

Migratory *O. mykiss* Colonizing a Natal Stream After Barrier Removal in the Methow River basin, WA

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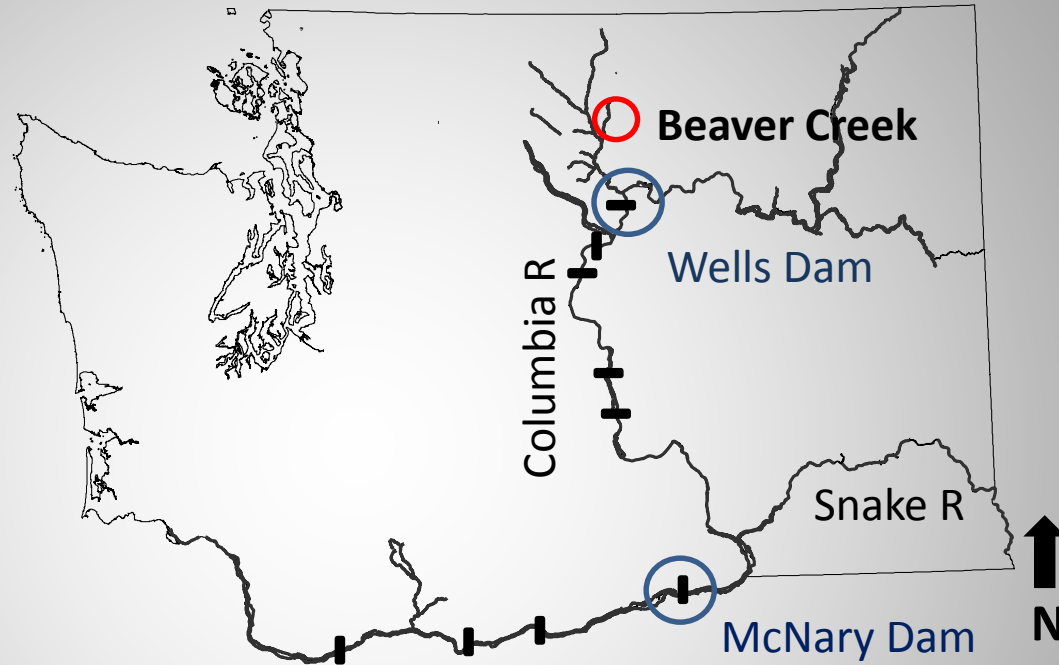


Willamette Science Review
February 2017

Study Area – tributary Methow River, upper Columbia Basin

Long mainstem migration (843 km)

9 mainstem dams



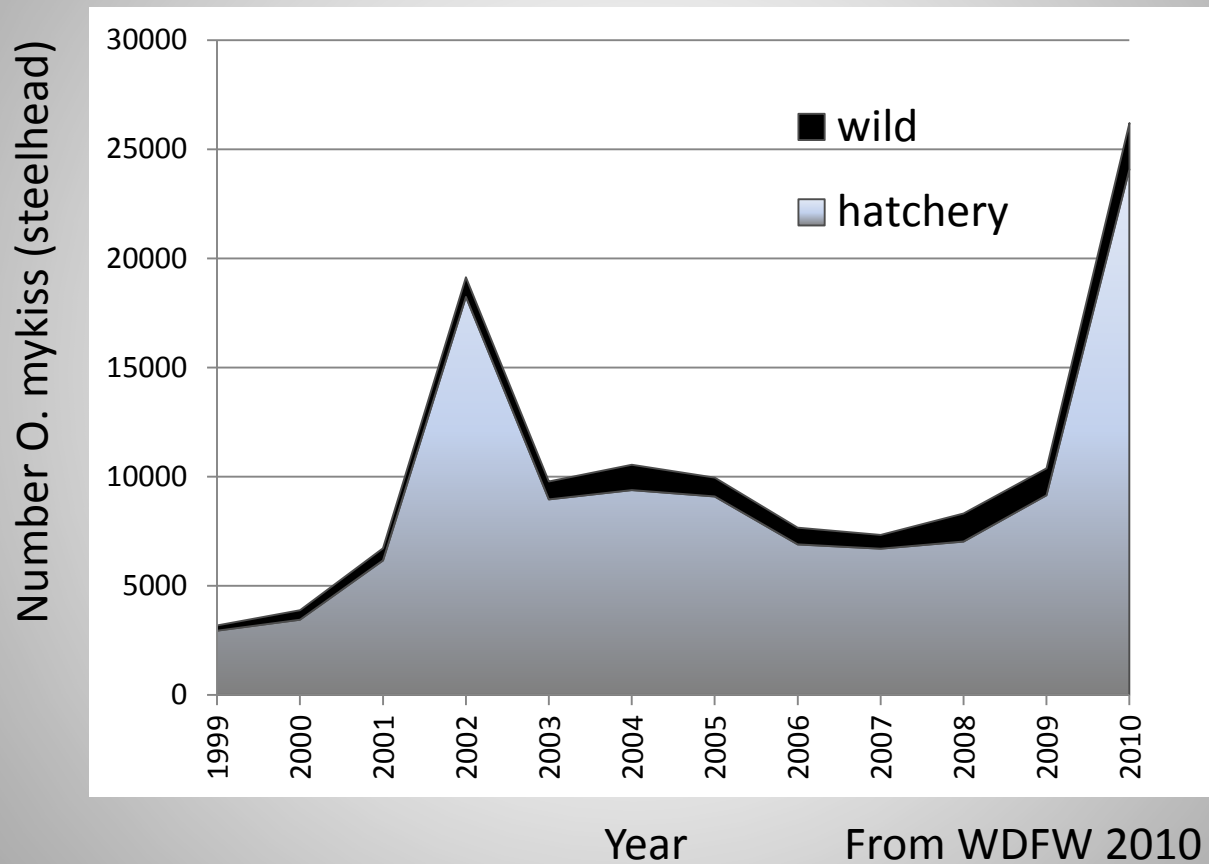
Upper Columbia Steelhead listed endangered 1997 -> threatened

Abundance	<5% extinction risk 100 yrs
Productivity	3,000 spawners
Spatial Structure	Previously occupied habitats
Diversity	Natural patterns genetic, phenotypic diversity

2010 Status Review
Not viable

Study Area - Steelhead returns to Wells Dam 1999-2010

80-90% returning adults hatchery-origin



Study Area - 7 Diversion dams redesigned in Beaver Creek 2002-2004



Objectives

- Do migratory steelhead establish a population in the re-opened habitat?
- Which source -> establishes a population?
 - Individual reproductive success
 - mate selection, successful phenotypes to next generation
 - Founder effect? Or low diversity
- What spatial extent of colonization 1 generation after re-open habitat?
 - Migration strategy (tag tracking)
 - Genetic

Three major processes shaping genetic structure ~

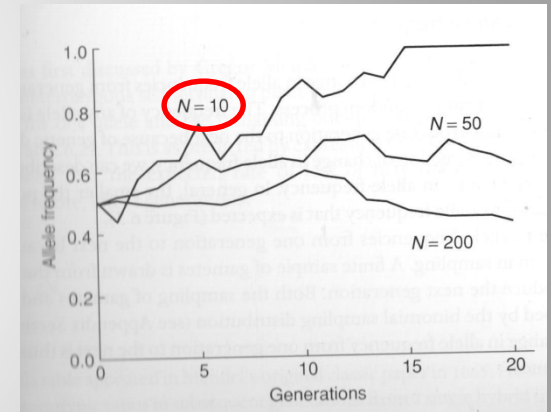
Gene Flow ~

Migration
Decreases genetic
Differences thru
mixing



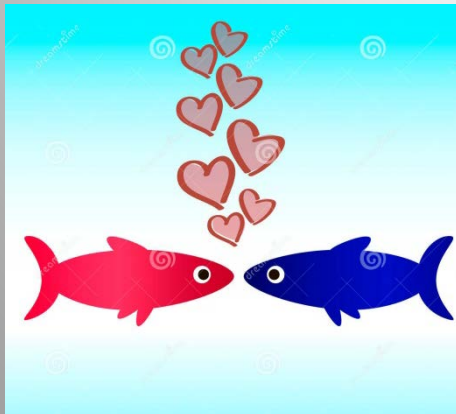
Drift ~

Increases genetic
Differences
Random fixation alleles
Due to finite popn size

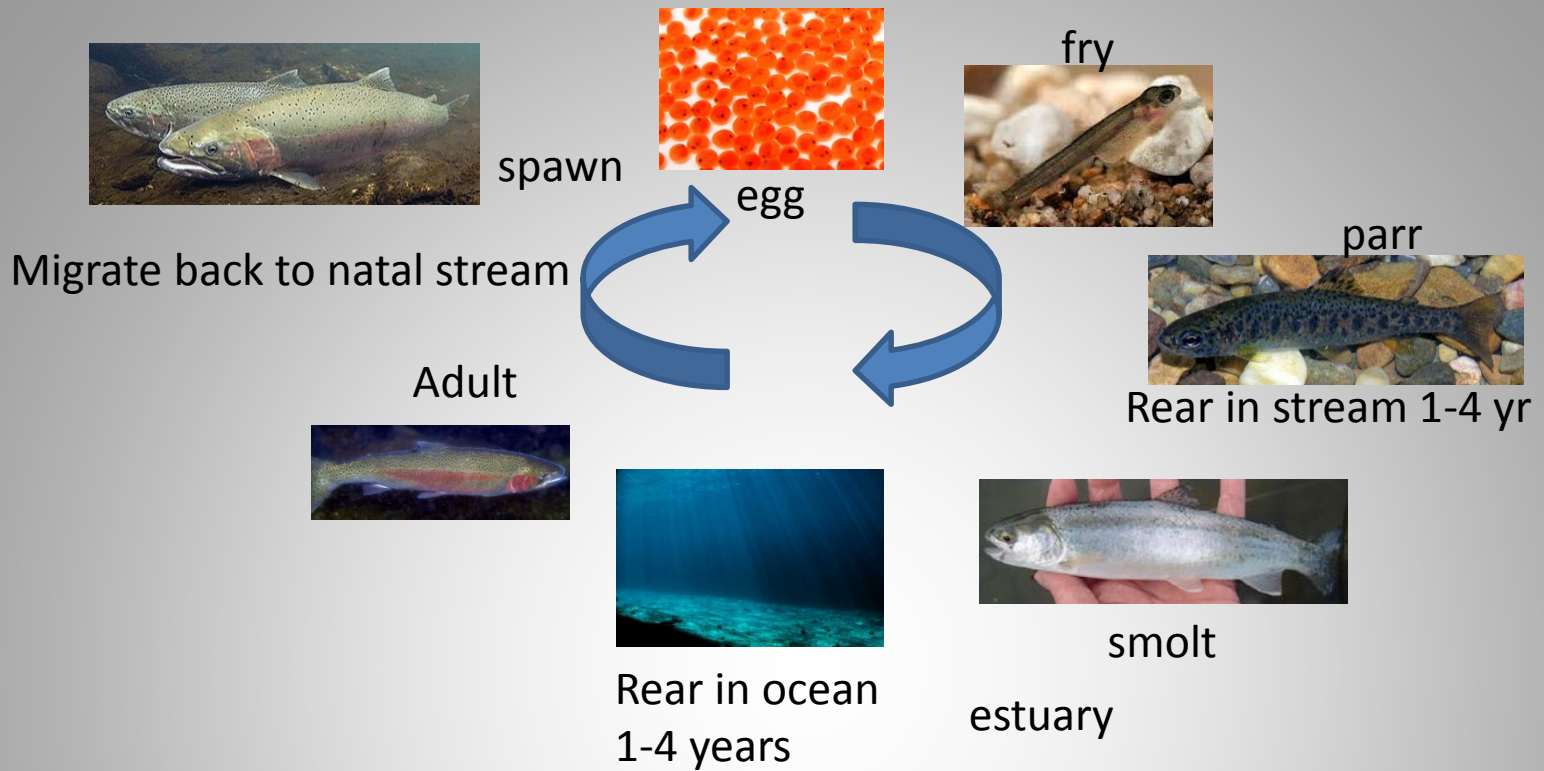


System of Mating ~

selection for trait – genetic link



Mutation
Selection



Life history diversity

Migration

Anadromous
Estuary

Steelhead

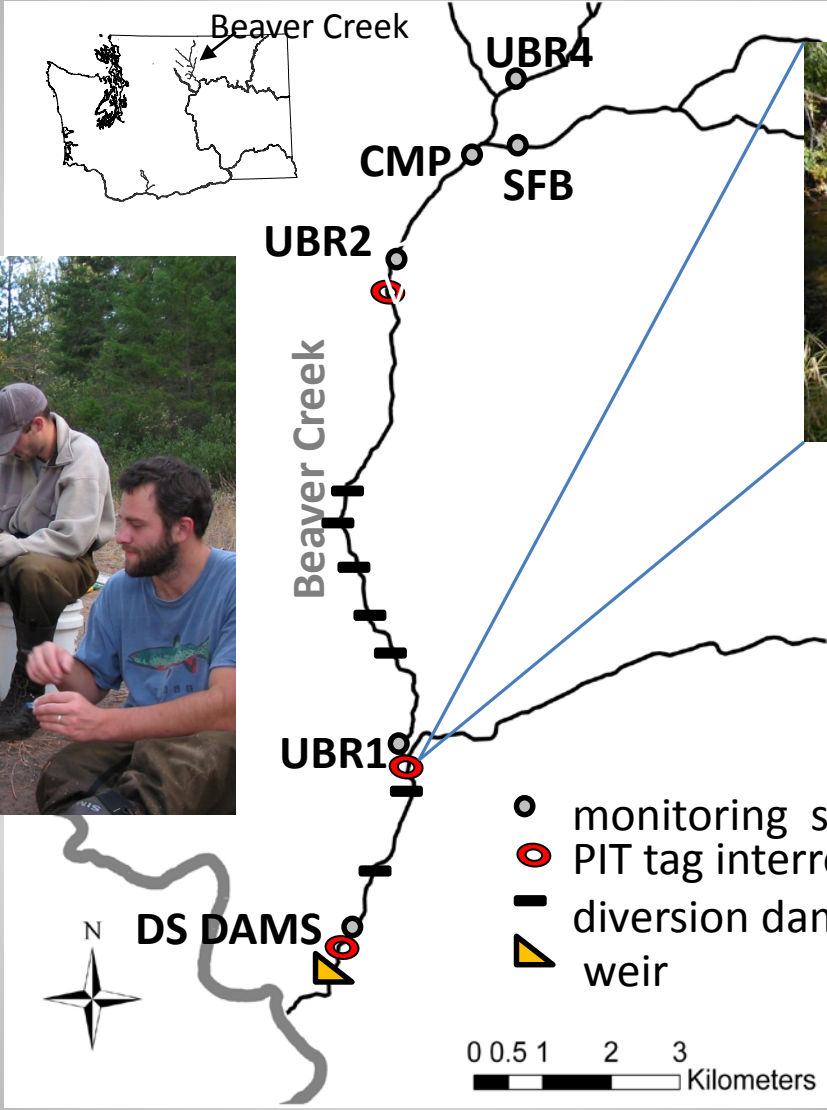
Fluvial (River)
Resident (Stream)
Adfluvial (Lake)

Rainbow Trout

Iteoparous
Overlapping generations

Fresh:salt

1:1	2:1	3:1
1:2	2:2	3:2
1:3	2:3	3:3
1:4	2:4	3:4



Downstream tag readers



Near mouth Methow Dams on Columbia R

Methods – Capture

- Upstream/downstream picket weir
 - Feb to Dec 2005, 2006, 2007, 2008
 - Adults on spawning migration
 - Parr outmigrating



- Electrofishing at monitoring sites
 - Juvenile rearing in tributary



Methods - Tagging

- Migration behavior was identified using PIT tag
- 16 digit alpha-numeric code
 - 3D9.1BF1FDC829
- Followed tags of juveniles reared in Beaver Creek to return as adults
 - PTAGIS

A screenshot of the PTAGIS web application interface. The page title is "COMPLETE TAG HISTORY". Below the title, there is a text box for entering tags, with instructions: "Enter one or more tags; separate multiple tags with a semicolon. You may also import a file of up to 300 tag codes. If you need the complete history for more than 300 tags, use the Query Builder in Advanced Reporting." There are several tabs for different views: "Summary Graphs", "Calculate Tag History", "Adult Ladder Detections", "Small-scale Site Detections", "Current Year Detections", and "Current Year Detections at Juvenile Bypass Sites". The "Calculate Tag History" tab is selected. Below the tabs, there is a form with a "Tag (Required)" label and a "Query on Tag:" label. The form contains a dropdown menu for "Tag" with "PIT tag" selected, a "From:" dropdown with "Code" selected, a "To:" dropdown with "Date" selected, a "Value:" input field, and an "Import file..." button.

Methods - Sample Selection

- Used Spawners from BY 2005 and 2006
- Queried tissue samples for analysis by length to match these brood years collected 2005-2008

Collection/BY age	2005	2006	2007	2008
2005	0			
2006	1	0		
2007	2	1	0	
2008	3	2	1	0

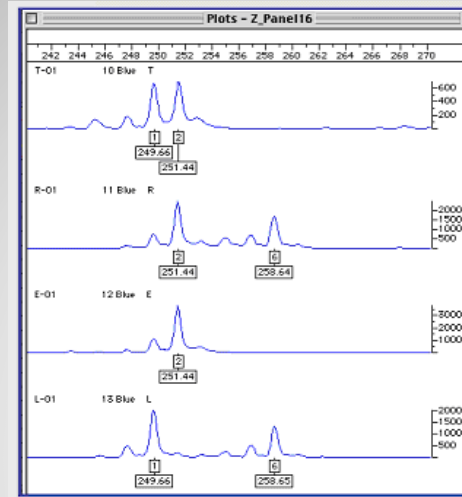
Collected Wells Hatchery tissue from WDFW for reference

Methods - Tissue collection and Genotyping

- Fin clip preserved in 95% EtOH
- DNA extracted
- PCR amplification optimized for each locus
- **16 usat loci** – analysis conducted at UI Aquaculture Research Station, Hagerman ID
 - 13 usat loci standardized (Stevensen et al. 2009)
 - *One102* (Olsen et al 2000), *Omm1036* and *Omm1046* (Rexroad et al 2002)

Parent – Offspring Matching

Exclusion tests with **1 mismatch** using Cervus > match 15 of 16 loci



Father	249	251
Mother	251	258
Child	251	251
Child	249	258

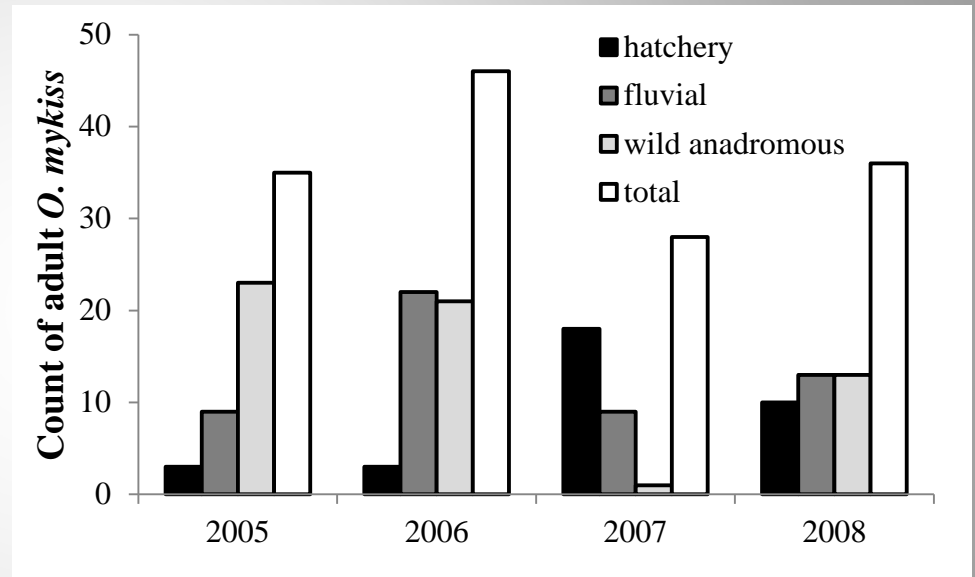
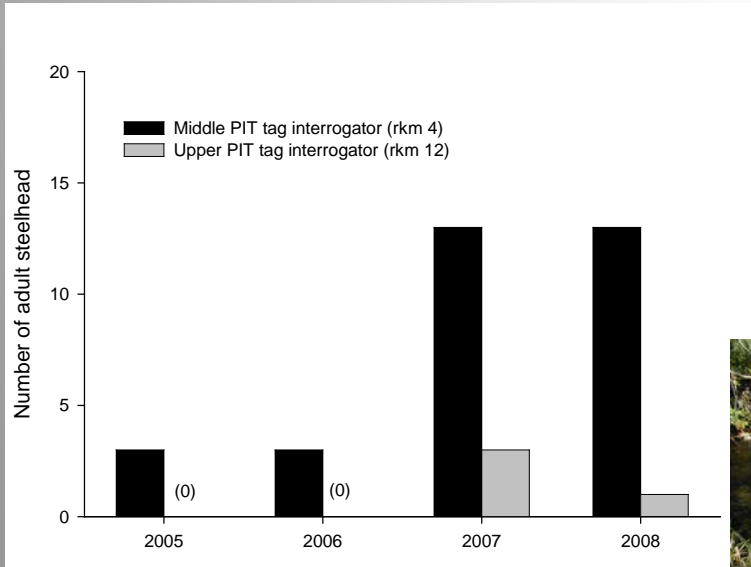
Relate Successful Reproduction to Mate Selection

- Use Spearman Rank correlation to look at association between mating pairs

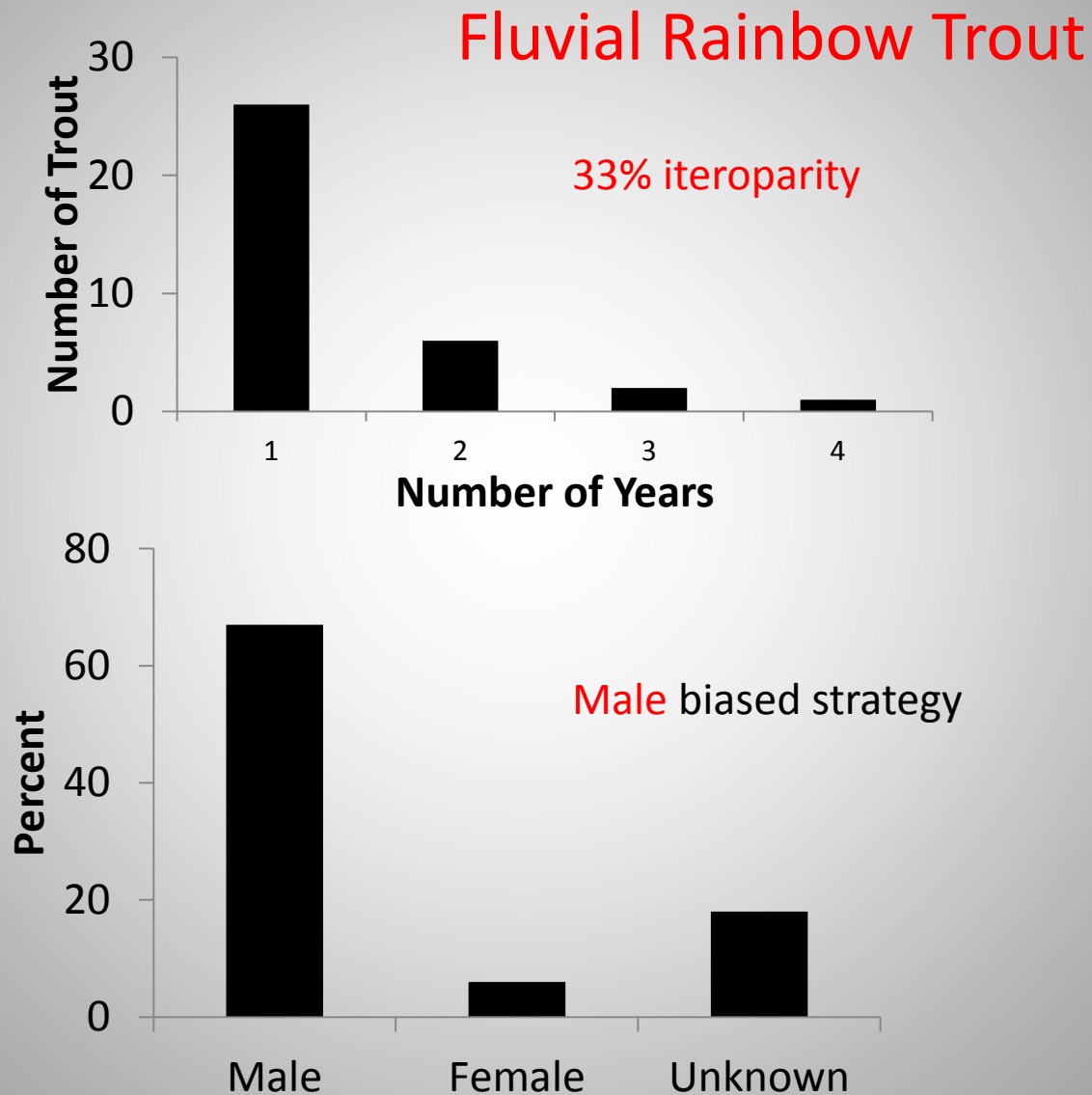
Change in Popn Genetics over Generation

- F_{ST} and Fisher exact tests

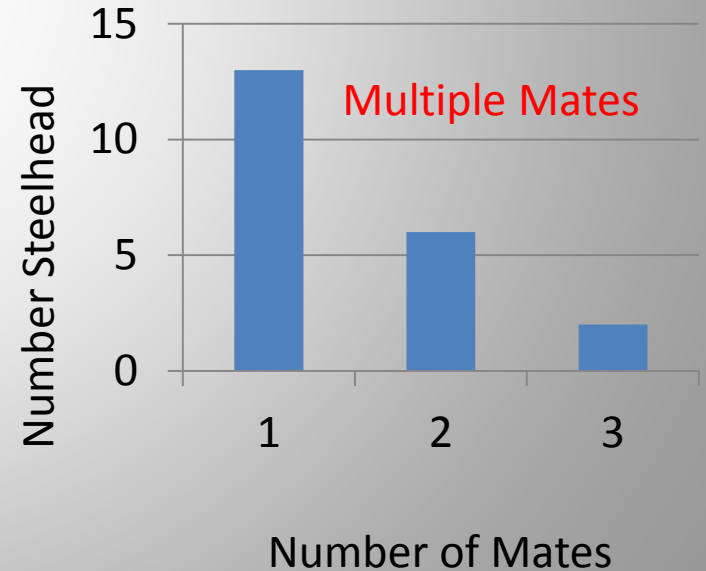
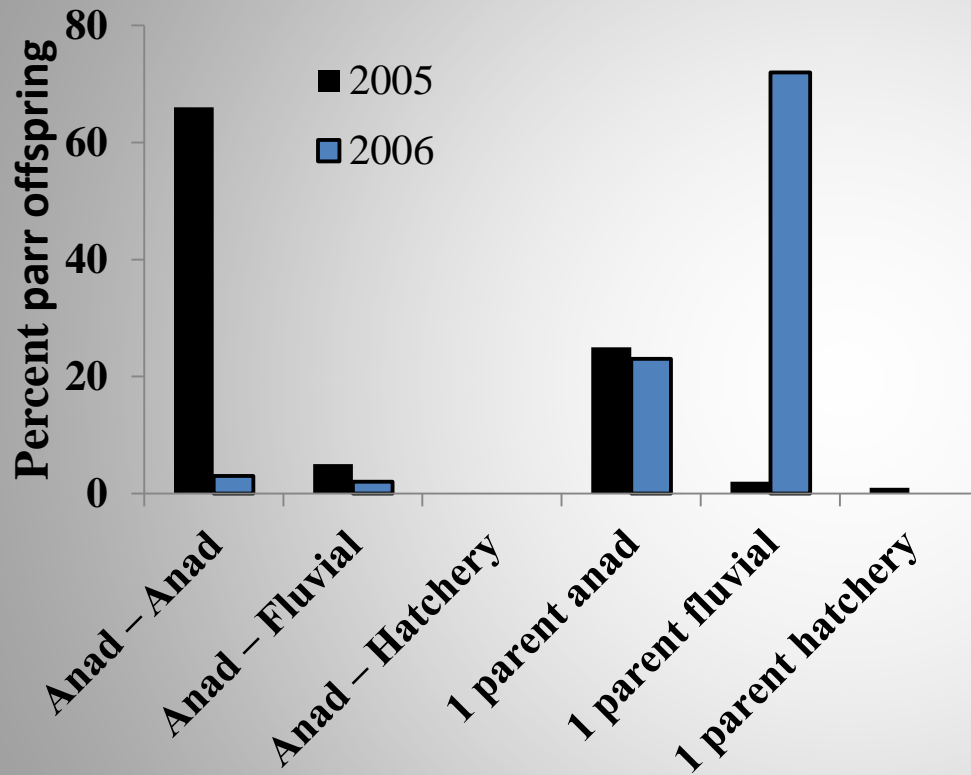
Results – Do steelhead enter the re-opened Habitat? Source?



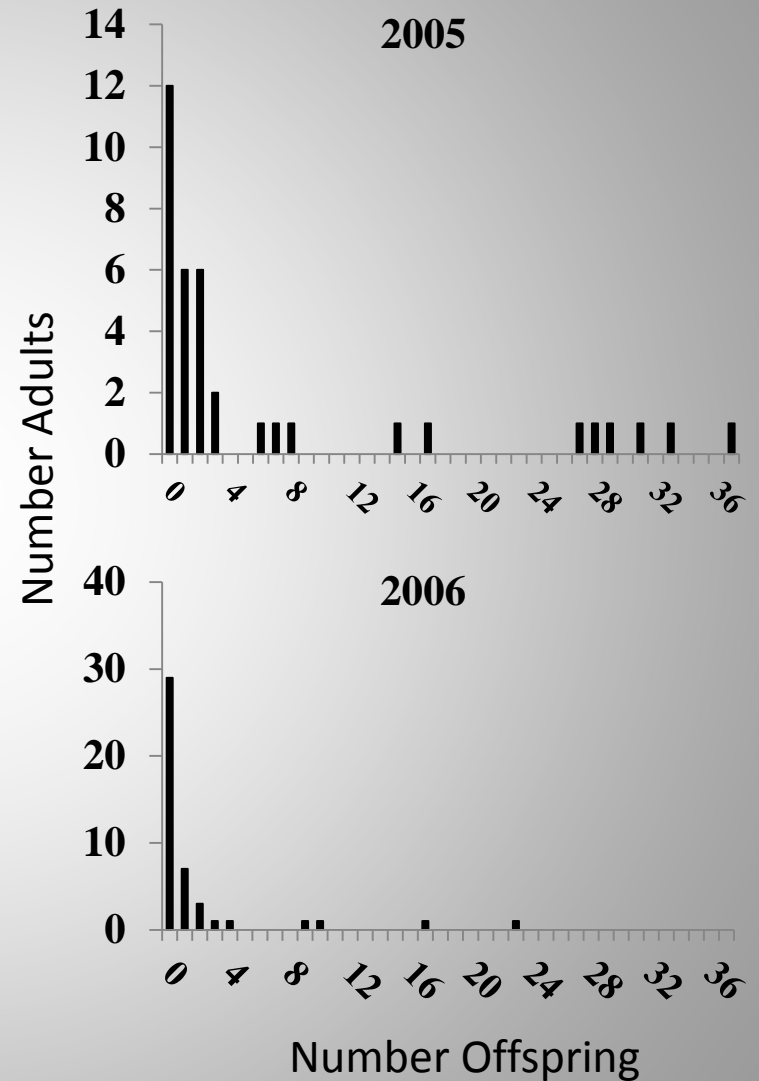
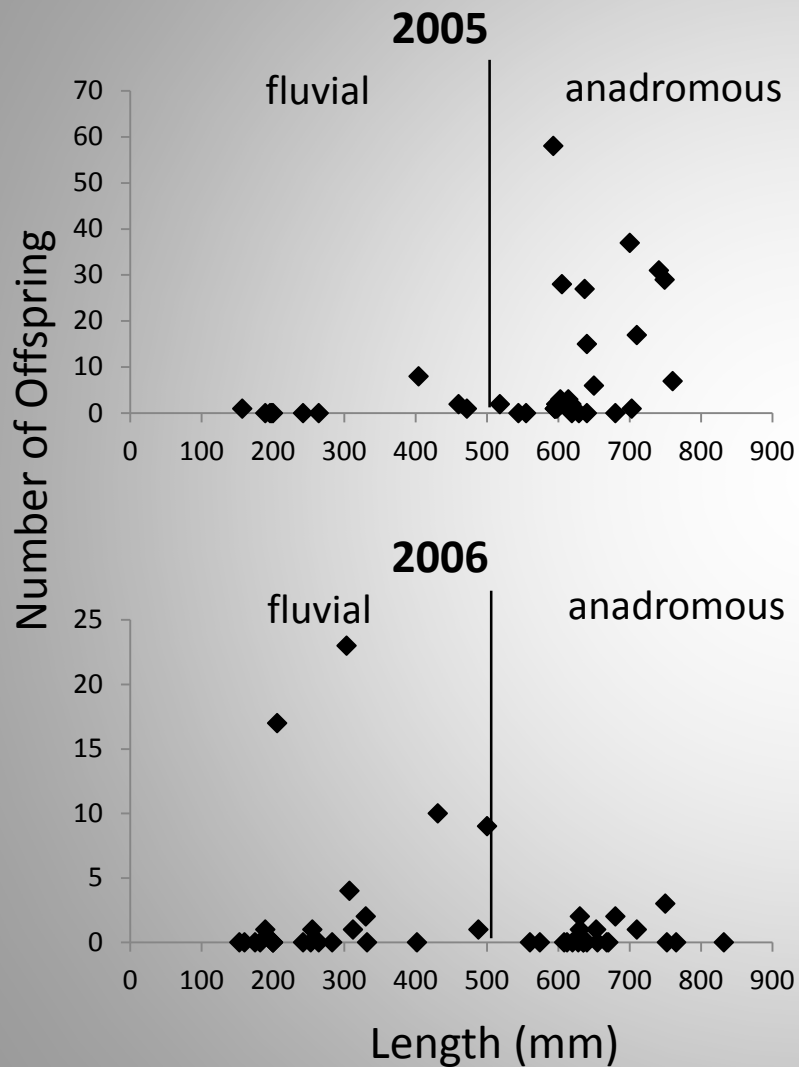
Results – Do steelhead colonize the re-opened Habitat? Source?



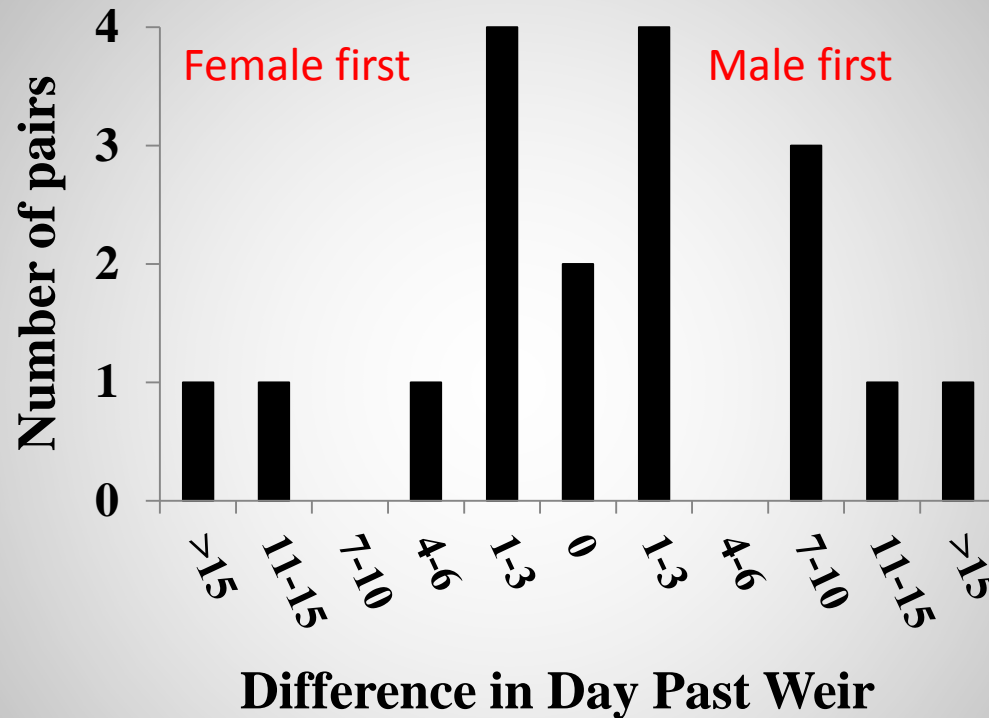
Results – Successful mate selection by source?



Results – Successful spawners by size/life history

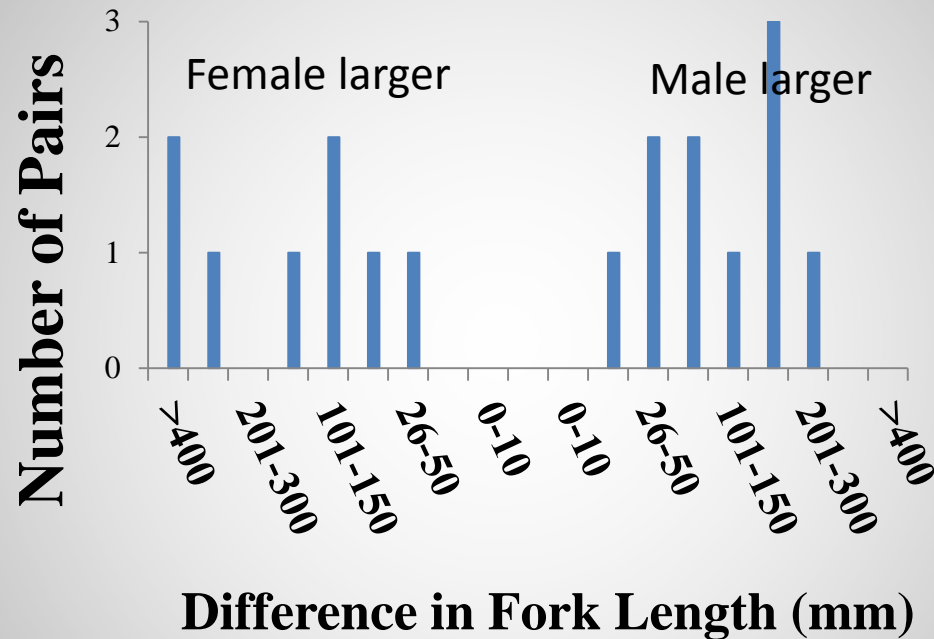


Results - What phenotypes were associated with successful mating?



- Sig. paired by day past weir (early-early, later-later) ($p < 0.001$, $\rho = 0.84$)

Results – What phenotypes were associated with successful mating?

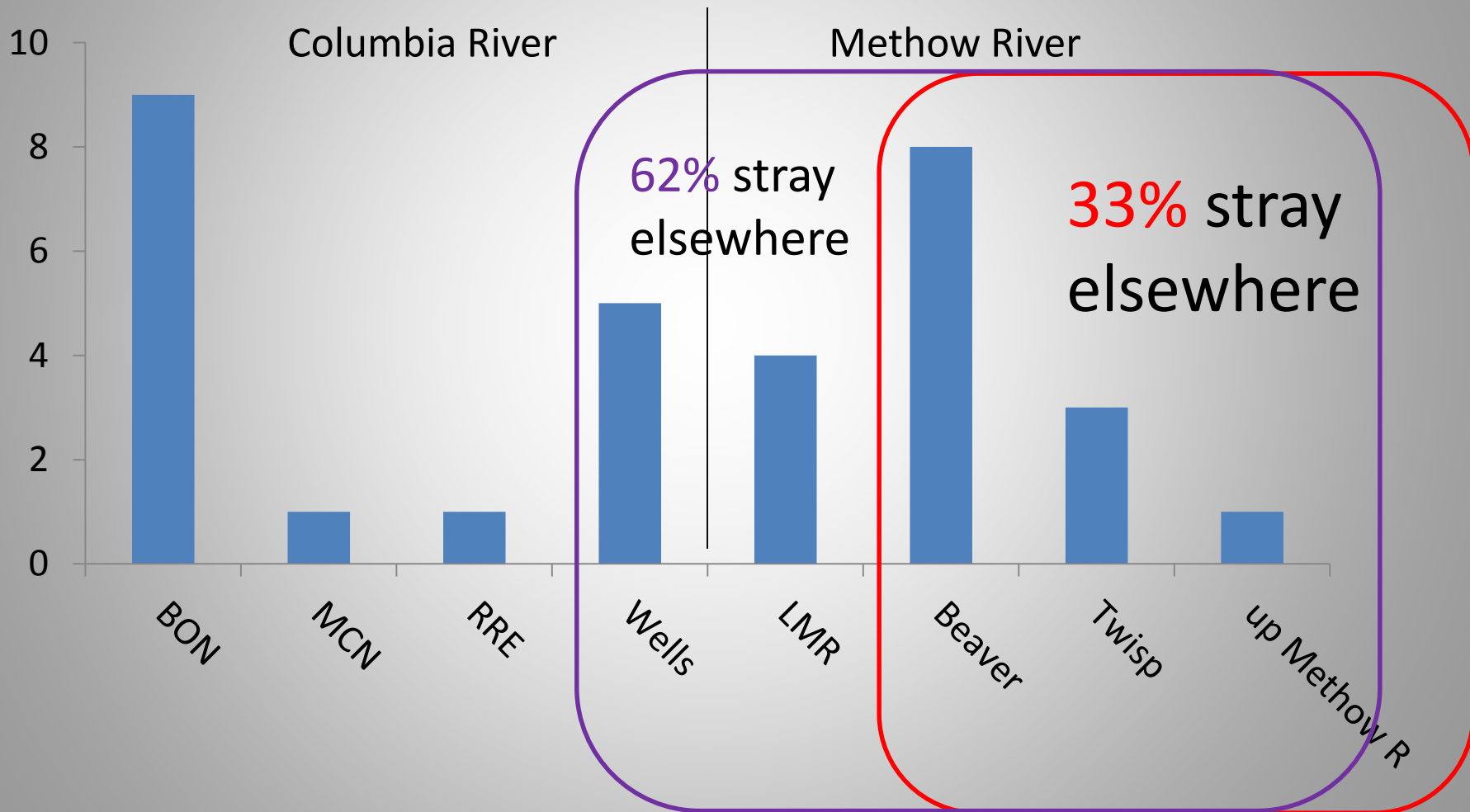


Sig. disassociation in size (larger-smaller) ($p=0.005$, $\rho=-0.72$)

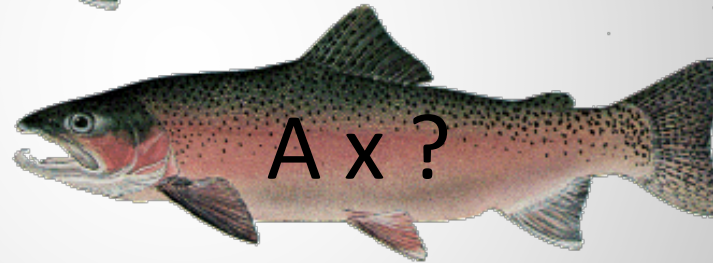
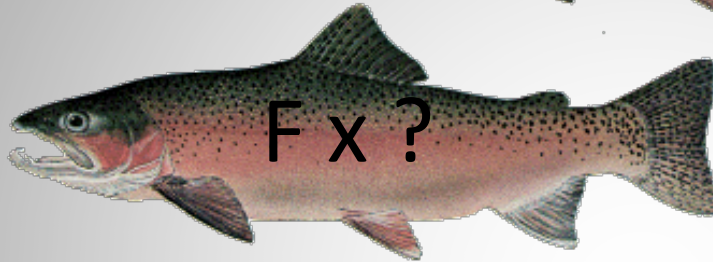
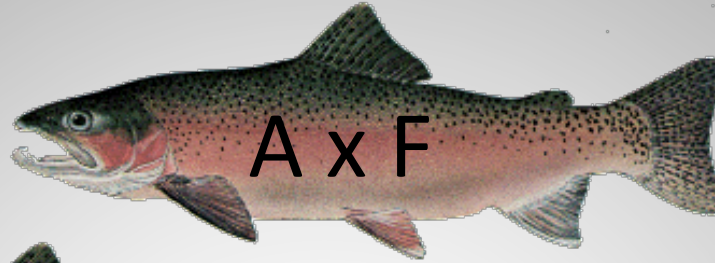
High genetic exchange among life history and generations

Random mating => no founder effect

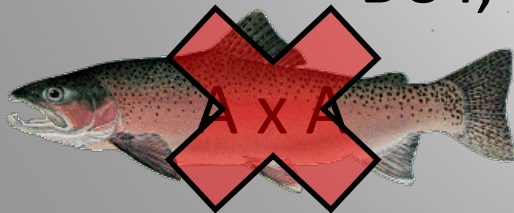
Results - Do steelhead colonize the reopened habitat?



Results - Returning Offspring as Adults



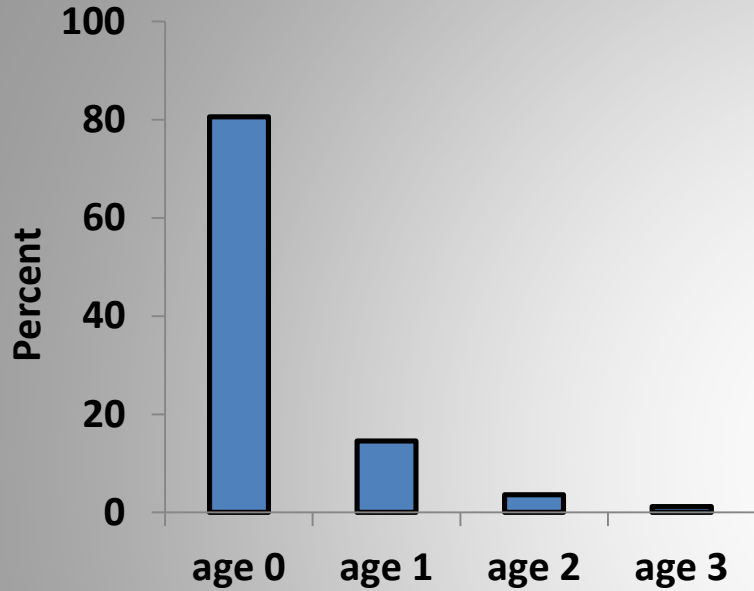
BUT, 50% parr progeny were **AxA** cross



Survival 1.3%

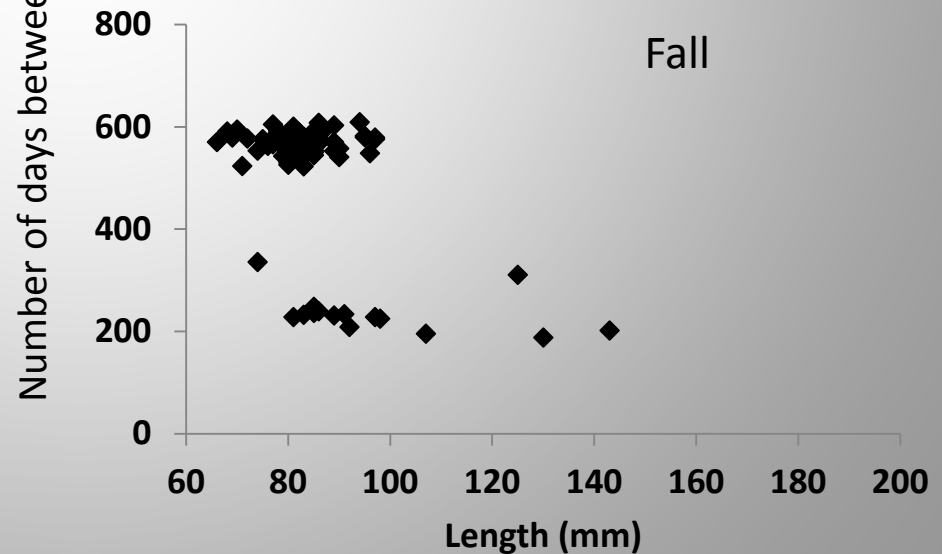
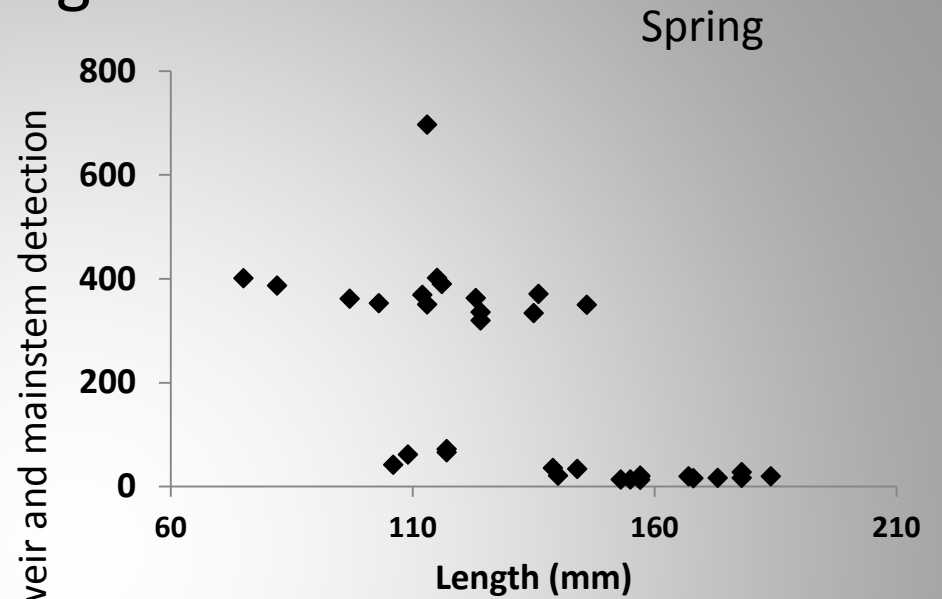
Results – Successful phenotypes?

Juvenile migration



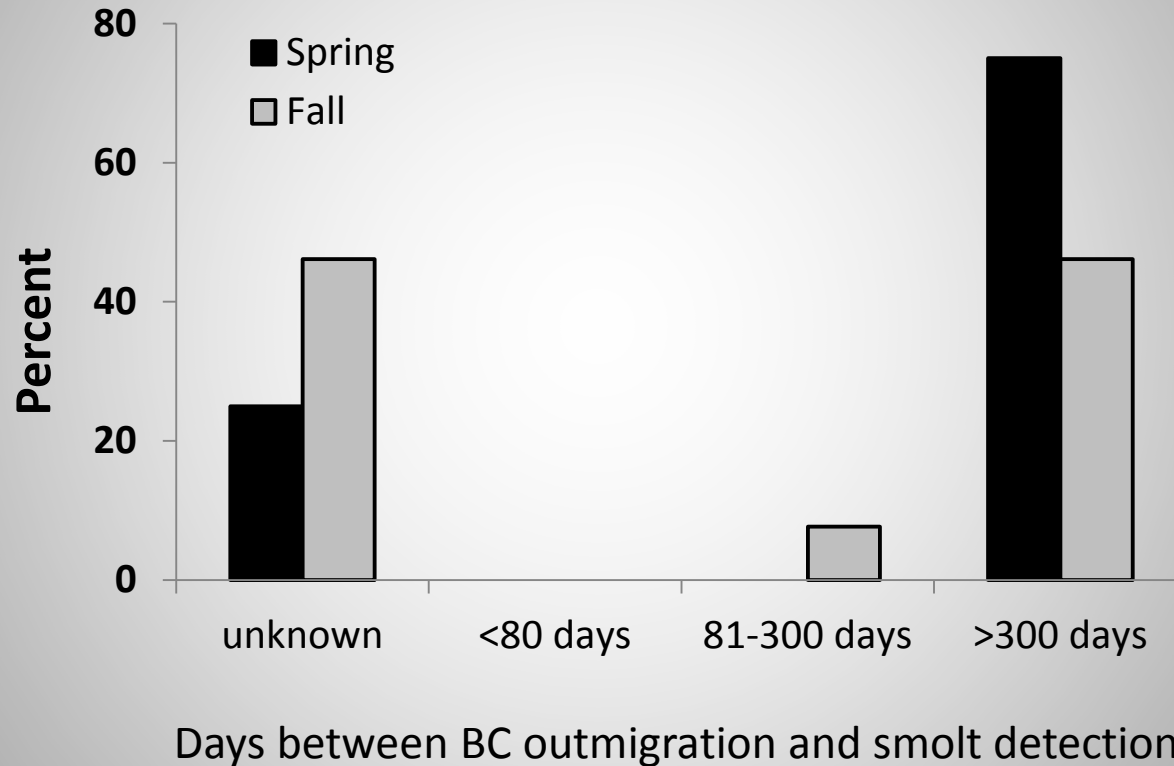
80% offspring captured
Age 0

Most parr reared >200 days
downstream from the natal tributary
before smolt outmigration



Results – Successful phenotypes? Juvenile Migration/Survival

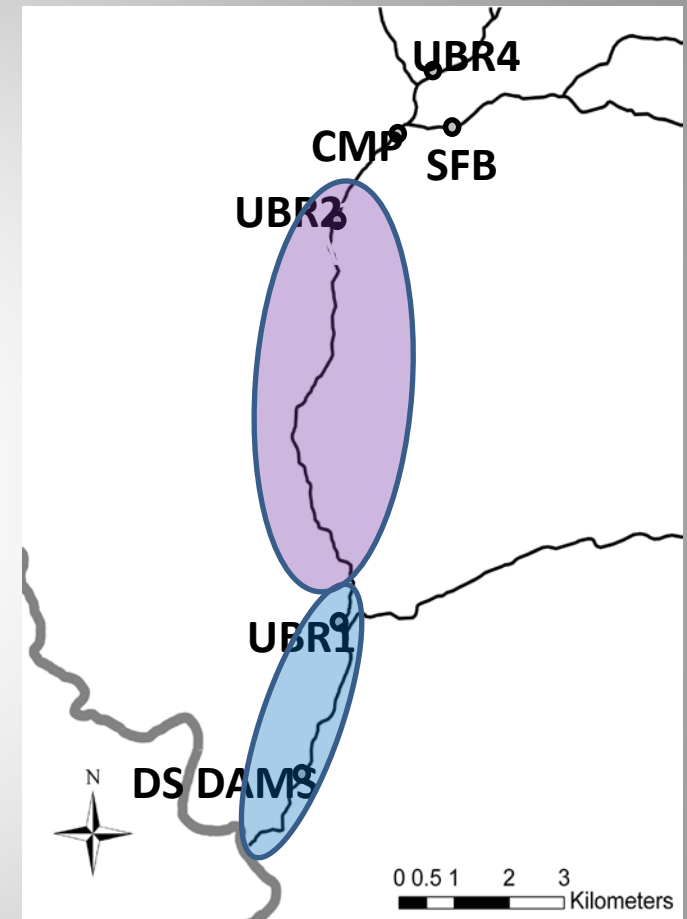
Most successful **adult returns** rear in –basin > 300 days



Results – Spatial extent of measurable changes?

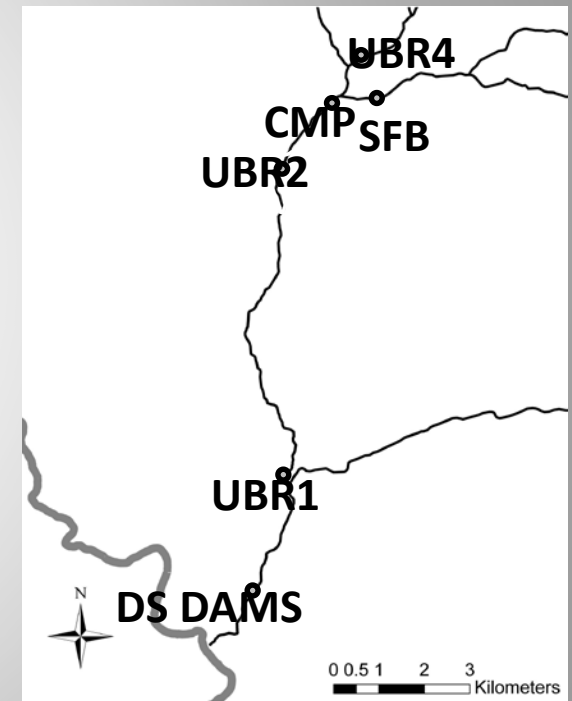
Site	Before Year	After Year	F_{ST}	Pval
DS Dam	2005	2009	0.014*	0.001*
UBR1	2004	2008	0.021*	<0.001*
UBR1	2004	2009	0.027*	<0.001*
CMP	2005	2009	0.002	0.047
UBR4	2004	2008	0.011*	0.009*
UBR4	2004	2009	-0.002	0.558
SFB	2005	2008	0.004	0.121
SFB	2005	2009	0.002	0.276

* Indicates statistical significance

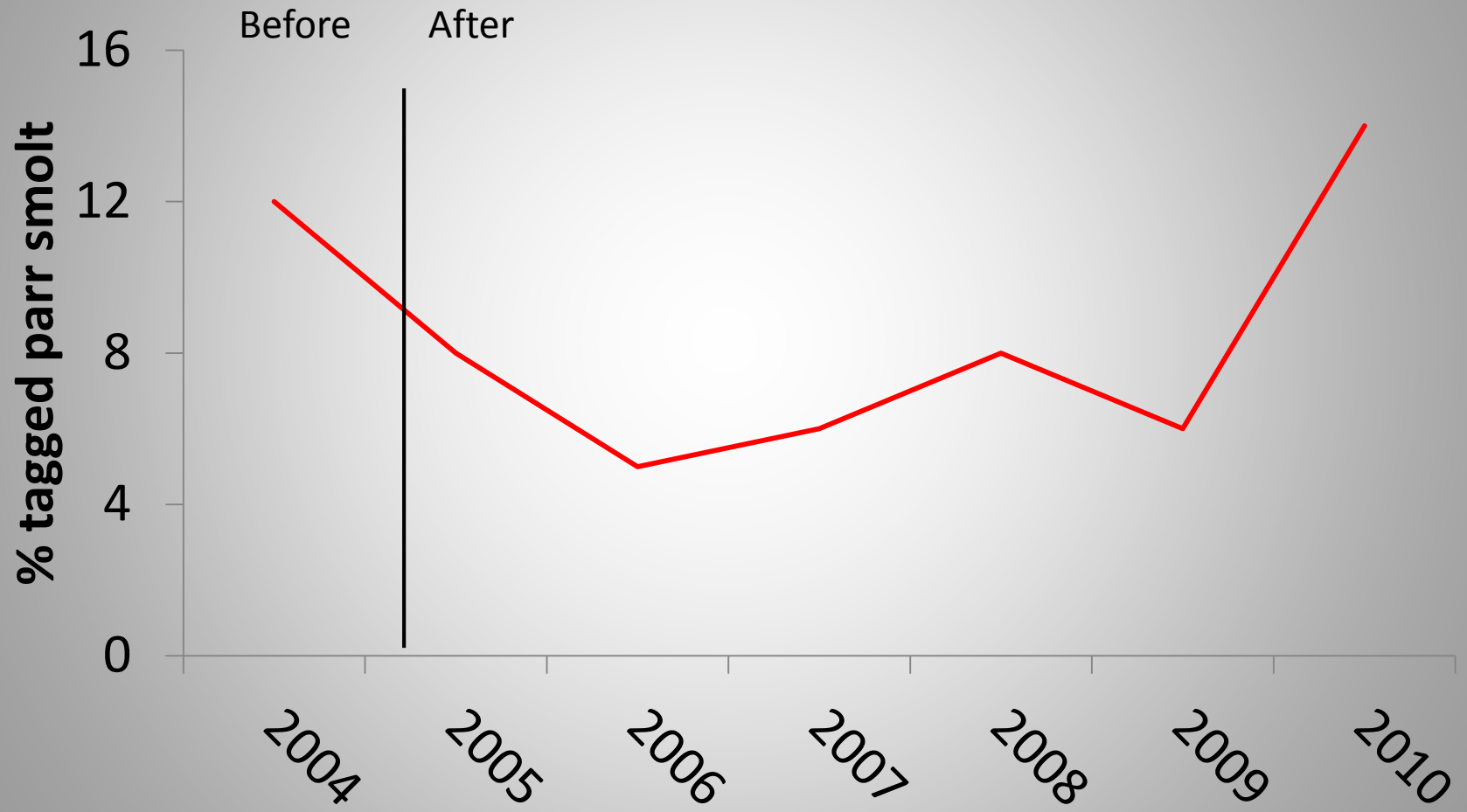


Results – Temporal Tests (sampling effect)

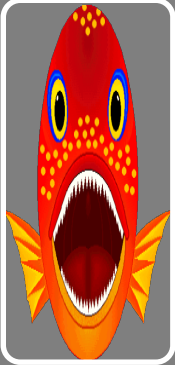
site	year	year	F_{ST}	Pval
UBR1	2008	2009	-0.003	0.253
UBR2	2008	2009	-0.004	0.880
UBR4	2008	2009	<-0.001	0.147
SFB	2008	2009	0.005	0.568



% smolt UBR1



Conclusions - Colonization



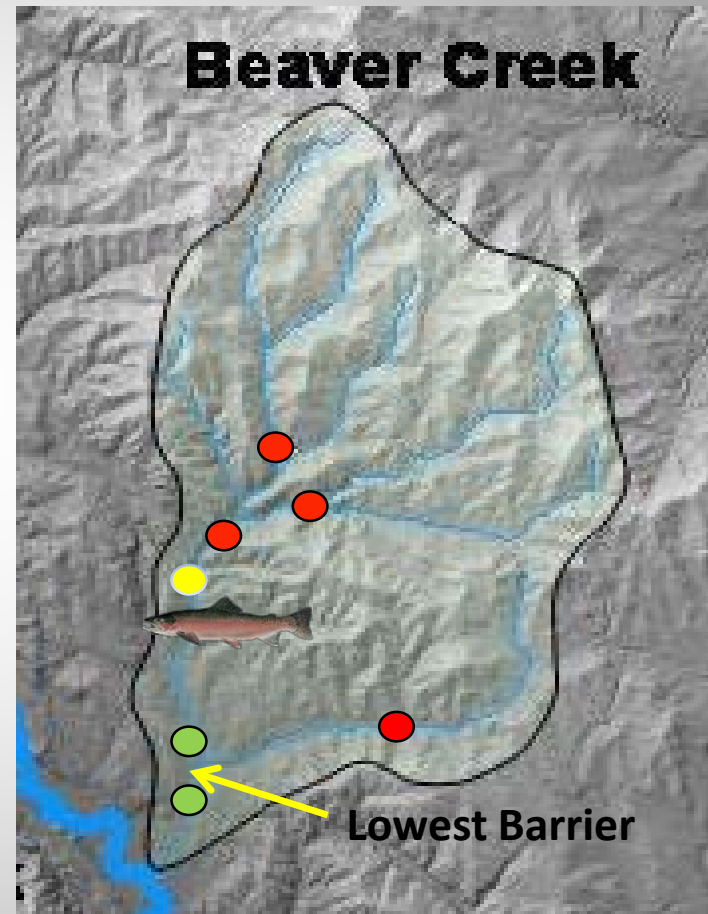
Before barrier removal

- Fragmented
- Smolts out, but no adult returns



After barrier removal

- Genetic shifts lowest site km 5
- Tag movement to middle site km 12
- Smolts out and adult returns



Conclusions – Indiv Success

- **Fluvial RBT** were key to re-colonization, gene flow and reserve of wild genotype
- **Hatchery** unsuccessful in early years of colonization
- **Phenotypes** of successful spawners shifted dramatically between 2005 and 2006
- Successful juvenile SH reared in the Methow R (or Wells Res) for **1 to 2 years** prior to smolt outmigration
- No clear relationship between number of offspring and returning adults



What is the **weakest link** in steelhead conservation?

- Phenotypes/genotypes under selection for adult survival and how these interact in time, space, density -> selection gradients
 - Interactions between rearing habitats and selection gradients influences fitness
- Aggressive work to understand, control or eliminate hatchery steelhead effects



Acknowledgements

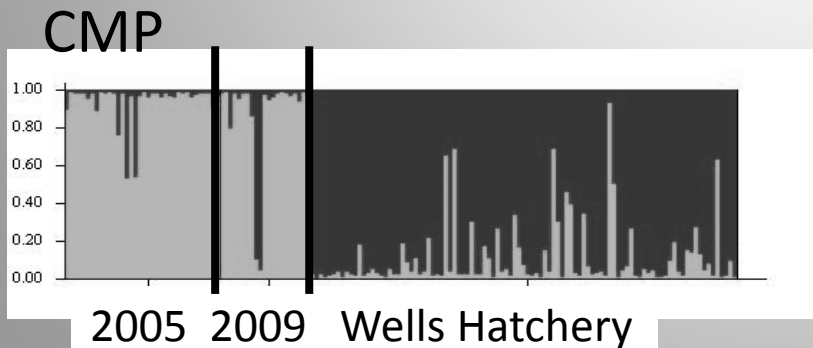
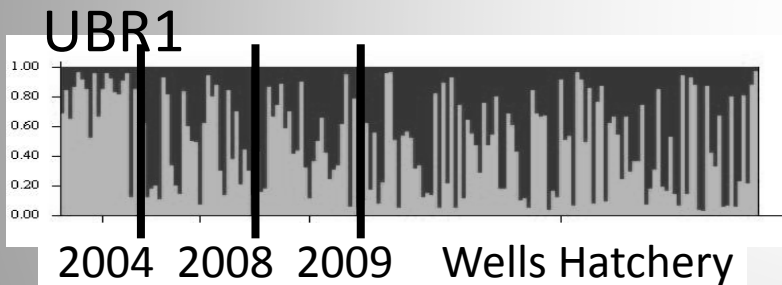
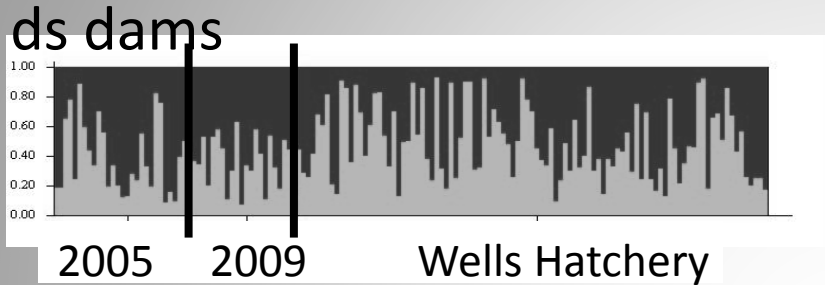
Funding provided by the Bureau of Reclamation

Data collection assistance (USGS) –
Kyle Martens, Wes Tibits, Brian Fisher

Lab analysis assistance Joyce Faler (Univ. of Idaho)

Coordination Greg Knott, Michael Newsom

Results - % Hatchery



Site	Before %	After %
DS Dams	40	35
UBR1	27	47
CMP	6	12

Gene Flow



Genetic Differentiation (F_{st})

	Fluvial	Wild Anad
Wild Anad	0.002 - ns	
Hatchery	0.006	0.004