to have common syndrome (Dingle 2006)



Anadromy

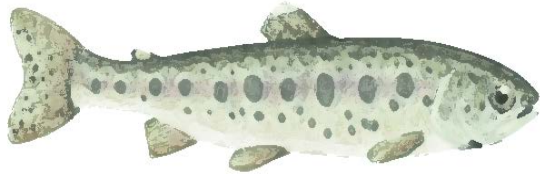
Oncorhynchus mykiss



— Freshwater

— Saltwater

Smoltification



Parr

Environmental cues

Physiology

Morphology

Behavior

Smolt



Genetic component

Objectives

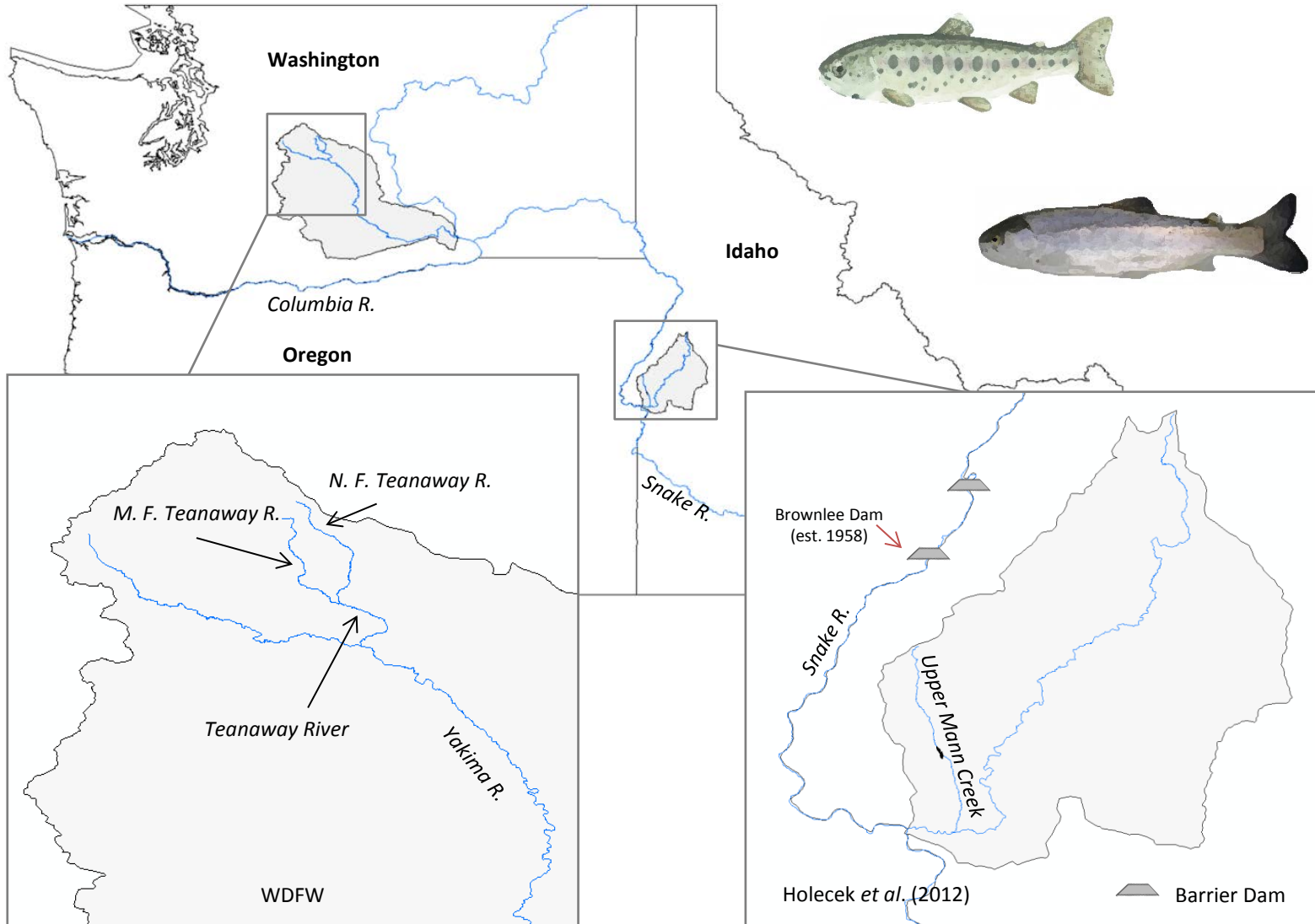
- Identify regions of the genome associated with migration
 - in a wild population of *O.mykiss* which maintains connection to ocean
 - in a wild population of *O.mykiss* sequestered for last 50 years behind barrier dam
- Are the same genetic regions associated with migration in both populations?
 - Is migration a derived trait?
 - Is migration locally adapted?

Genetics of Anadromy

Genome-Wide Association Study (GWAS)

- Samples
 - Wild populations of segregating individuals
- Genetic Markers
 - Thousands distributed throughout the genome
- Statistics
 - Marker/Trait associations

Samples



Samples



Yakima River, WA

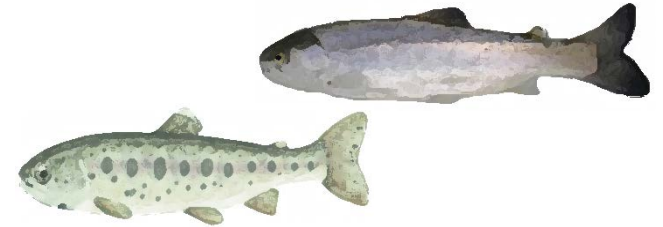
- Electrofishing by WDFW
- PIT tagged in Spring 2008 recovered in Summer/Fall
- Resident RBT = mature w/ gametes
- Smolt = PIT array detection at downstream dam



Upper Mann Creek, ID

- Screw trap (March-June 2009)
- Parr = fish >1 yo with gametes and/or parr marks
- Smolts = silver fish >1 yo w/out parr marks

Samples



	Smolts	Residents	Total
Yakima R.	29	98	127
Upper Mann Cr.	28	27	55
Total	57	125	182

	Smolts	Residents	Total
Female	45	28	73
Male	12	97	109
Total	57	125	182

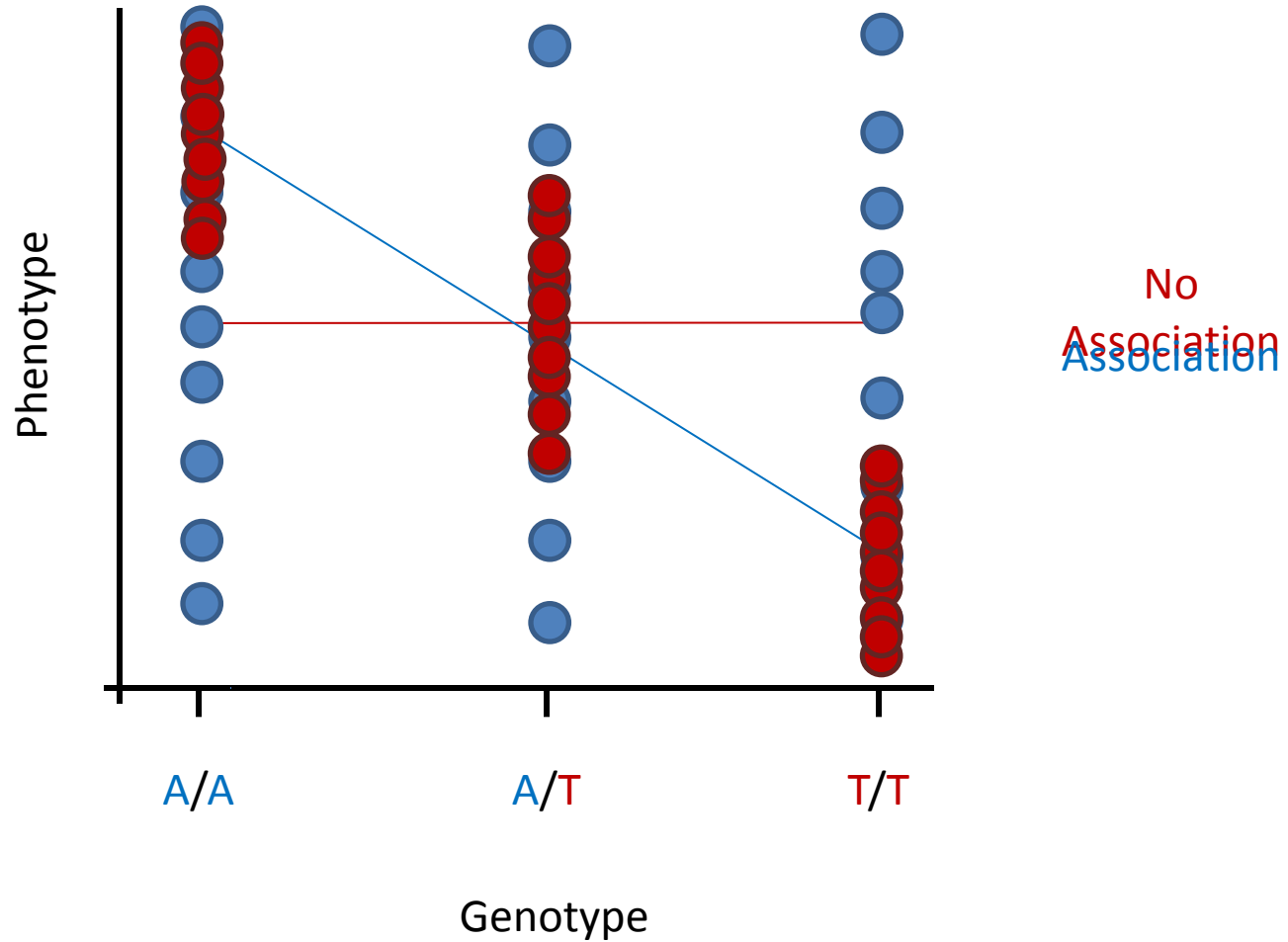
Genetic Markers

- Restriction-site Associated DNA (RAD) tag sequencing
 - Thousands of markers distributed throughout the genome
- OmyY1 – molecular sex marker

Genetic Markers

- 12,073 Polymorphic RAD-tag SNPs
- 8,219 (68%) SNPs aligned perfectly to loci from Miller *et al.* (2012) and Hecht *et al.* (2012)
- 1,148 (14%) SNPs had been assigned to a linkage group.

Statistics



Statistics

Global GWAS – Yakima River GWAS – Upper Mann Creek GWAS

GLM

$$y = X\beta + S\alpha + Qv + e$$

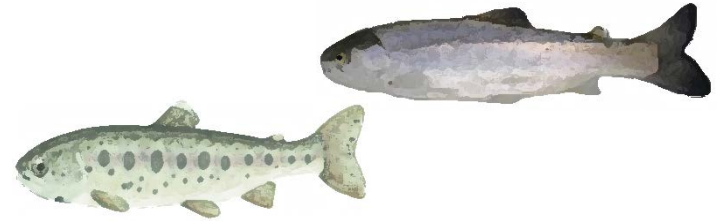
$$\textit{Life-History} = \textit{SNP} + \textit{sex} + \textit{STRUCTURE} + e$$

MLM

$$y = X\beta + S\alpha + Qv + Zu + e$$

$$\textit{Life-History} = \textit{SNP} + \textit{sex} + \textit{STRUCTURE} + \textit{kinship} + e$$

Results - GWAS



Population	# Loci	# Sig. Loci GLM	# Sig. Loci MLM
Global	5,019	58	219
Yakima River	4,338	107	50
Upper Mann Creek	6,039	22	138

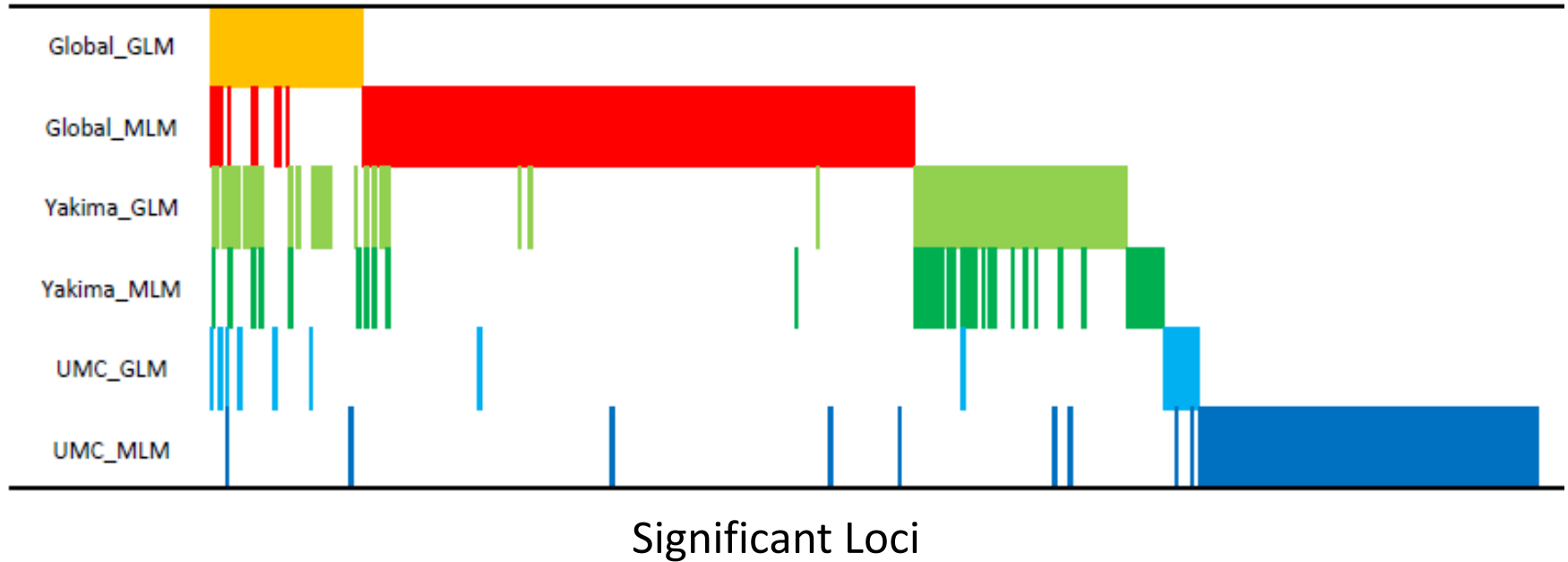
504 loci detected overall

267 loci detected in Global analyses

123 loci detected in Yakima River analyses

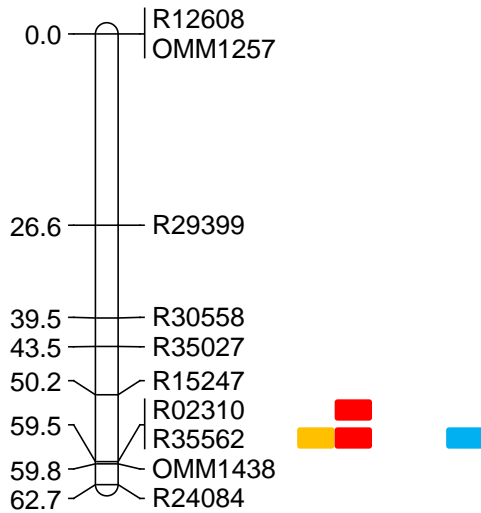
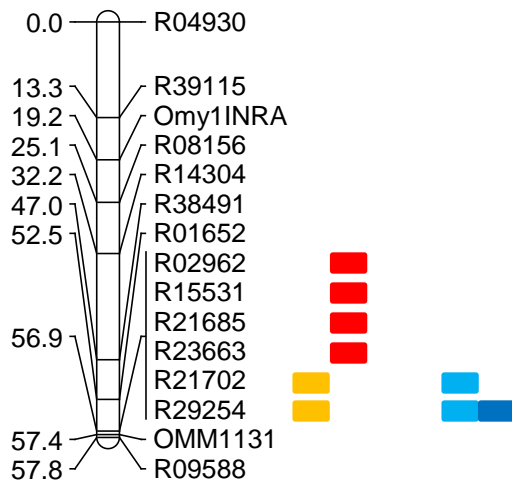
157 loci detected in Upper Mann Creek analyses

Results - Marker Overlap



Omy02

Omy10

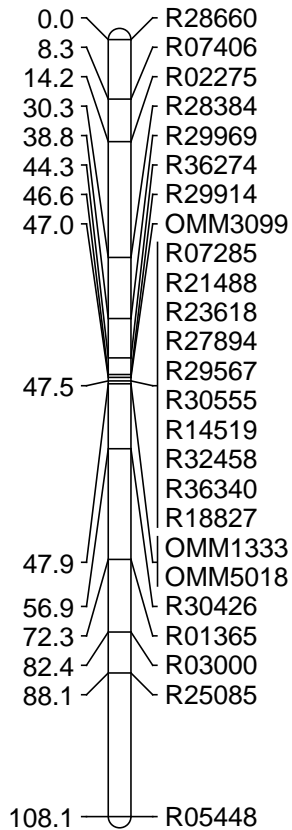


Nichols *et al.* (2008)
Martínez *et al.* (2011)

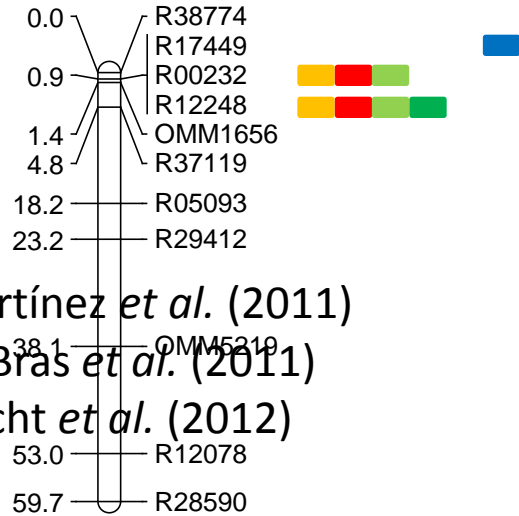


Linkage map adapted from Miller *et al.* (2012)

Omy11



Omy12



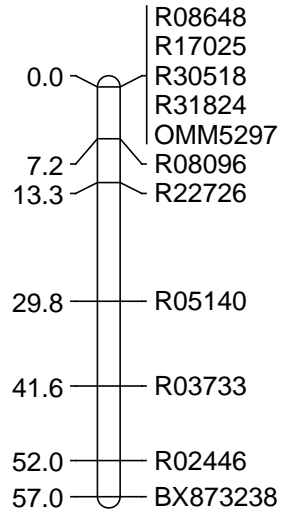
Martínez *et al.* (2011)
 Le Bras *et al.* (2011)
 Hecht *et al.* (2012)

Nichols *et al.* (2008)
 Wringe *et al.* (2010)
 Le Bras *et al.* (2011)
 Martínez *et al.* (2011)
 Hecht *et al.* (2012)

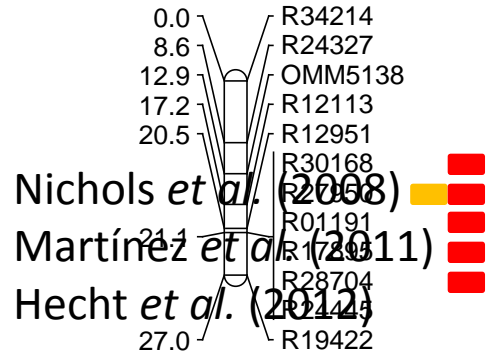


Linkage map adapted from Miller *et al.* (2012)

Omy18



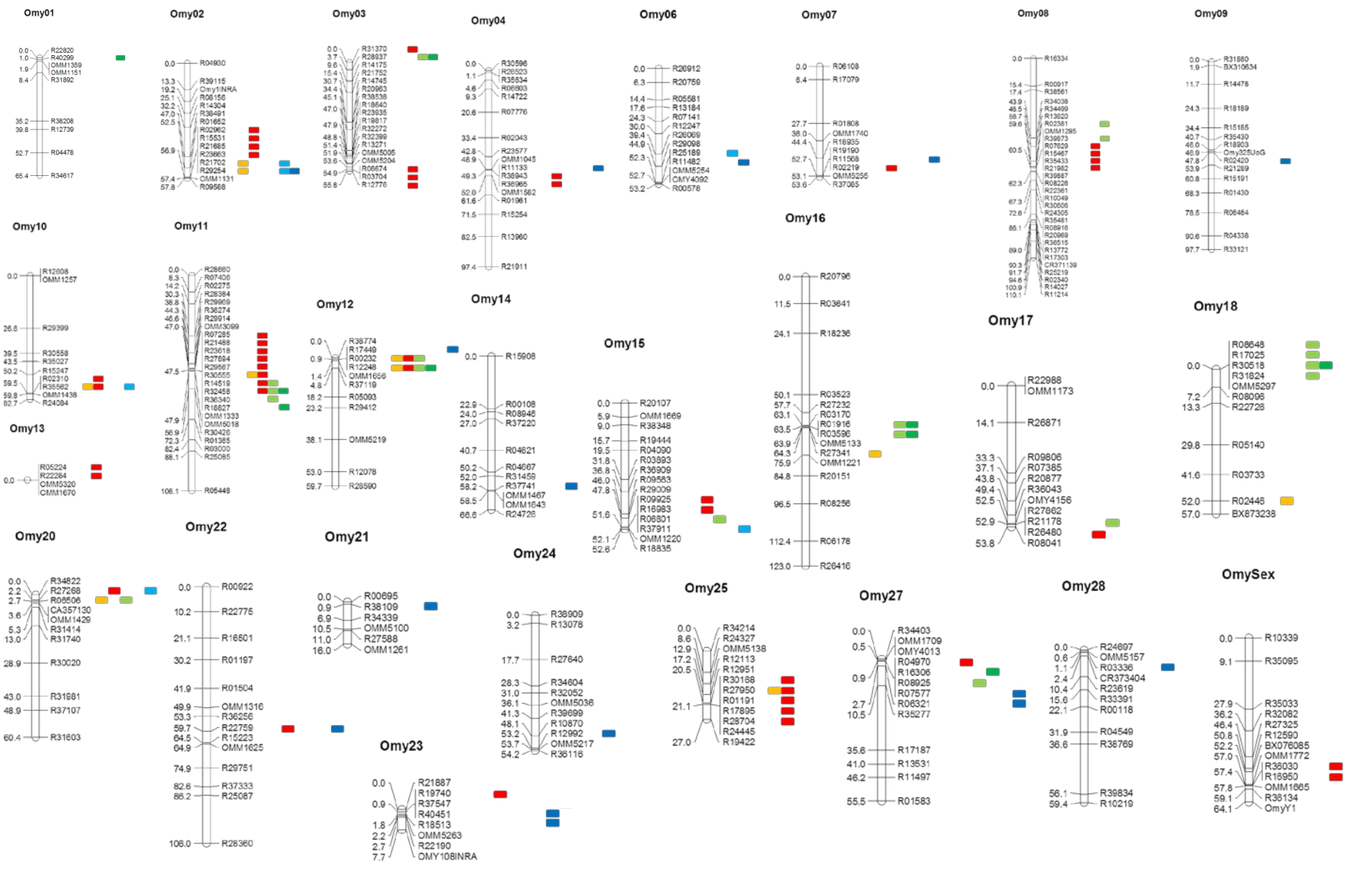
Omy25



Le Bras *et al.* (2011)



Linkage map adapted from Miller *et al.* (2012)



Linkage map adapted from Miller *et al.* (2012)

Conclusions

- Identified 504 loci associated with the propensity to migrate in two wild populations of *O.mykiss*
- Several mapped loci localize to QTL regions previously detected suggesting some conserved mechanisms between populations
- Some loci are unique to each population, suggesting locally adapted mechanisms

Conclusions

- UMC continues to exhibit genetic variation for propensity to migrate despite 50 years sequestration above a barrier dam
- **Does this mean if passage to the ocean is restored anadromy in Upper Mann Creek would be reestablished???**



Genome-wide association reveals genetic basis for the propensity to migrate in wild populations of rainbow and steelhead trout

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Thank You

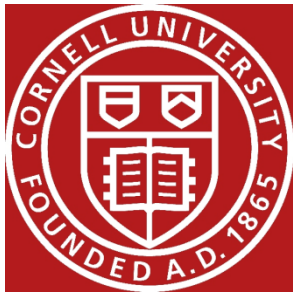
Contact: Ben Hecht
Email: hecb@critfc.org



Scott M. Blankenship
Cherril Bowman



Dennis Scarnecchia
Rob Lyon
IBEST CRC



Alex Lipka



Garrett McKinney



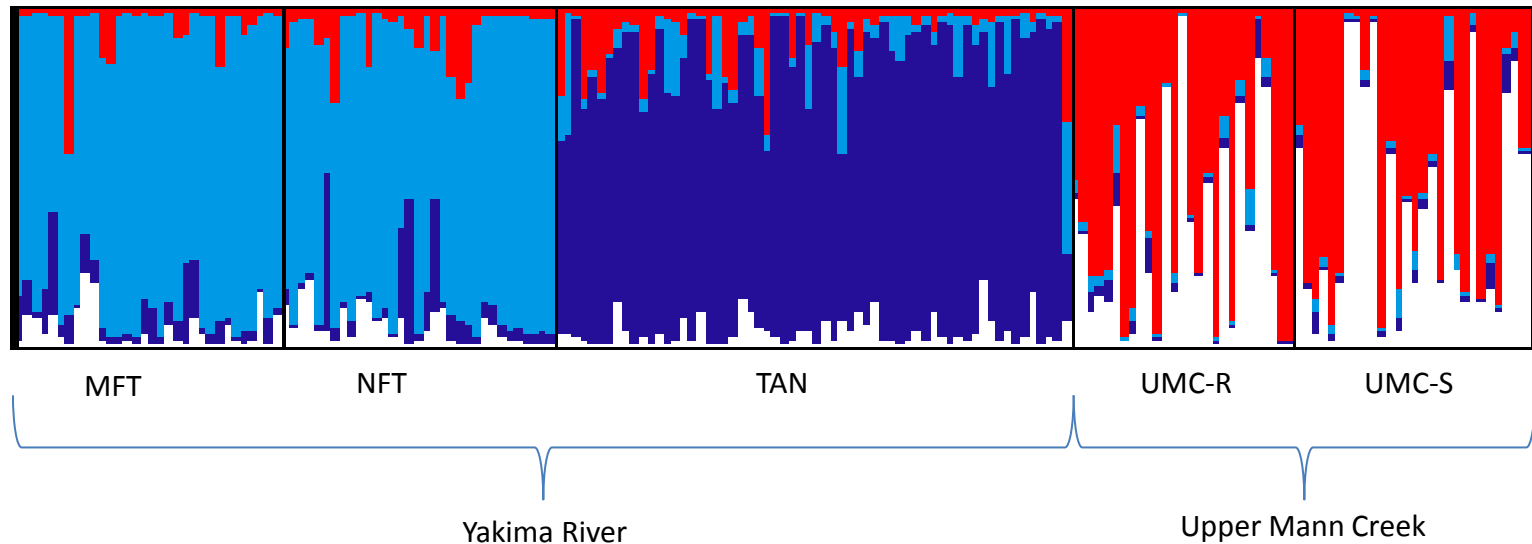
Mike Miller
Doug Turnbull
GCF



Megan Moore
Travis Jacobson
Andrew Matala

Results - Structure

K = 4



Estimated using programs STRUCTURE and CLUMPP using a subset of 1,000 SNPs with 100% genotype frequency and $MAF \geq 0.10$. Figure generated by program DISTRUCT.

RADseq

DNA




sbfl digestion



P1 Ligation



Sonication 



Size Select



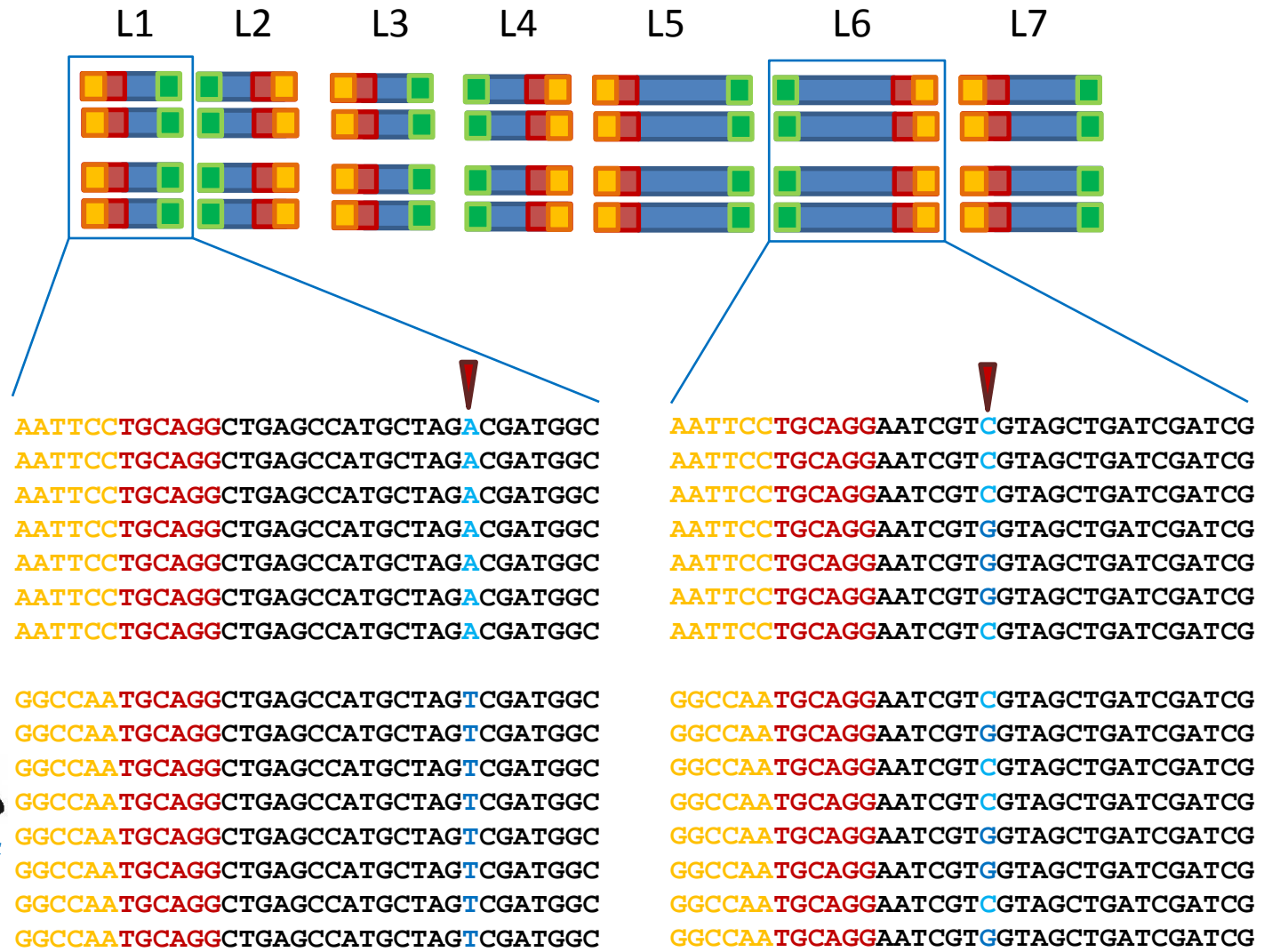
P2 Ligation



PCR

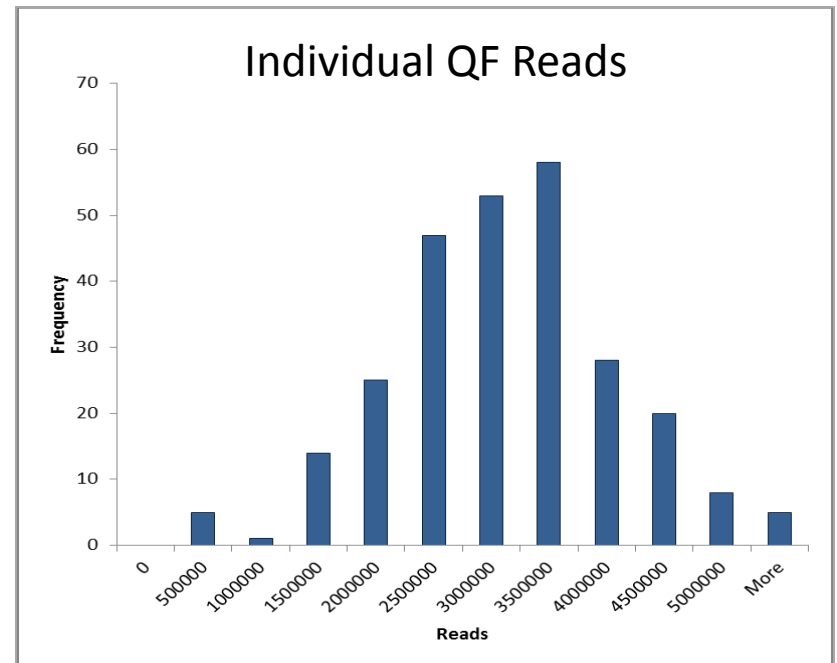
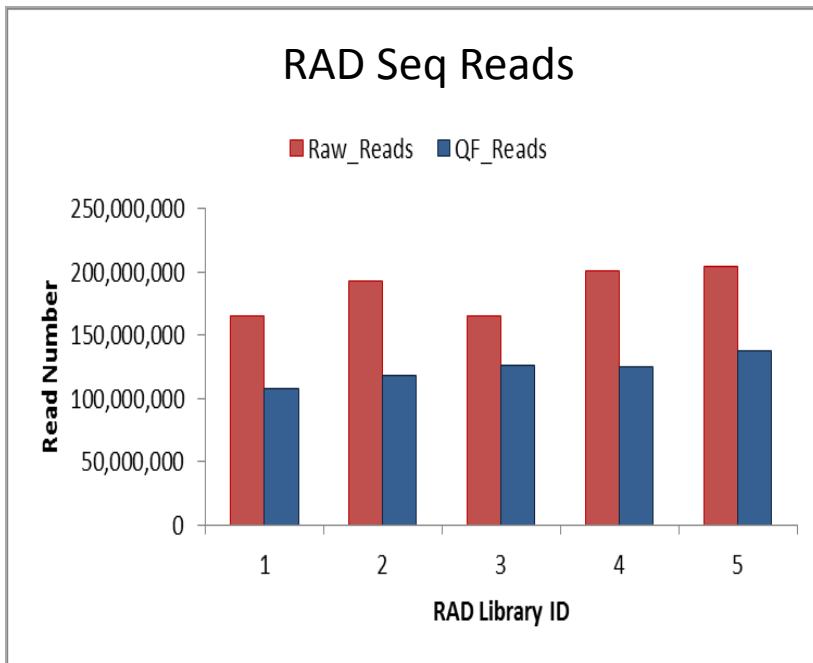


Genotyping by sequencing



Results - RAD

- 5 RAD libraries
- 38-39 barcoded samples per library
- Avg. 185M raw & 123M QF reads per library
- 189 total individuals sequenced
- Avg. 2.8M QF reads per individual
- 12,073 polymorphic loci detected



Linkage group assignment of significant loci

Linkage group	Global		Yakima		Upper Mann Creek		Total
	GLM	MLM	GLM	MLM	GLM	MLM	
OmySex		2					2
Omy1	1	1	1	2		1	6
Omy2	2	4			2	1	9
Omy3		4	1	1			6
Omy4		2				1	3
Omy5							0
Omy6					1	2	3
Omy7		1				1	2
Omy8		5	2				7
Omy9						1	1
Omy10	1	2			1		4
Omy11	1	8	3	2			14
Omy12	2	3	2	1		1	9
Omy13		2	1	1			4
Omy14						1	1
Omy15		2	1		1		4
Omy16	1		3	2			6
Omy17		1	1				2
Omy18	1		4	1			6
Omy19	1		1				2
Omy20	1	1	1		1		4
Omy21		1				1	2
Omy22		1			1	2	4
Omy23		2				2	4
Omy24						1	1
Omy25	1	6					7
Omy26							0
Omy27		1	1	1		2	5
Omy28						1	1
Total	12	49	22	11	7	18	119

Linkage group assignment based on alignment of RAD markers to Miller *et al.* (2012) and Hecht *et al.* (2012)