

Genomic time-series data reveal signatures of selection in wild redband trout populations



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Redband trout mechanisms research

- This research identified links between genetic and phenotypic diversity to allow predications of adaptive responses of populations to environmental change.

ORIGINAL ARTICLE

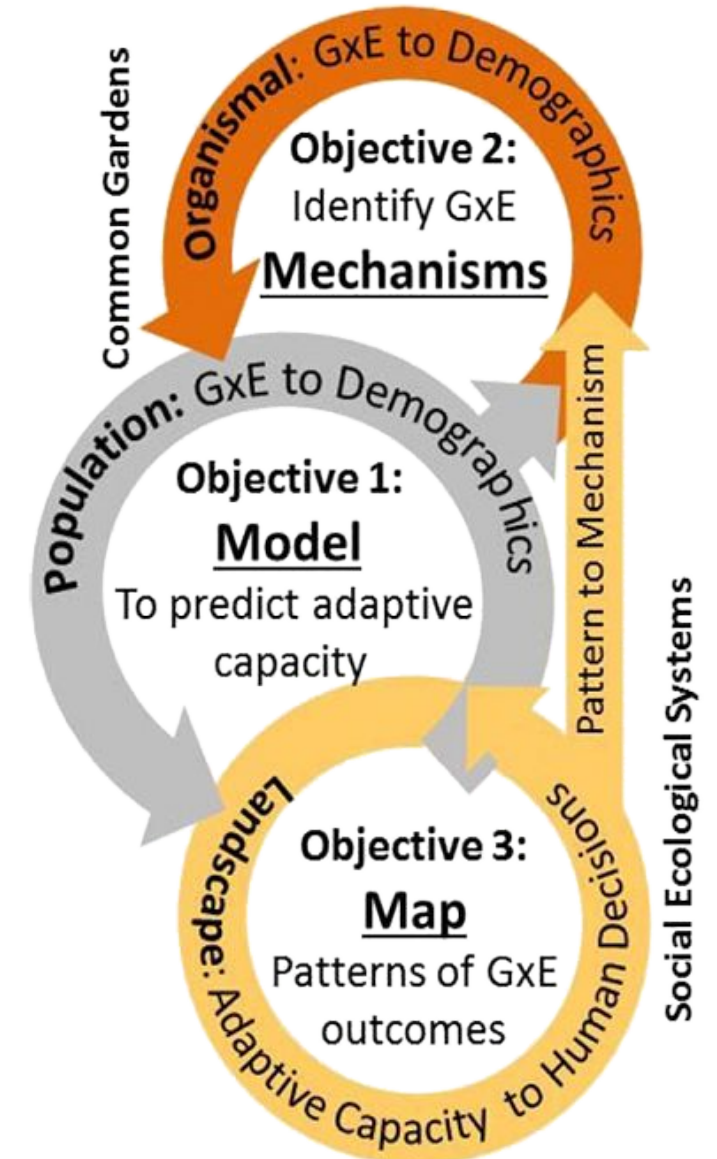
MOLECULAR ECOLOGY WILEY

cerk - Whole genome resequencing reveals genomic regions associated with thermal adaptation in redband trout
protection of cardiovascular systems during heat stress

greb1 - Whole genome resequencing identifies local adaptation associated with environmental variation for redband trout
associated with migration timing in anadromous steelhead and chinook

rock1 - Whole genome resequencing identifies local adaptation associated with environmental variation for redband trout
associated with migration timing in anadromous steelhead and chinook

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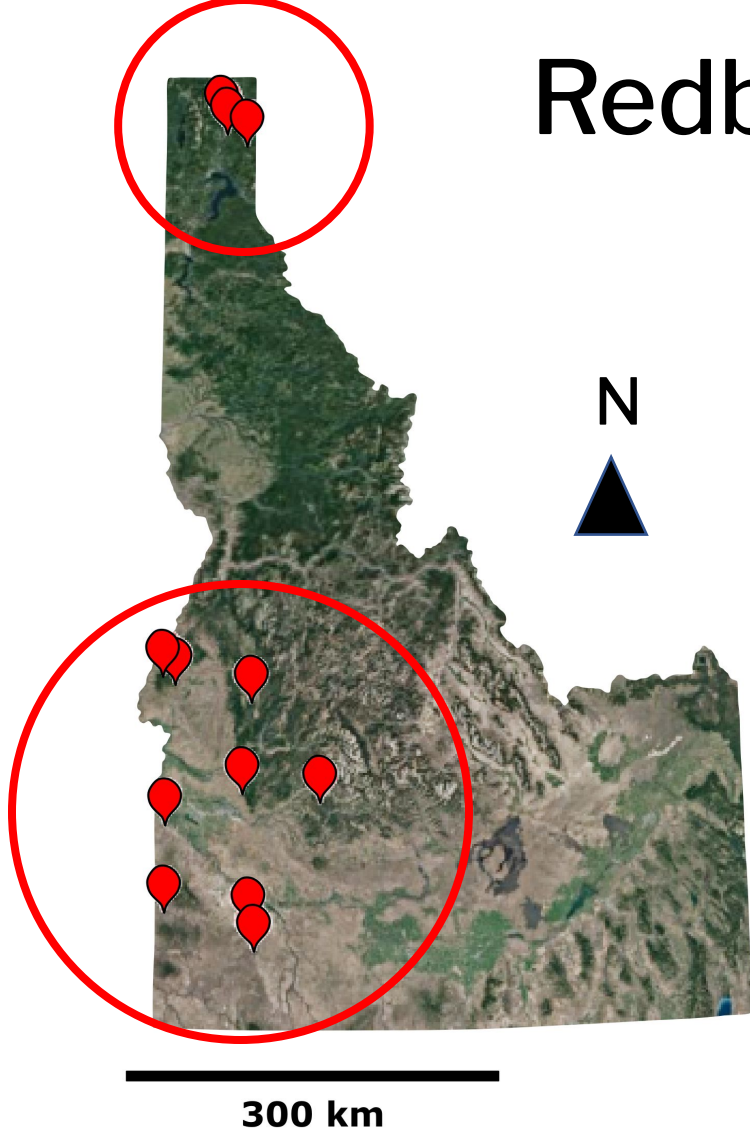


Do genomic time series data show signatures of selection in wild populations?

Research objectives

- (1) Identify temporal changes in allele frequencies due to natural selection.
- (2) Characterize overlap between the genomic regions that we found to exhibit signatures of selection and those identified by previous redband trout mechanisms work.
- (3) Identify correlations between temporal fluctuations in allele frequencies and environmental variables.

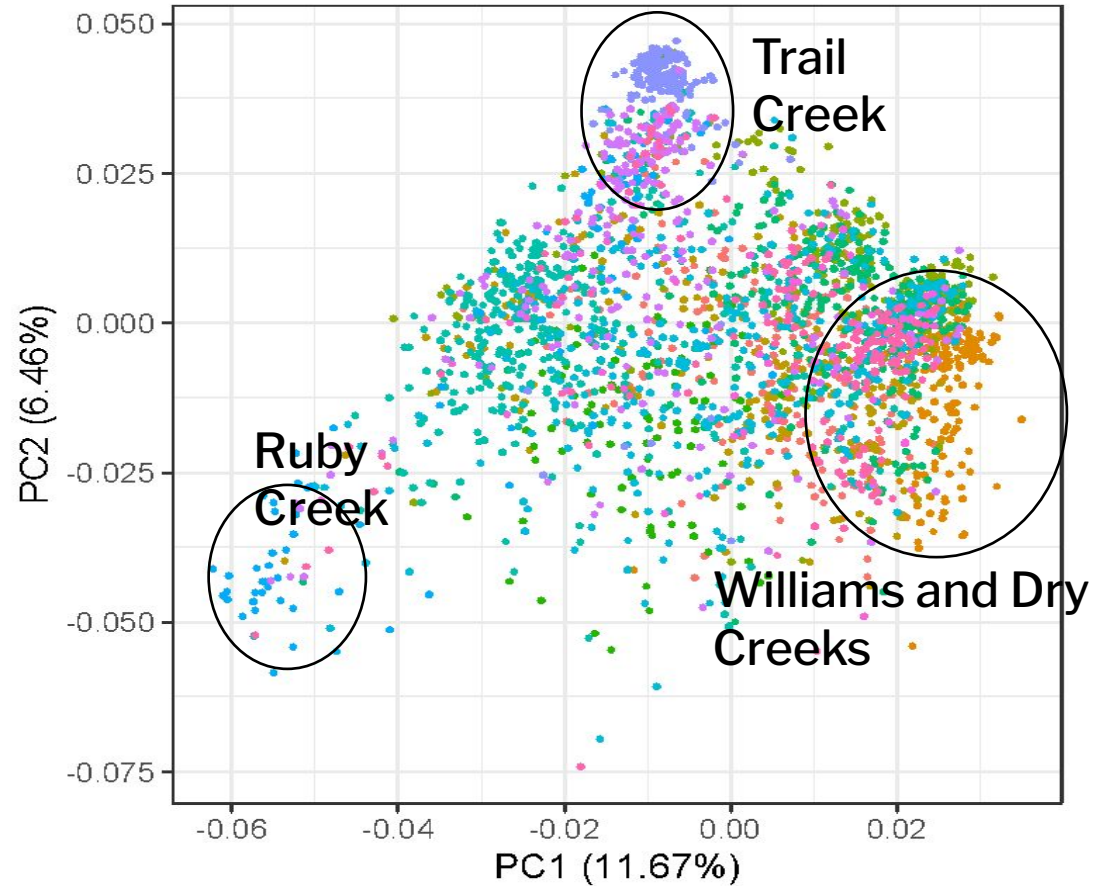
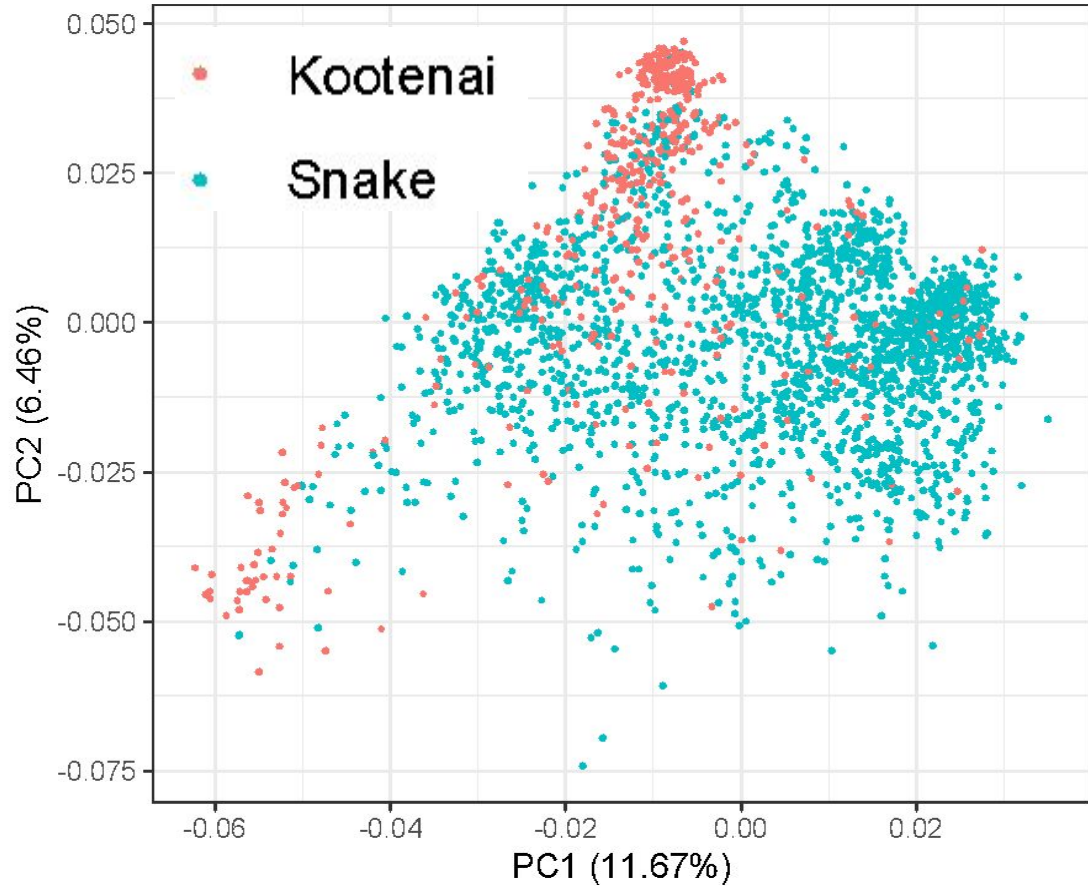
Redband trout study populations



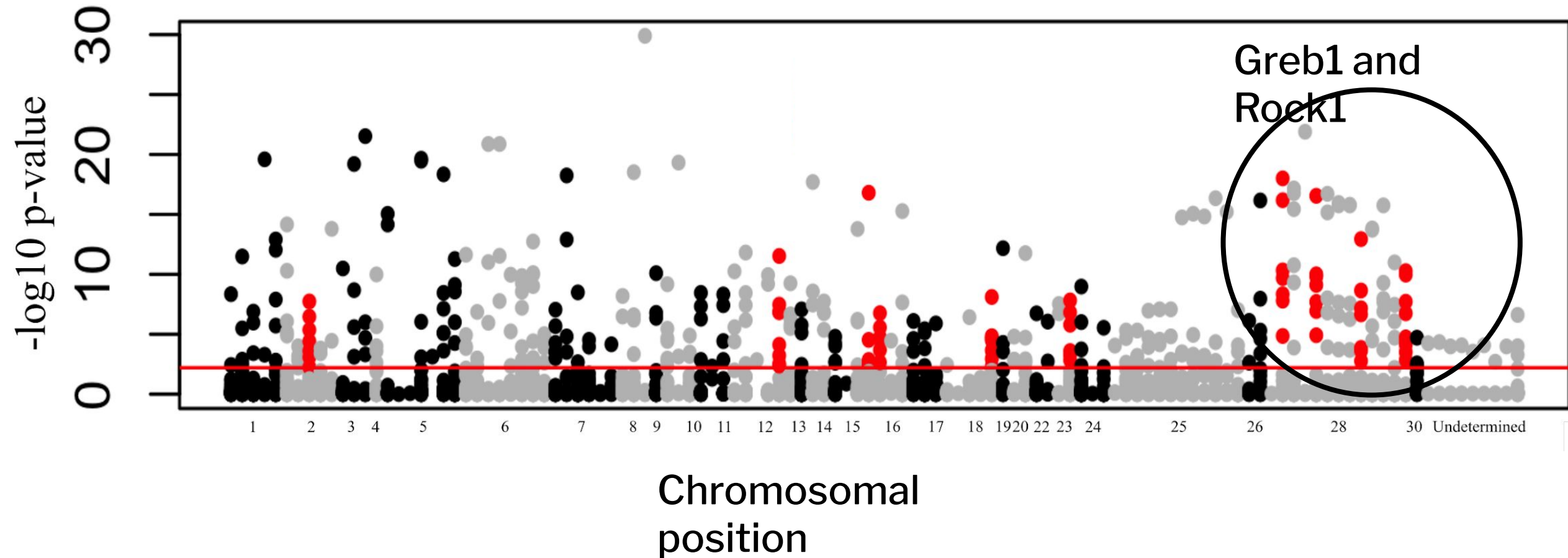
Population	Years sampled																							
	98	99	00	01	02	03	04	05	06	07	08	09	10	11	12	13	14	15	16	17	18	19	20	21
Big Jacks Creek	■				■																		■	■
Dry Creek											■				■				■				■	■
Duncan Creek				■		■																■	■	
Fawn Creek								■						■				■	■			■	■	
Jump Creek				■																				■
Keithley Creek							■						■			■		■	■			■	■	■
Little Jacks Creek	■												■					■	■			■	■	
Mann Creek							■															■	■	■
Ruby Creek									■													■		
Callahan Creek									■													■	■	■
Trail Creek																						■	■	■
Whiskey Jack Creek		■																				■		
Williams Creek						■																■	■	■

- SNP panel: 243 neutral markers and 129 “adaptive” markers
- We generated SNP data for 2648 individuals

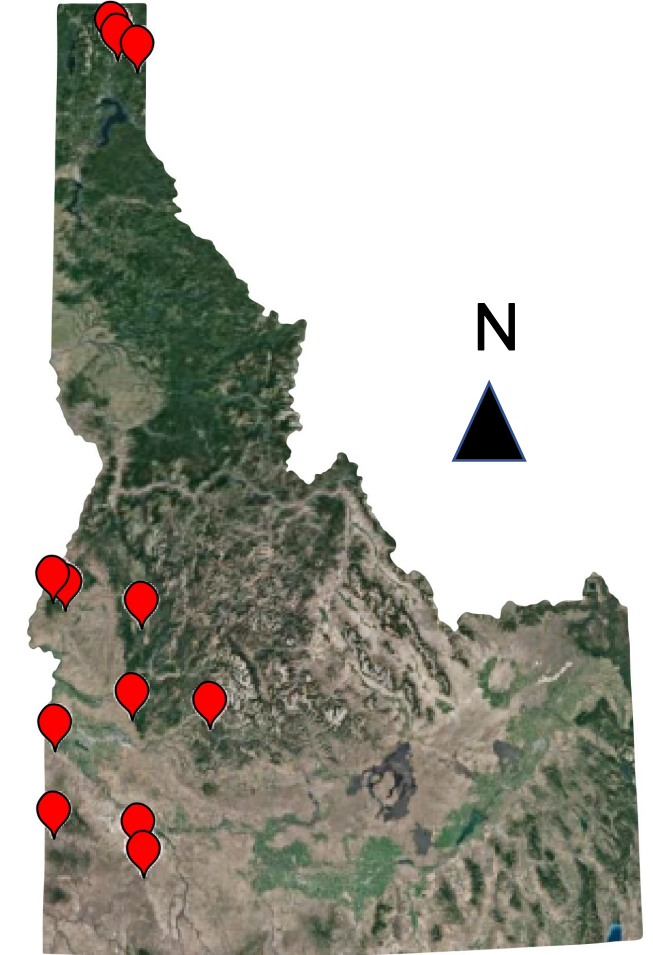
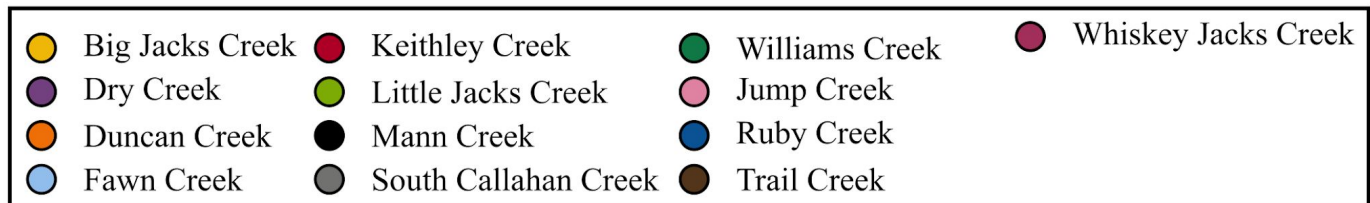
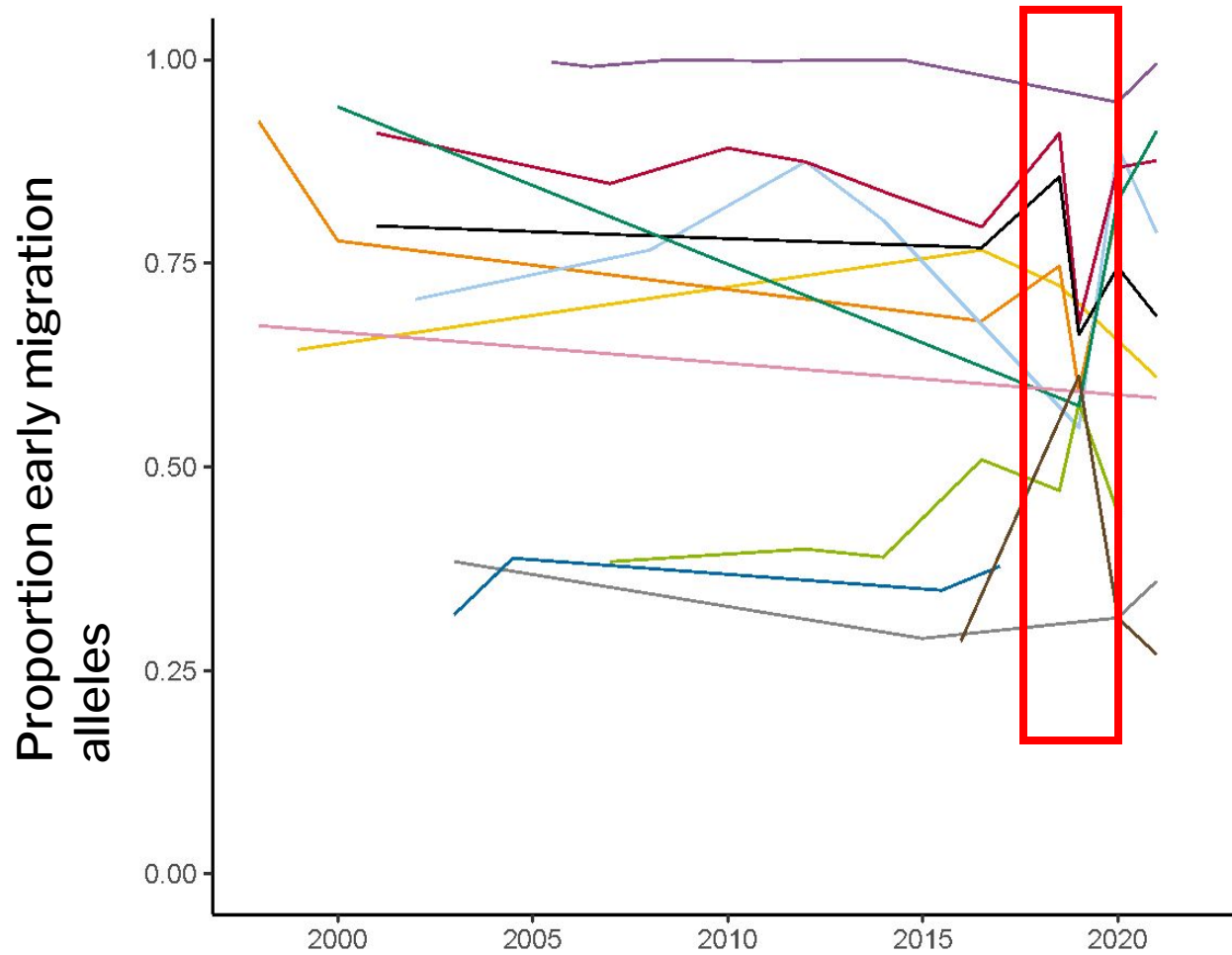
Genotype PCAs of adaptive loci show genetic differentiation between drainages and populations



We identified statistically significant signatures of selection in wild redband trout!

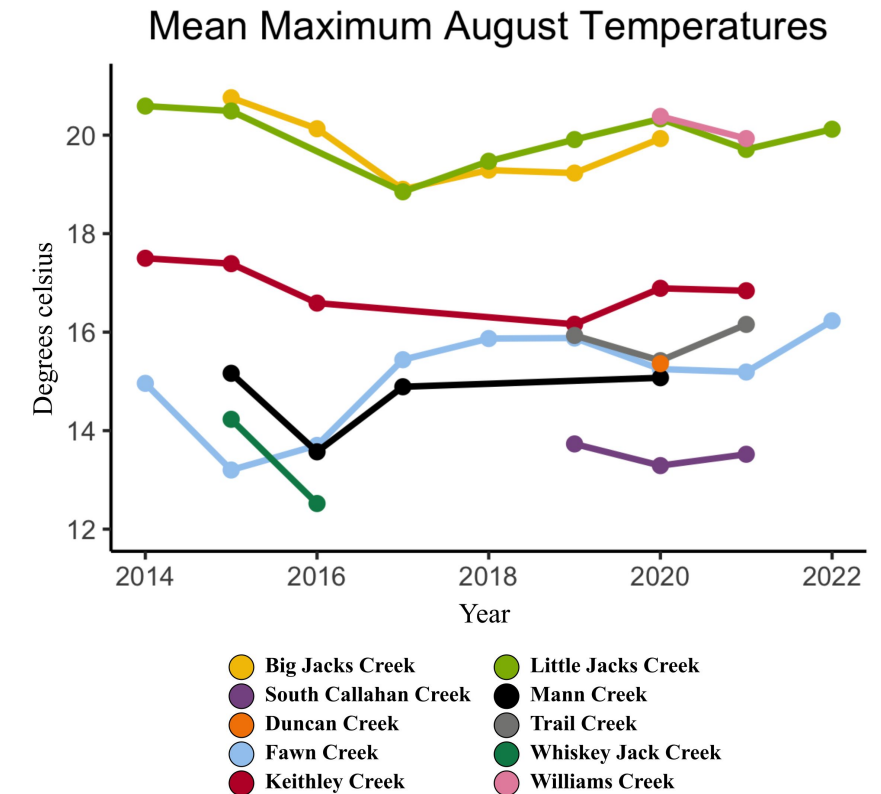


rock1 and *greb1* temporal dynamics



Are environmental fluctuations driving genomic changes in redband trout populations?

Variable category	Significant association?
Spring maximum temperatures	No
Summer maximum temperatures	No
Timing of spring temperature increases	No
Droughts	No
Timing of peak spring water flows	No
Amount of spring water flow	No
Minimum summer water flows	No



Summary and future directions

- The time-series dataset revealed several SNPs under selection in wild redband trout populations
- Kootenai and Snake River Basins exhibit distinct temporal patterns of genetic change
- *greb1* and *rock1* appear to be major targets of selection in redband trout populations, resulting in major interannual allele frequency changes
- The environmental forces responsible for the fluctuations remain unclear and will be the focus of our ongoing work.

