

The genetic and evolutionary basis of phenotypic variation in Pacific salmon informs conservation and management

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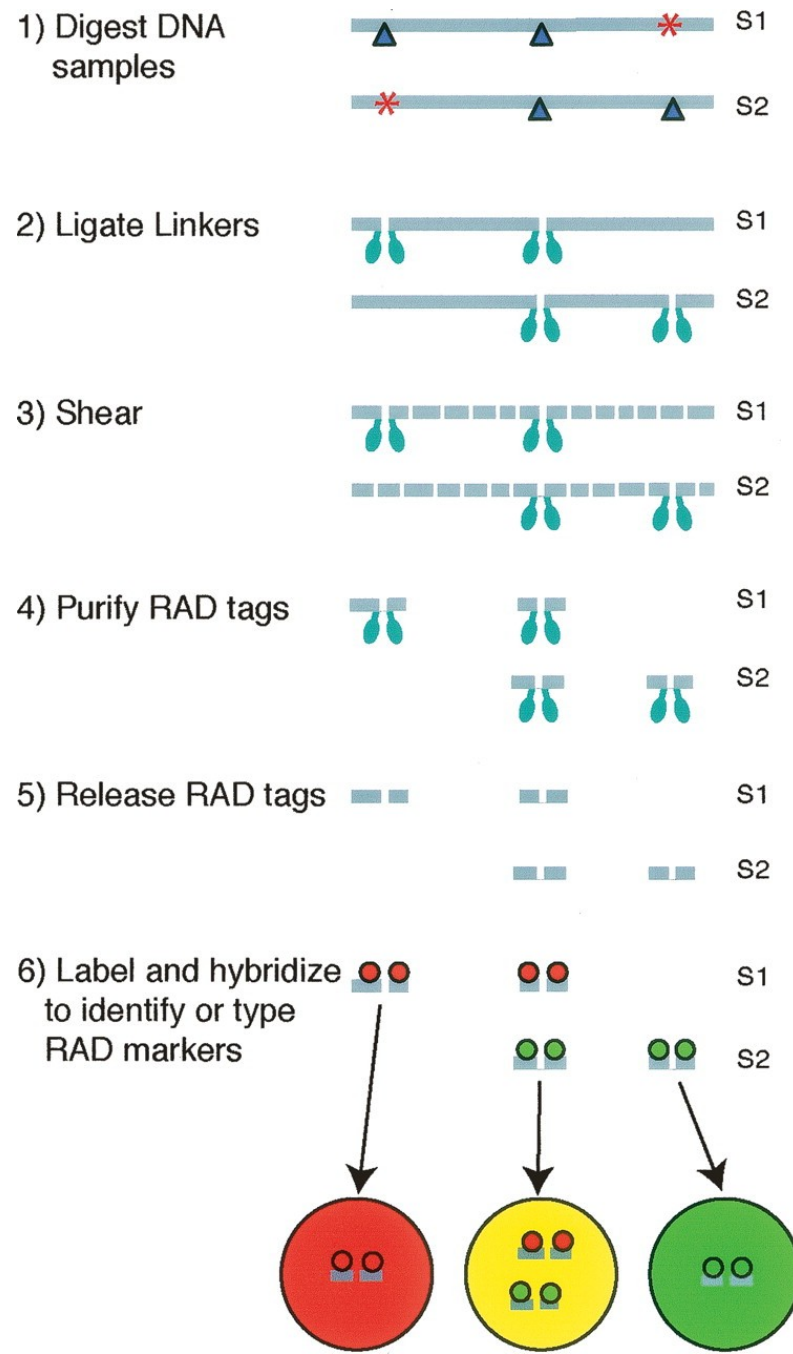
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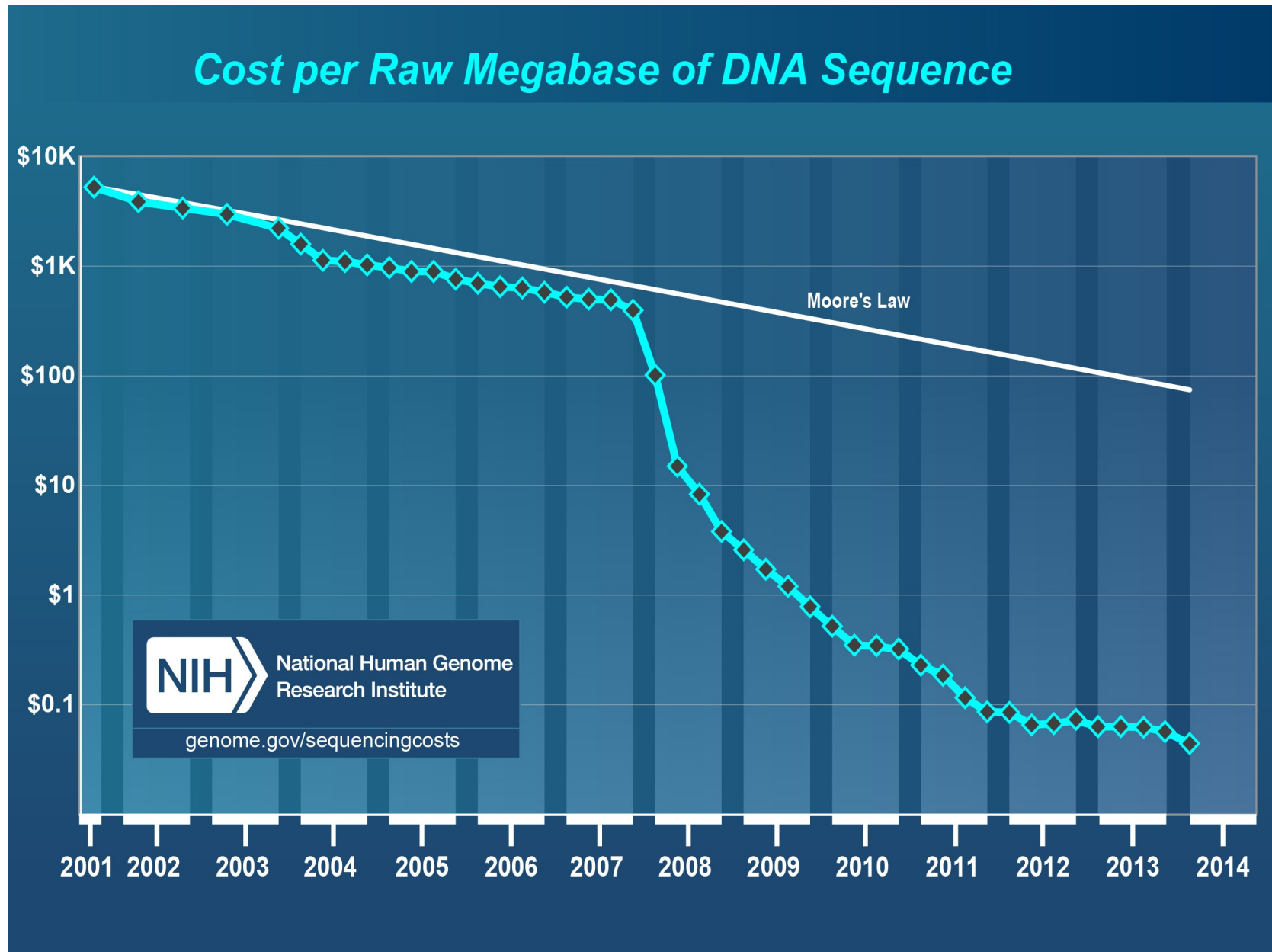
Genomics has enabled explorations into the genetic and evolutionary basis of natural phenotypic variation.

“Over the past century, much has been learned about the genetic basis of [phenotypic variation] in a handful of model organisms. In addition, a large pool of phenotypic variation exists throughout the amazing diversity of the millions of species outside of the laboratory, the genetic basis of which has been relatively unexplored. Methods that facilitate the rapid identification of the genes that underlie ... natural phenotypic variation will help to provide a much deeper understanding of many biological processes.”

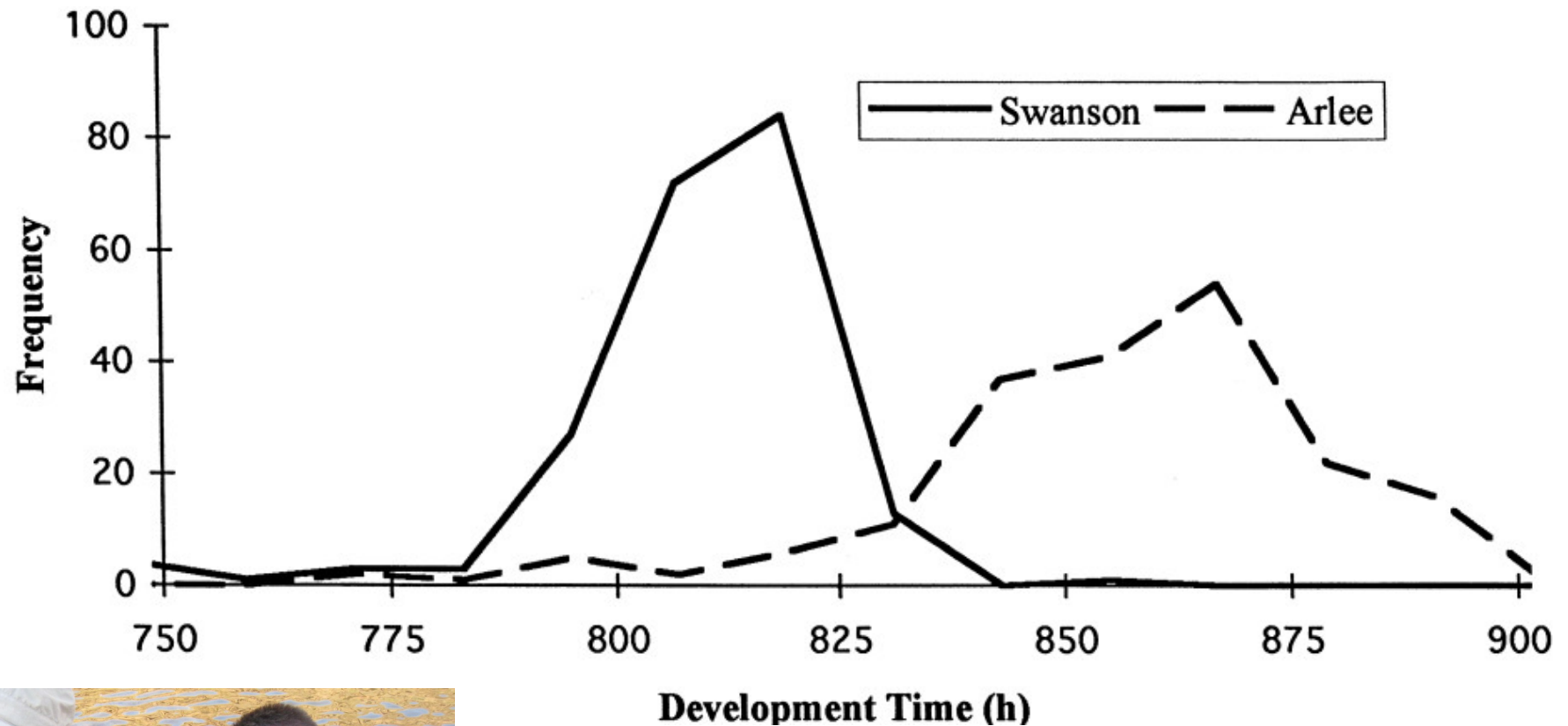
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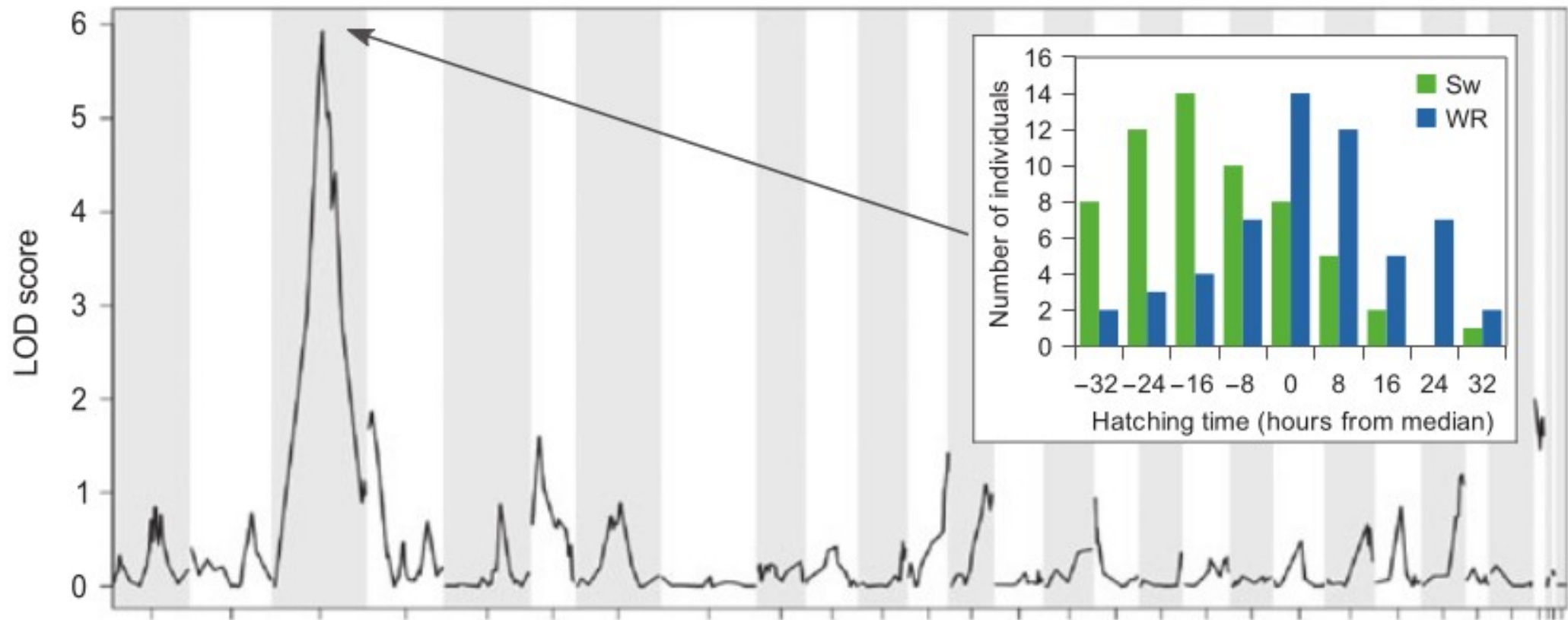
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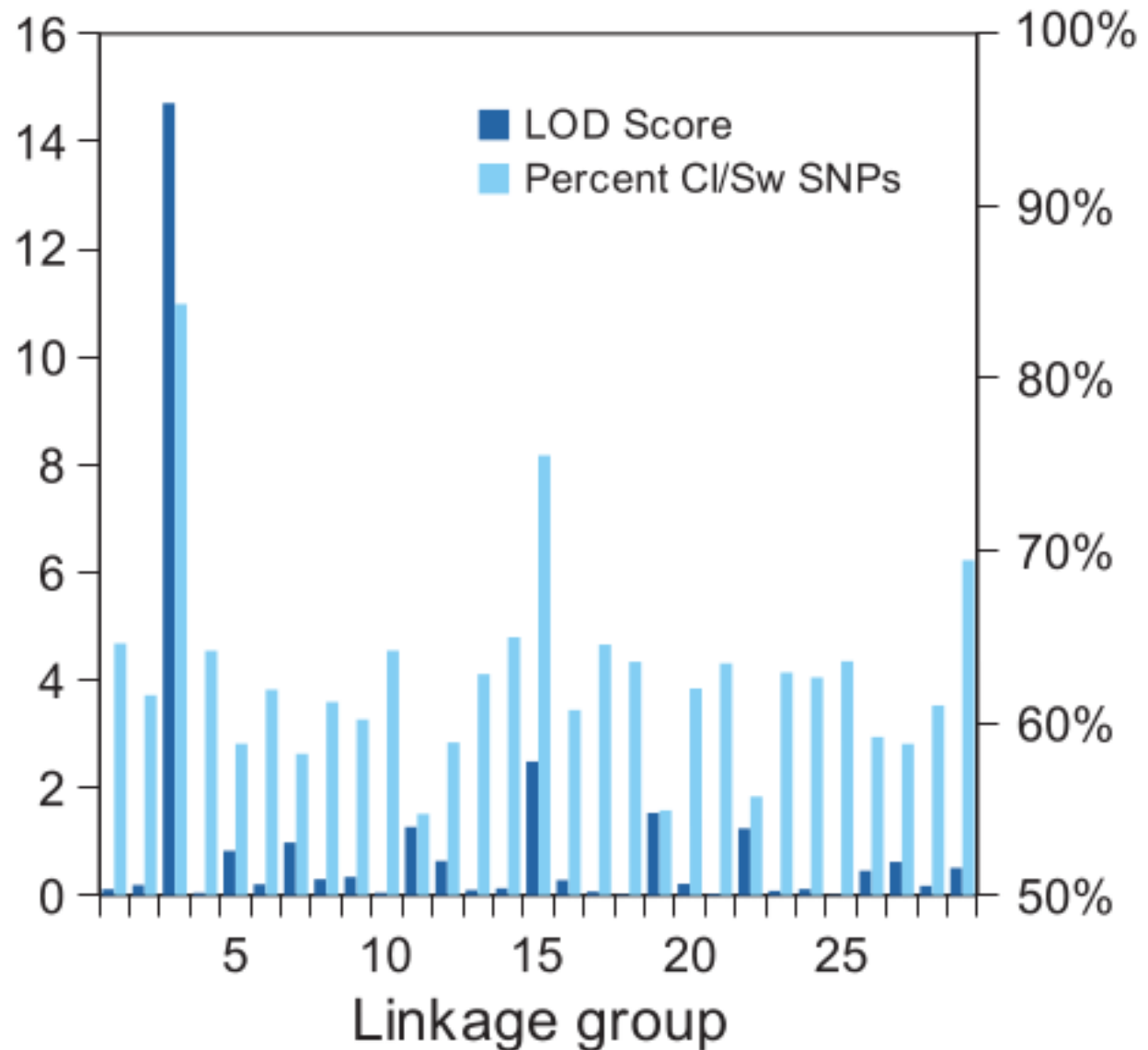
My first genomics study in salmonids explored development rate variation in rainbow trout.



We found a single major effect locus for development rate on chromosome 5.



A conserved haplotype was responsible for rapid development rate in geographically distant populations.



We predicted this evolutionary mechanism would be common and discussed its conservation implications.

“Parallel adaptation is common [in Pacific salmon] with two classic examples [being] beach and stream spawning within sockeye and adult run-timing variation within chinook and steelhead. ... Based on our results and the fact that anadromy could facilitate the flow of genetic material over great distances, we predict that most cases of parallel adaptation in anadromous salmonids will be achieved through the repeated utilization of the same adaptive alleles... This hypothesis can be readily tested using genomic technologies similar to those presented here.”

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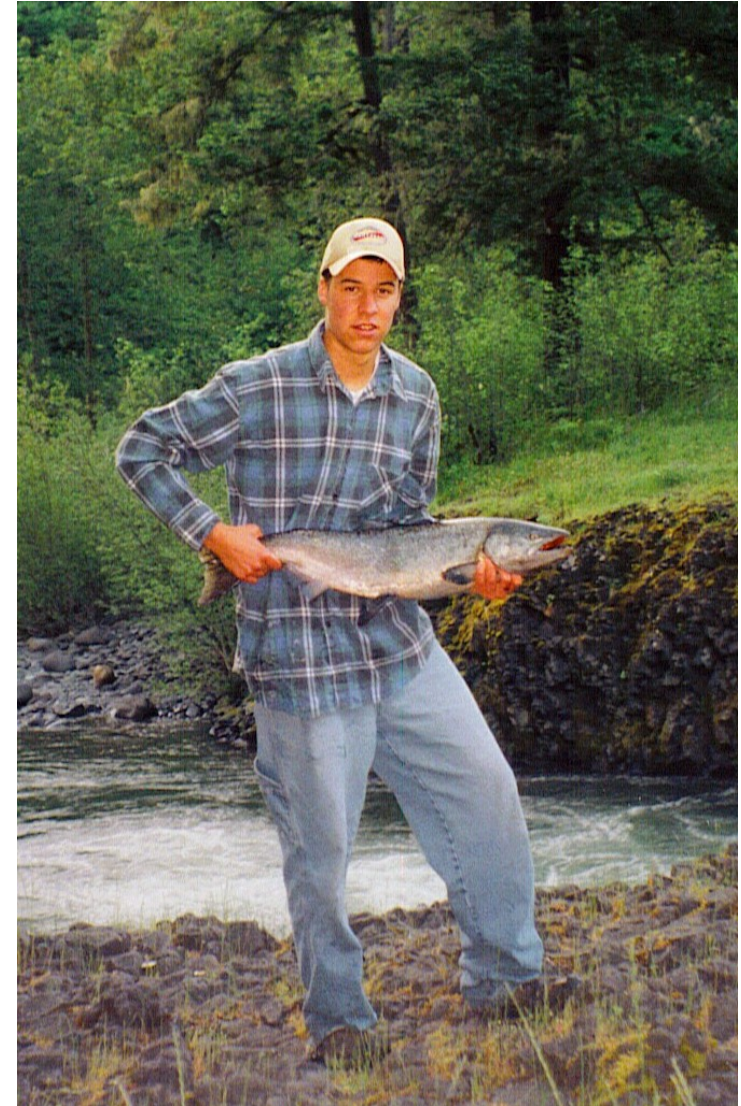
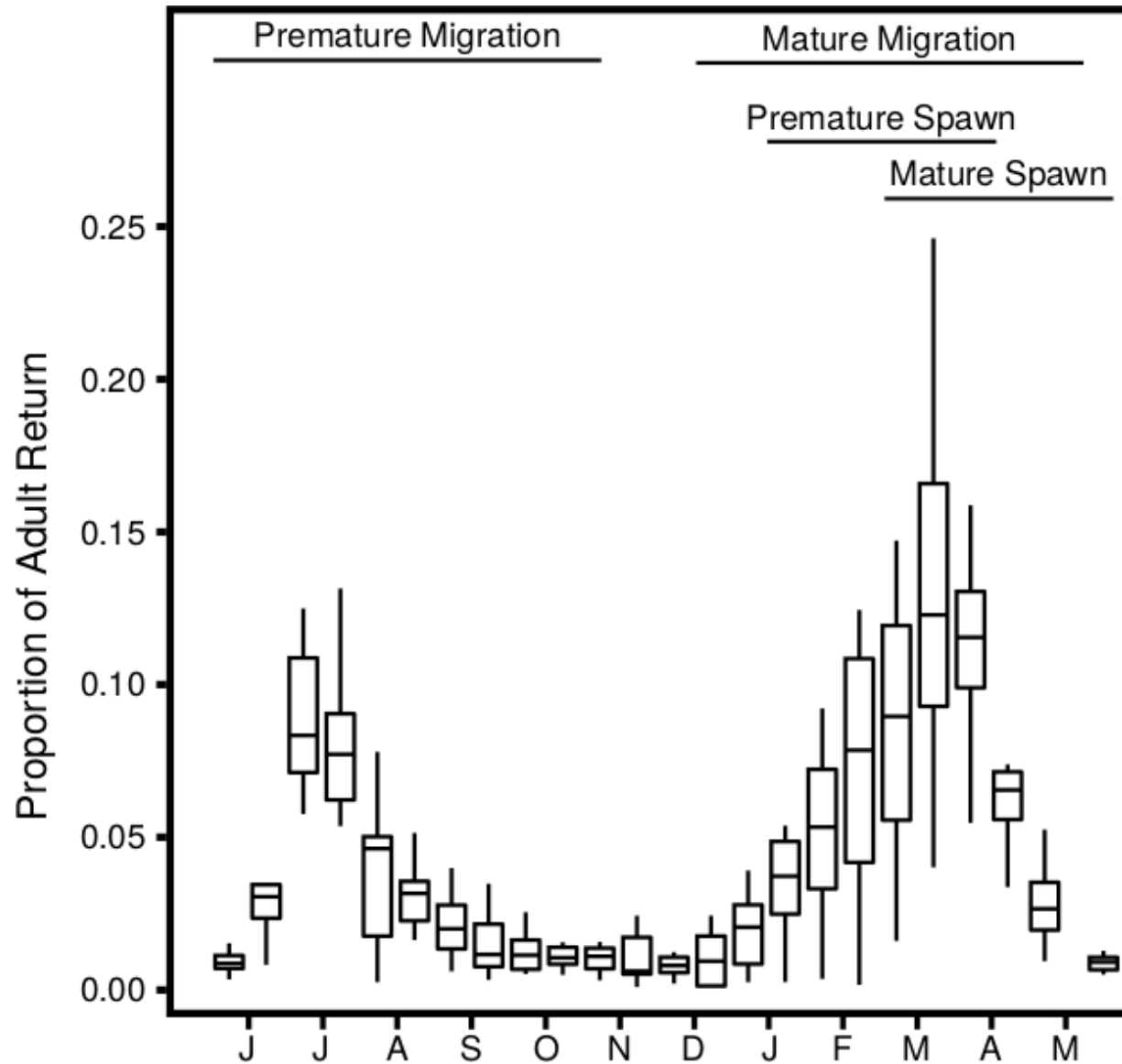
“The repeated use of adaptive genetic variation across distant geographical areas also underscores the importance of conserving populations throughout a species range for the future adaptability of that species. Particular populations could serve as reservoirs for alleles that become important for the successful adaptation of other populations upon environmental changes. For example, southern populations probably contain alleles that confer adaptation to warmer conditions, and these alleles could be [used] by more northern populations as temperatures increase. Unfortunately, many southern populations are already extinct and others too depressed to provide adequate stray-based gene flow. Thus, the extinction or depression of some populations could hinder the future adaptability of others.”

A conserved haplotype controls parallel adaptation in geographically distant salmonid populations

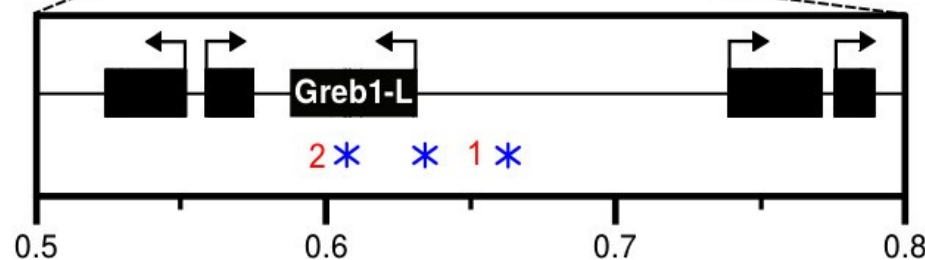
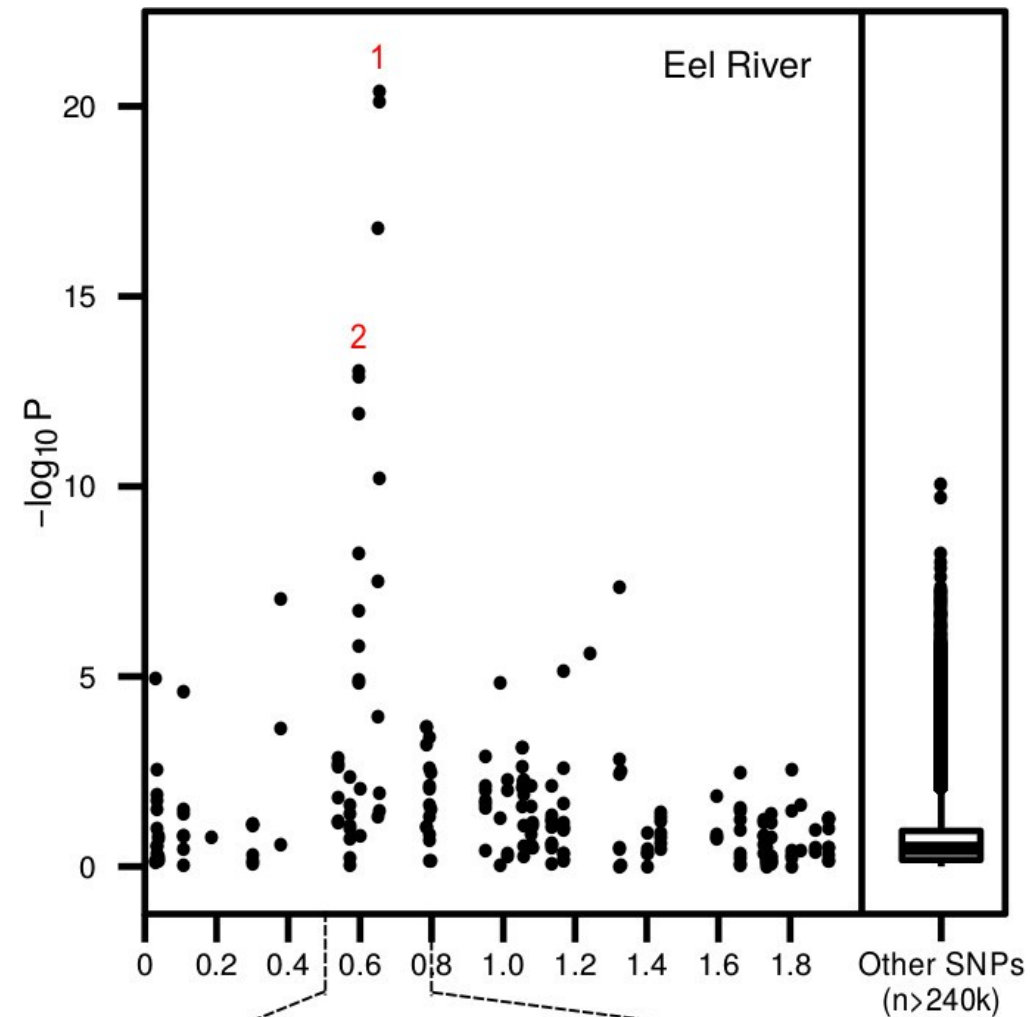
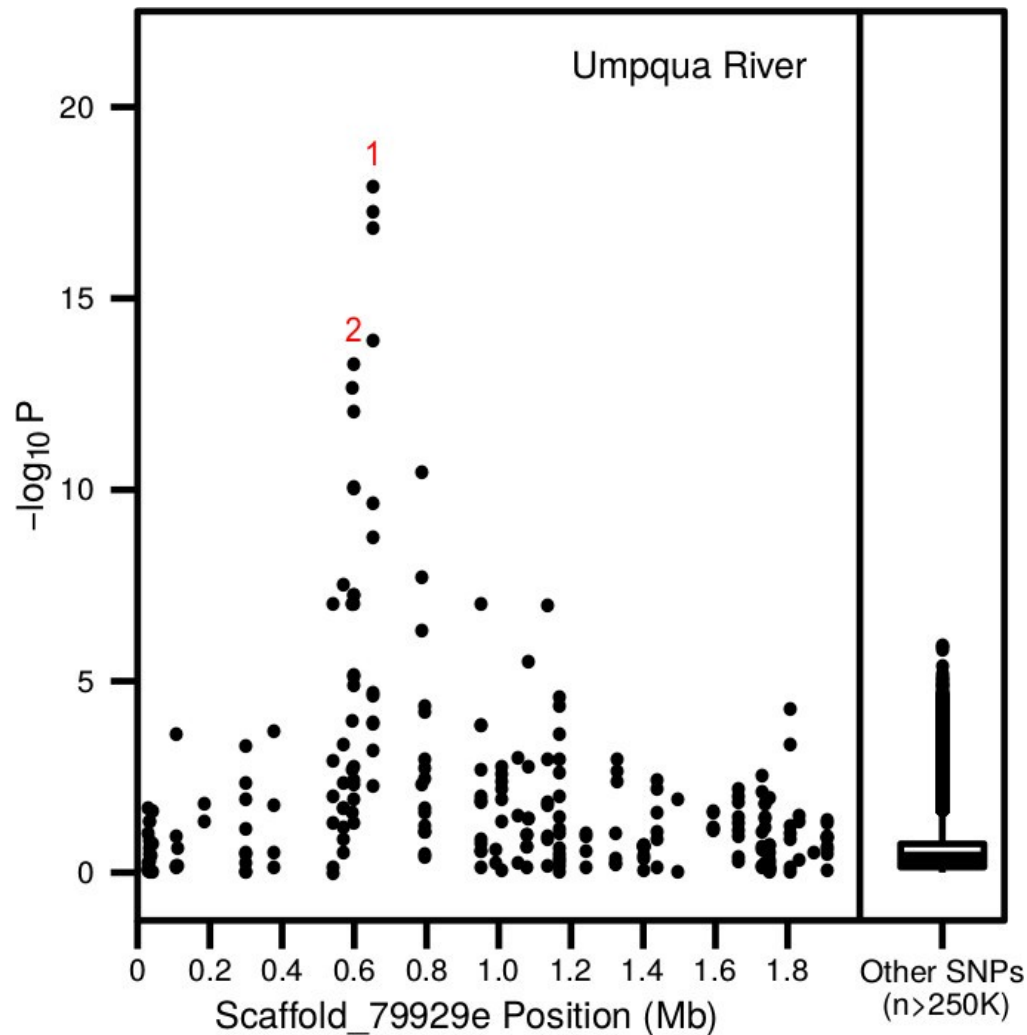
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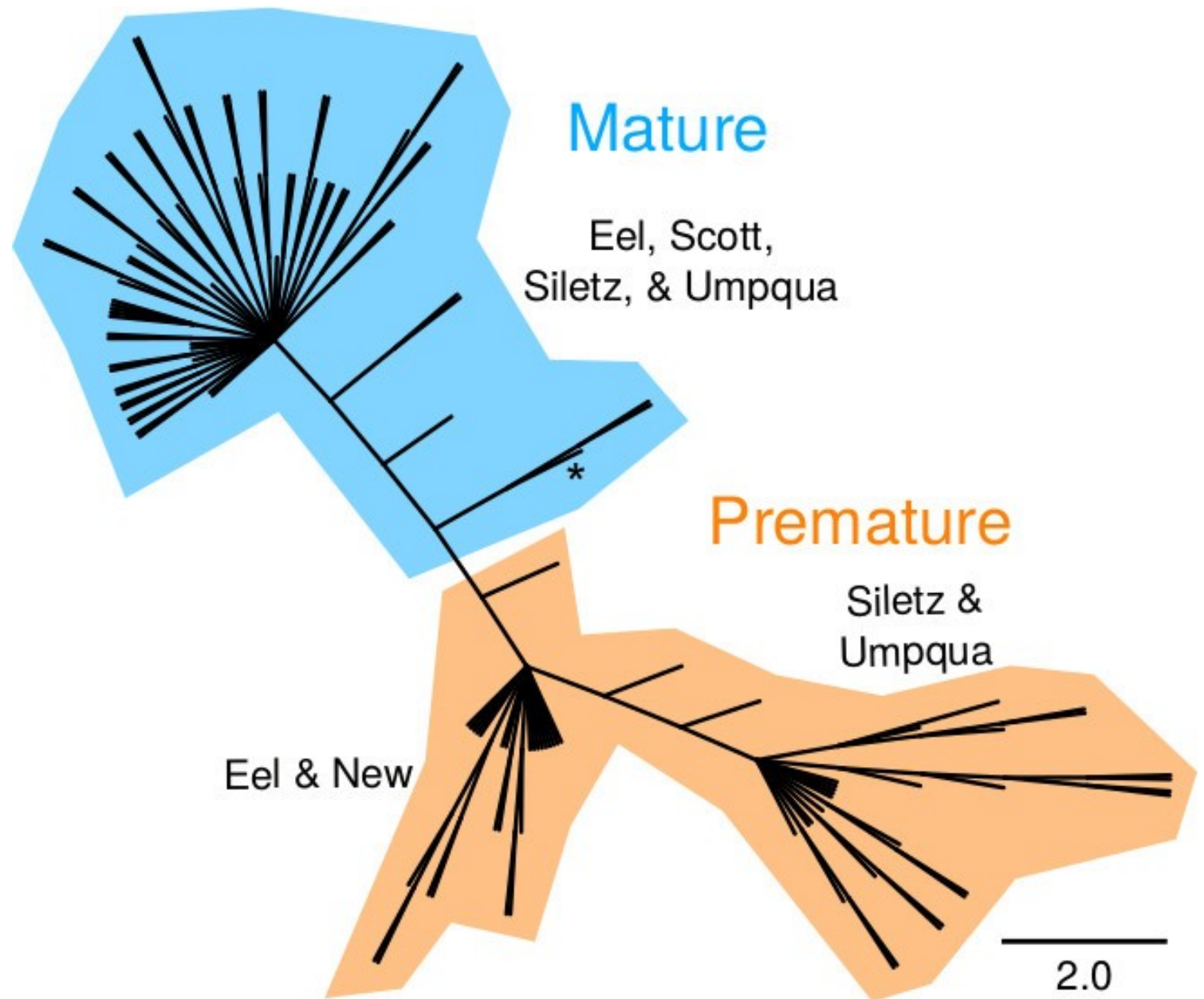
My new lab at UC Davis decided to focus on run-timing variation in Chinook and steelhead.



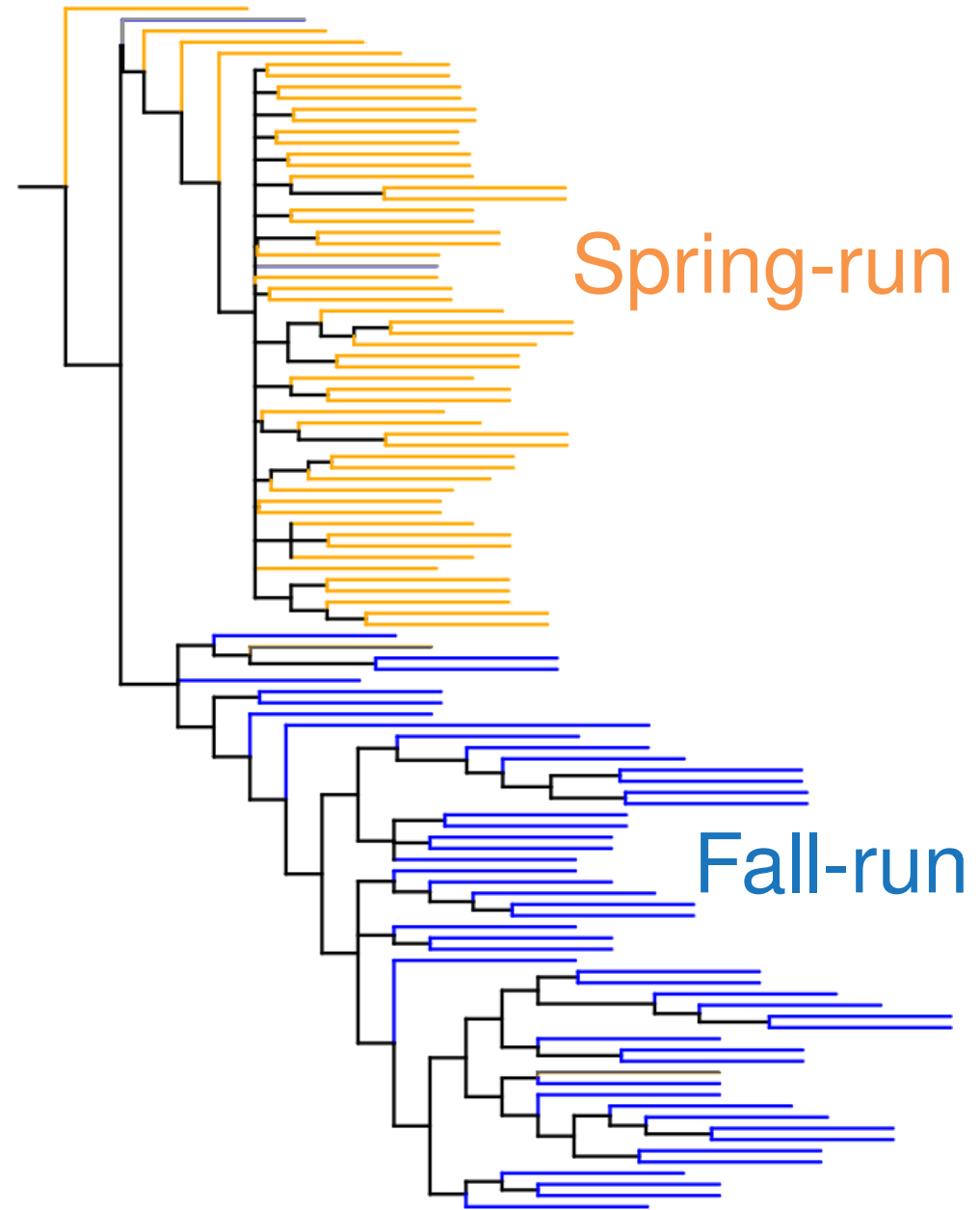
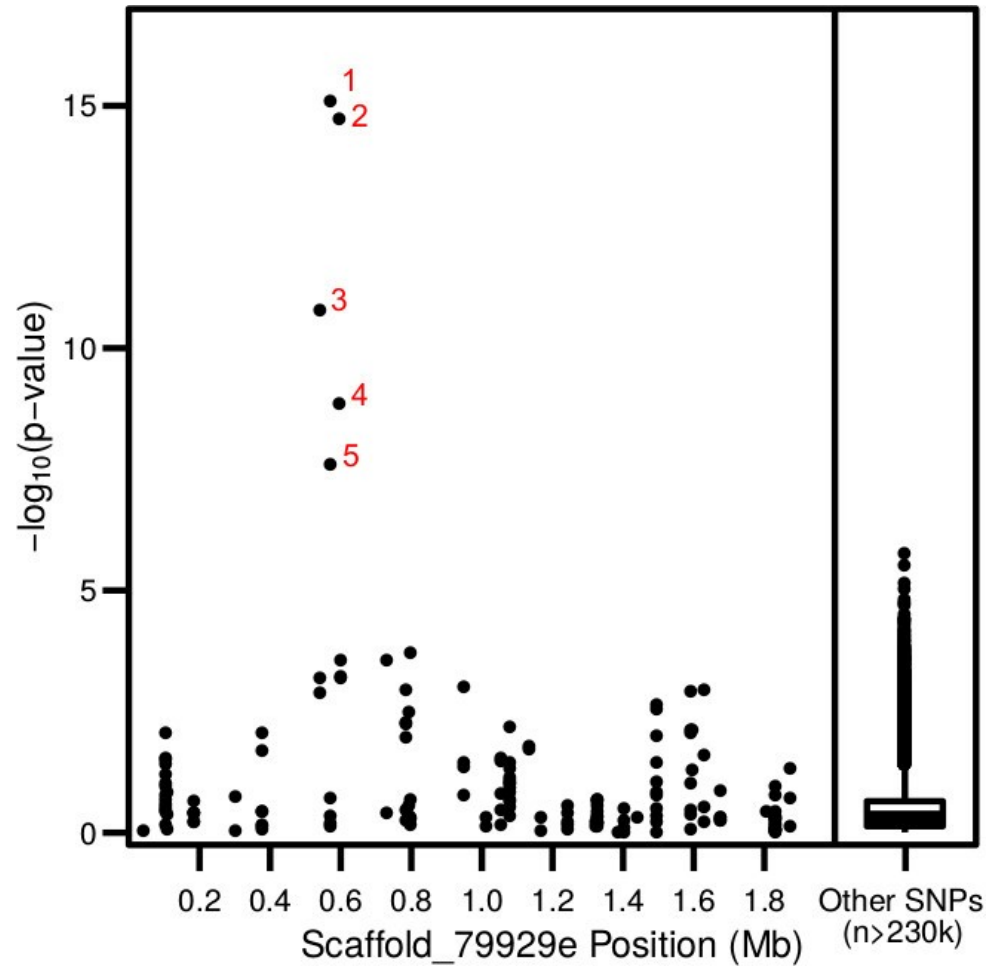
We found a single locus completely associated with summer run-timing in multiple steelhead populations.



A single ancient allelic evolutionary event is the ultimate source of all summer-run (aka premature) alleles.



The same genetic and evolutionary mechanism explains premature migration (aka spring run-timing) in Chinook too.



We discussed the conservation implications of our results and this evolutionary mechanism.

“If current premature migration alleles are lost, new premature migration alleles and the phenotype they promote cannot be expected to reevolve in time frames relevant to conservation planning... Alleles with a large effect on phenotype are expected to be rapidly lost from a population when there is strong selection against the phenotype they promote... [The premature migration allele] cannot be expected to be maintained as standing variation in populations that lack the premature migration phenotype.”

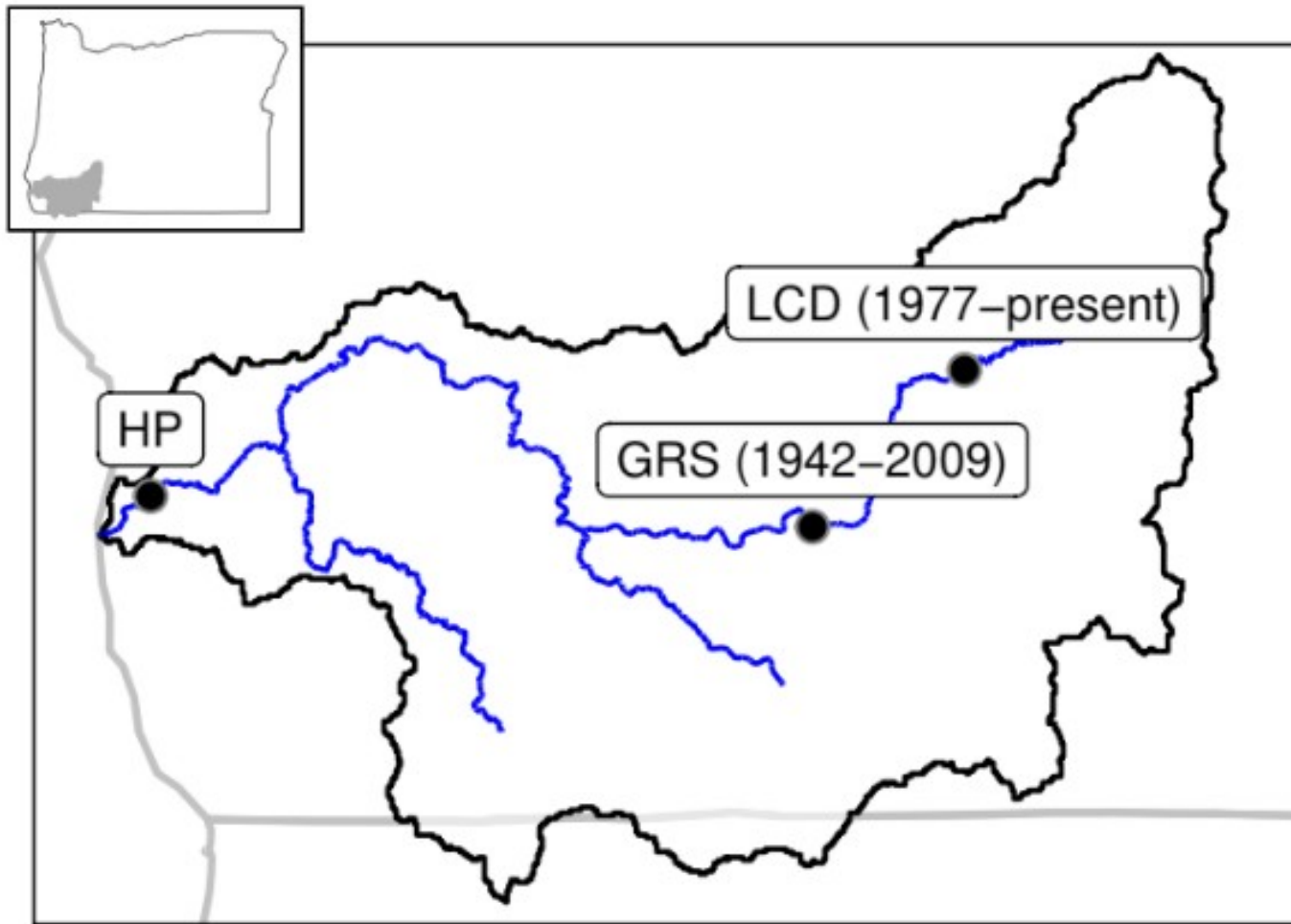
We discussed the conservation implications of our results and this evolutionary mechanism.

“Thus, although evolving the premature migration phenotype in new locations could be rapid if robust premature migrating populations are present in proximate locations, the widespread extirpation and decline of premature migrating populations has greatly diminished the potential restoration and expansion of premature migration.”

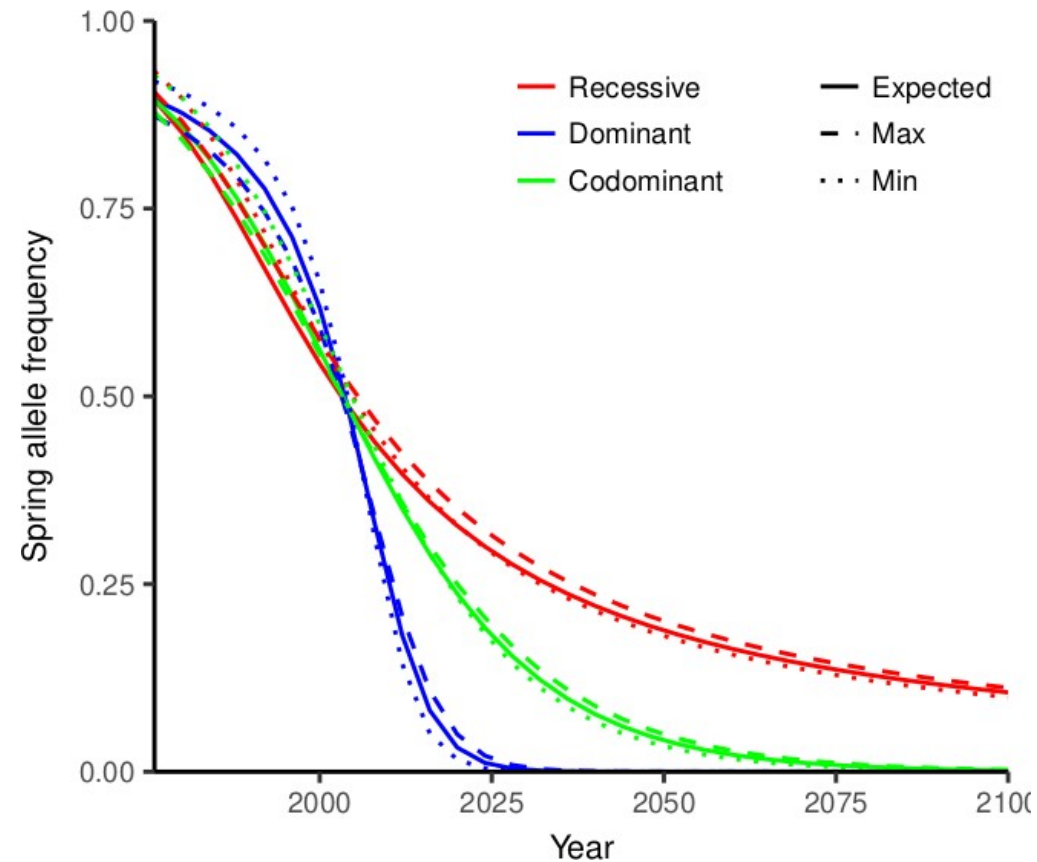
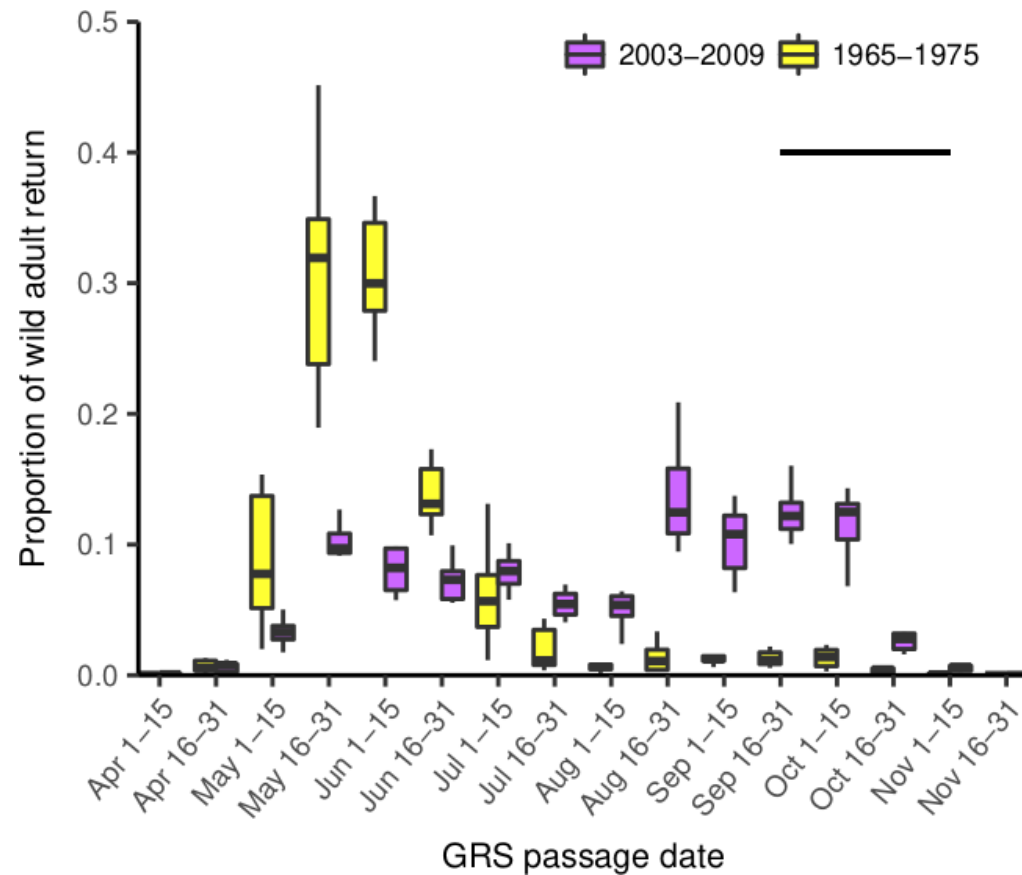
The evolutionary basis of premature migration in Pacific salmon highlights the utility of genomics for informing conservation

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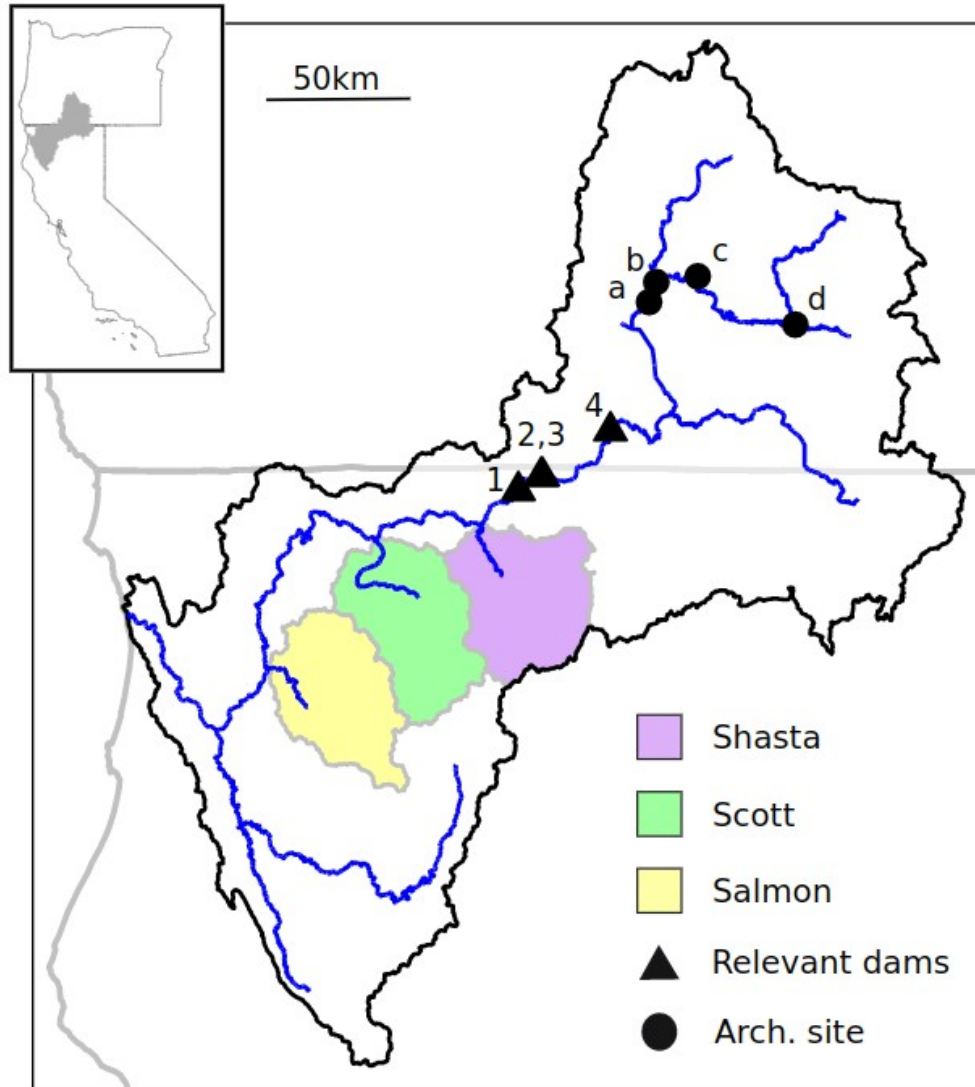
We focused on Rogue and Klamath Chinook to further explore the implications of our results for conservation and restoration.



Rogue Chinook have experience a dramatic phenotypic and genotypic shift since LCD construction.



The Shasta and Scott Rivers are not serving as sustainable reservoirs of the spring-run allele.



Location	Date spring Chinook last observed	Number of samples	Spring-run allele frequency
Salmon	present	116	0.20
Shasta	1930's	440	0.002
Scott	1970's	432	0.002

We discussed the conservation implications of our results and this evolutionary mechanism.

“Our findings suggest that widespread declines and extirpation of the spring-run phenotype and allele will challenge reestablishment of the spring-run phenotype [upon Klamath dam removal] and future restoration projects. These results reveal the mechanisms and consequences of human-induced phenotypic change and highlight the need to conserve and restore critical adaptive variation before the potential for recovery is lost.”

Anthropogenic habitat alteration leads to rapid loss of adaptive variation and restoration potential in wild salmon populations

Tasha Q. Thompson^{a,b,1}, M. Renee Bellinger^{c,2}, Sean M. O'Rourke^{a,b,2}, Daniel J. Prince^{a,b,2}, Alexander E. Stevenson^d, Antonia T. Rodrigues^e, Matthew R. Sloat^f, Camilla F. Speller^{g,h}, Dongya Y. Yang^e, Virginia L. Butlerⁱ, Michael A. Banks^c, and Michael R. Miller^{a,b,1}

The same evolutionary mechanism has been observed for other important traits in salmon.

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An ancient selective sweep linked to reproductive life history evolution in sockeye salmon

Andrew J. Veale^{1,2} & Michael A. Russello ¹

The same evolutionary mechanism has been observed for other important traits in salmon.

LETTER

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Sex-dependent dominance at a single locus maintains variation in age at maturity in salmon

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Conclusions

- Many adaptive traits are influenced by loci with a large phenotypic effect.
- Alleles from a single evolutionary event are used repeatedly across geographic space.
- Large effect alleles are susceptible to loss under selection against the phenotype they promote.
- Current conservation policy was not designed for and can fail in this situation.