# COMPARATIVE GENOMICS OF RAINBOW TROUT:

are genes associated with migration conserved between populations?



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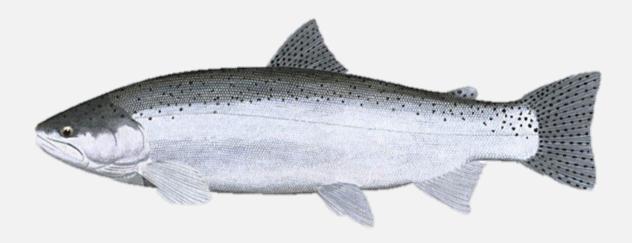
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**Texas Christian University** 

# ONCORHYNCHUS MYKISS

- 2 ecotypes
- Morphological distinction
- Conservation implications
- Économical importance

#### Steelhead Trout



#### Rainbow Trout



#### Goal

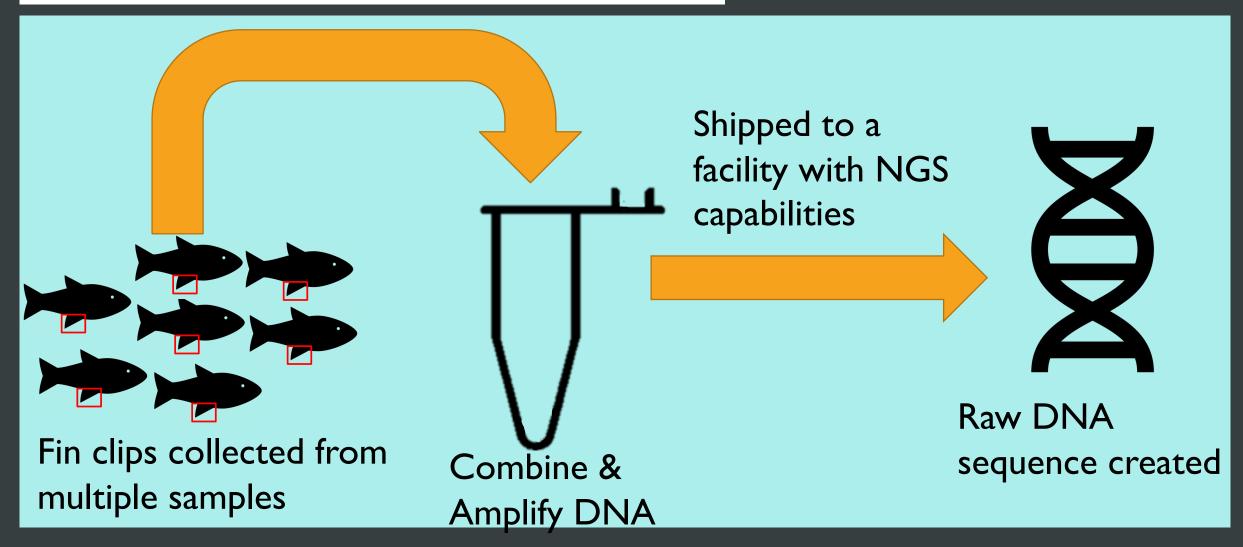
Evaluate the genetic basis of migration in 2 populations of rainbow trout from Sashin Creek, AK and Little Sheep Creek, OR

# **Objectives**

- Utilize Pooled sequencing to obtain genomic information from migrant and resident trout from each site
- Identify alleles related to migratory or resident ecotypes within these populations
- Determine if associated alleles are shared in multiple populations

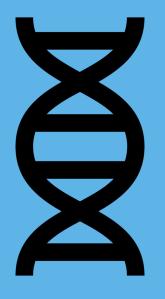
#### POOLED SEQUENCING

Repeat for each of the 6 sample populations

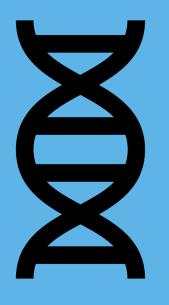


## **SEQUENCING RESULTS**

#### **Migrant Sequences**



Sashin



Little Sheep

#### **Resident Sequences**

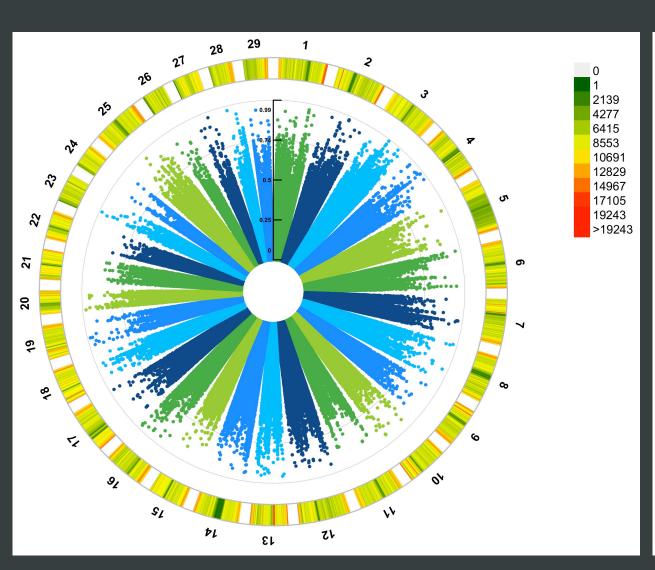


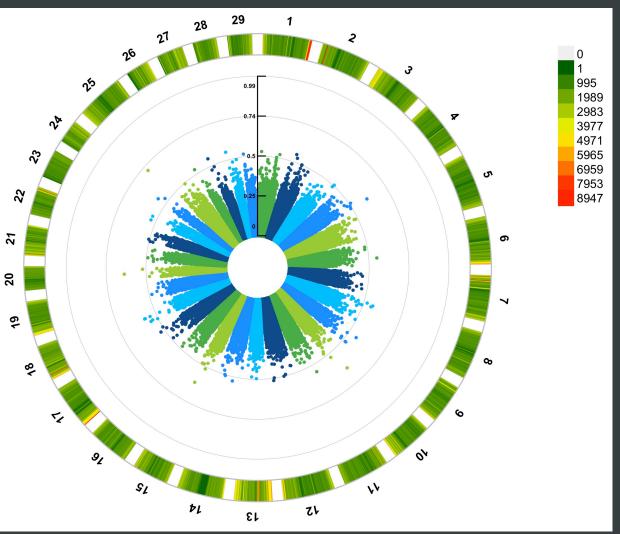
Sashin



Little Sheep

# F<sub>ST</sub> ESTIMATES





Sashin Creek

Little Sheep Creek

# Positions with shared ecotype-dependent alleles in Sashin and Little Sheep Creek

CHR	LSC F <sub>ST</sub>	Sas F <sub>ST</sub>	Gene (if present)	BP
I	0.297	0.509	phosphatidylinositol-specific phospholipase C, X domain containing I	13331
3	0.316	0.684	-	74564628
4	0.275	0.930	leptin receptor	34759942
5	0.278	0.520	DnaJ homolog, subfamily C, member 6	80722208
8	0.416	0.605	tumor protein D53 homolog	17055130
25	0.289	0.510	-	66224036

## **FINDINGS**

- Pooled sequencing provided a fine-scale approach to comparing genomes in both Sashin and Little Sheep Creek
- Sashin and Little Sheep Creek did not show the same degree of differentiation
- There are areas within the genome that show similar selection signatures in both populations
- More populations would be necessary to show the degree and extent of these findings

#### **ACKNOWLEDGEMENTS**



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