

Genetic Comparisons Between Migrants And Residents *Oncorhynchus mykiss* From The Upper Yakima River

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Outline

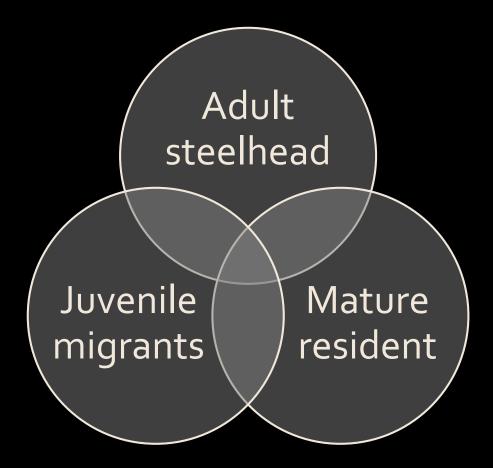
- Background/Concept
- Project Description
- Genetic Results
- Conclusions/ Future Applications

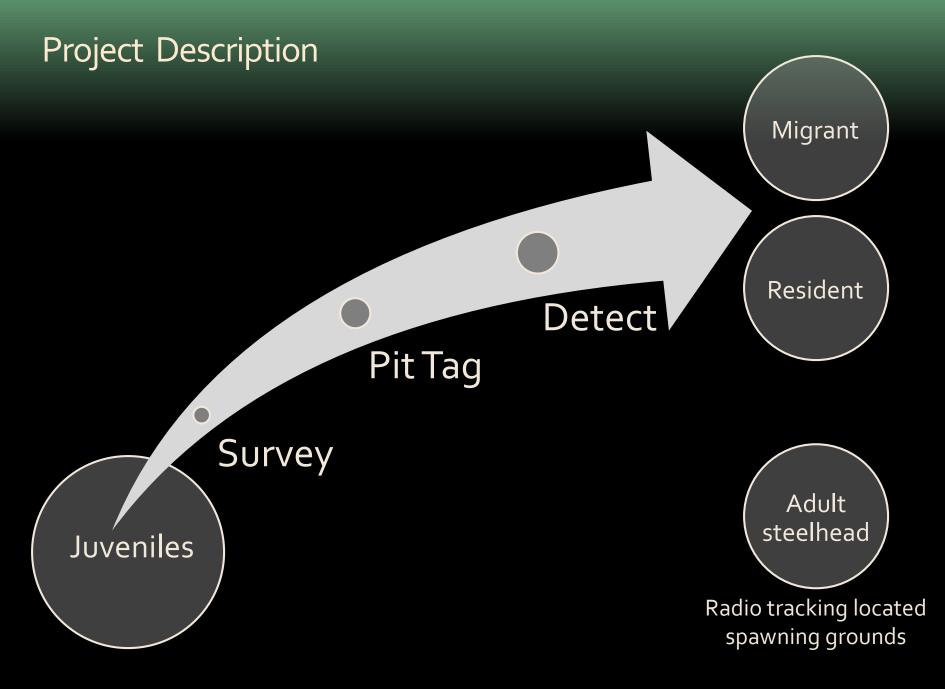
Background

- Previous genetic studies have documented genetic differences among Yakima River steelhead populations
- Genetic studies have generally found little evidence of genetic interactions between steelhead and non-native hatchery *O. mykiss* (i.e., rainbow trout) stocked in the Yakima Basin

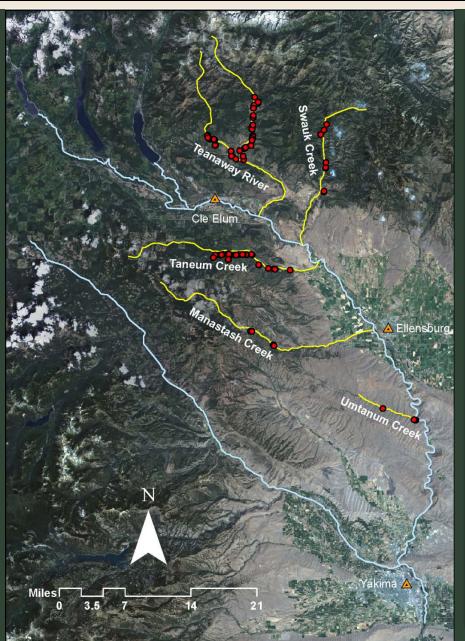
 Limited information is available regarding the genetic affinities between steelhead and native resident *O. mykiss* in the Yakima River. Concept

Investigate the genetic and geographic relationships among *O. mykiss* life history forms





Collections



Population	Sample size
'06 Teanaway Migrants	27
'07 Teanaway Migrants	31
'08 Teanaway Migrants	18
Teanaway Spawners	130
'06 Teanaway Residents	18
'07 Teanaway Residents	137
'08 Teanaway Residents	106
'08 Swauk Residents	31
'07 Taneum Migrants	9
Taneum Spawners	16
'06 Taneum Residents	19
'07 Taneum Residents	24
'08 Taneum Residents	49
'06 Manastash Residents	8
'08 Umtanum Residents	19

Genetics Analysis

Genetic Analysis

- Genetic diversity
- Allelic associations

Hardy-Weinberg equilibrium Linkage disequilibrium

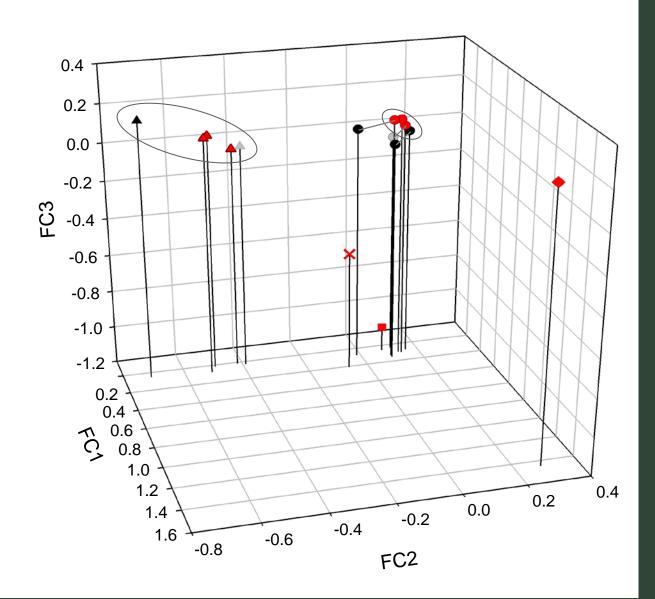
Collection comparisons

Overall genetic differentiation
Factorial correspondence analysis

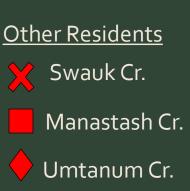
Genetic Analysis - Summary

- Genetic diversity high 76% to 83%
- Random associations of alleles within and between genetic loci
- Generally, collections from the same tributary had statistically equivalent allele frequencies and F_{ST} that were small or equivalent to zero.
- Generally, collections from different tributaries had statistically different allele frequencies and F_{ST} statistically significant from zero

Factorial Correspondence Analysis







Migrants

Residents

Concluding Remarks

Conclusions

- All three life history stages (i.e., residents, migrants, and anadromous adults) from the same location were more genetically similar than the same life history stage was between tributaries
- Residents from the five tributaries were genetically differentiated
- Upper Yakima River O. mykiss were genetically differentiated, where collection location appeared more informative regarding genetic affinity than life history category

Applications

- Acknowledge population structuring
- Regional context SPAN standardized genetic baseline Fishery assessment Escapement estimation Viability analysis

- Residualization
- Interactions with cutthroat trout (O. clarki)
- Geospatial analysis

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Steelhead information

Yakama Nation