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Challenges and opportunities for genetics-based fisheries management of recently diverged stocks

Acknowledgments

STUDENTS/POSTDOCS:

- Andrew Veale (Postdoc, 2014-16)
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- Stephanie Kirk (MSc, 2010)
- Bryson Sjodin (MSc, 2018)
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MITACS Accelerate

Genome BritishColumbia

Freshwater Fisheries Society of BC

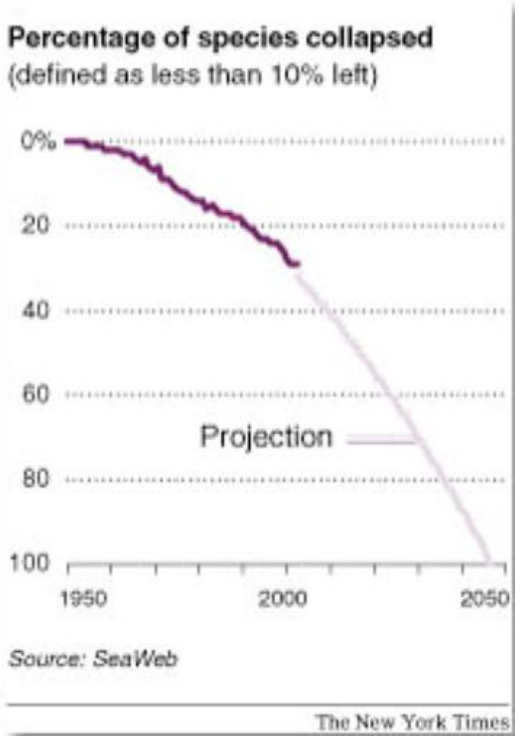
Okanagan Nation Alliance

Fisheries collapse?

Impacts of Biodiversity Loss on Ocean Ecosystem Services

Boris Worm,[1]* Edward B. Barbier,[2] Nicola Beaumont,[3] J. Emmett Duffy,[4] Carl Folke,[5,6] Benjamin S. Halpern,[7] Jeremy B. C. Jackson,[8,9] Heike K. Lotze,[1] Fiorenza Micheli,[10] Stephen R. Palumbi,[10] Enric Sala,[8] Kimberley A. Selkoe,[7] John J. Stachowicz,[11] Reg Watson[12]

SCIENCE VOL 314 3 NOVEMBER 2006



- Predicted that by 2048 the ocean would be empty of fish
- Reported fishing stocks had collapsed in 29 percent of the world's fisheries

GENOME 10K

GenomeCanada

FISH SPECIES COMPLETED/IN PROGESS:

- Great white shark
- Chinese sturgeon
- Bowfin
- Bichir
- European freshwater eel
- Orange roughy
- Blind cave fish
- Atlantic herring
- Bighead carp
- Wuchang bream
- Silver carp
- Rare gudgeon
- Tiger tail seahorse
- Lanternfish
- Golden arowana
- Japanese seabass
- Large yellow croaker
- Tongue sole
- Inshore hagfish
- Sea lamprey
- Japanese lamprey
- Elephant shark
- Little skate
- Spotted gar
- Japanese medaka
- Zebrafish
- Southern platyfish
- Atlantic cod
- Three-spined stickleback
- Zebra mbuna
- Tigerfish
- Golden mbuna
- Happy cichlid
- Blue mbuna
- Pacific bluefin tuna
- Atlantic salmon
- Rainbow trout
- Channel catfish
- Fugu
- Freshwater pufferfish
- Indonesian coelocanth
- South African coelocanth
- Nile tilapia
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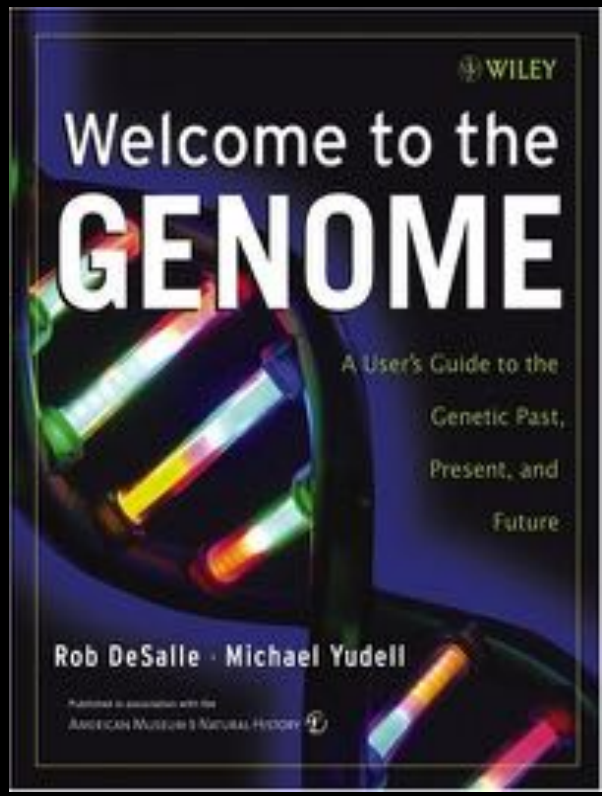


Genetics-based fisheries management

- Distribution of neutral genetic variation
- Applications:
  - defining stocks
  - analyzing mixtures
  - identifying specimens
  - monitoring restocking initiatives
  - guiding aquaculture operations

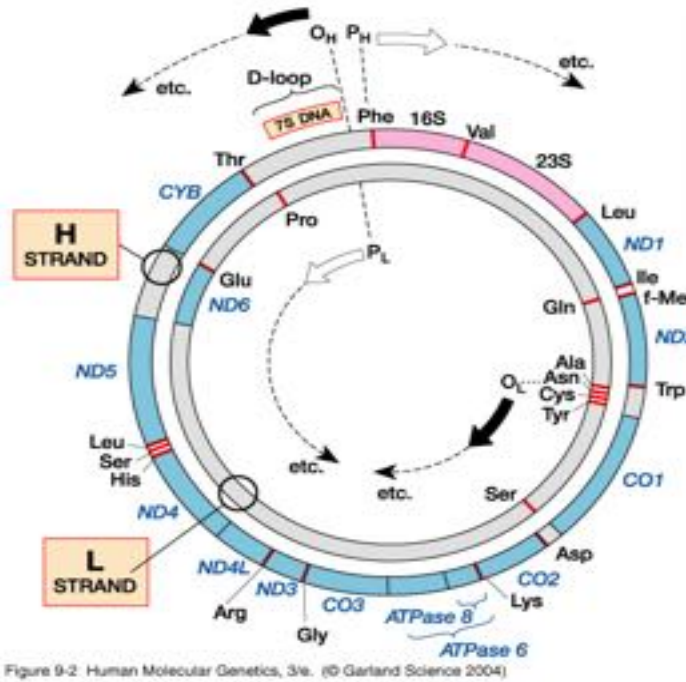
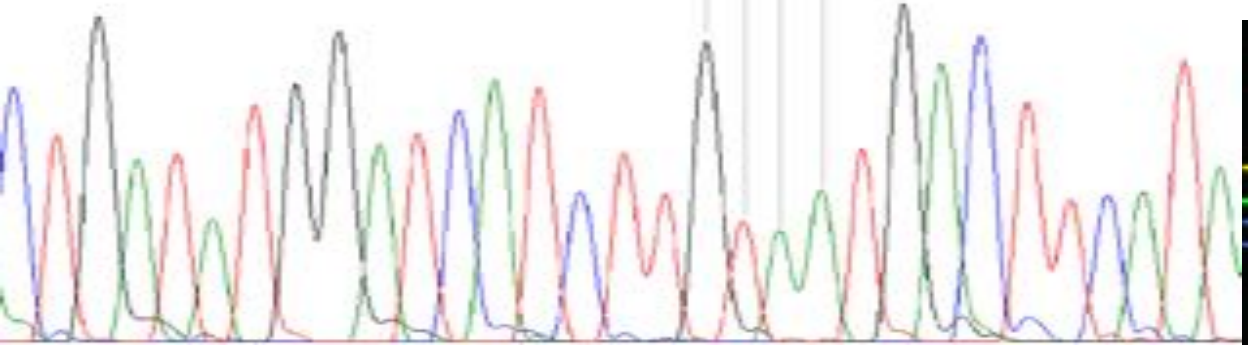
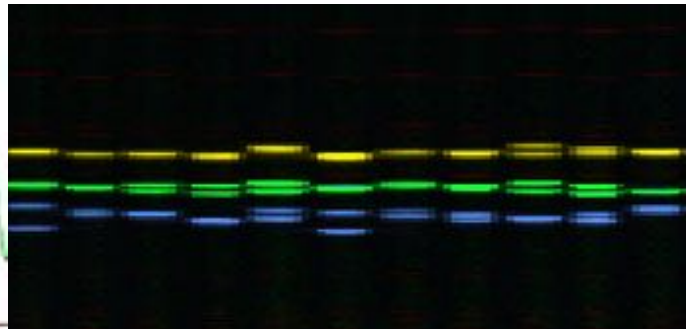


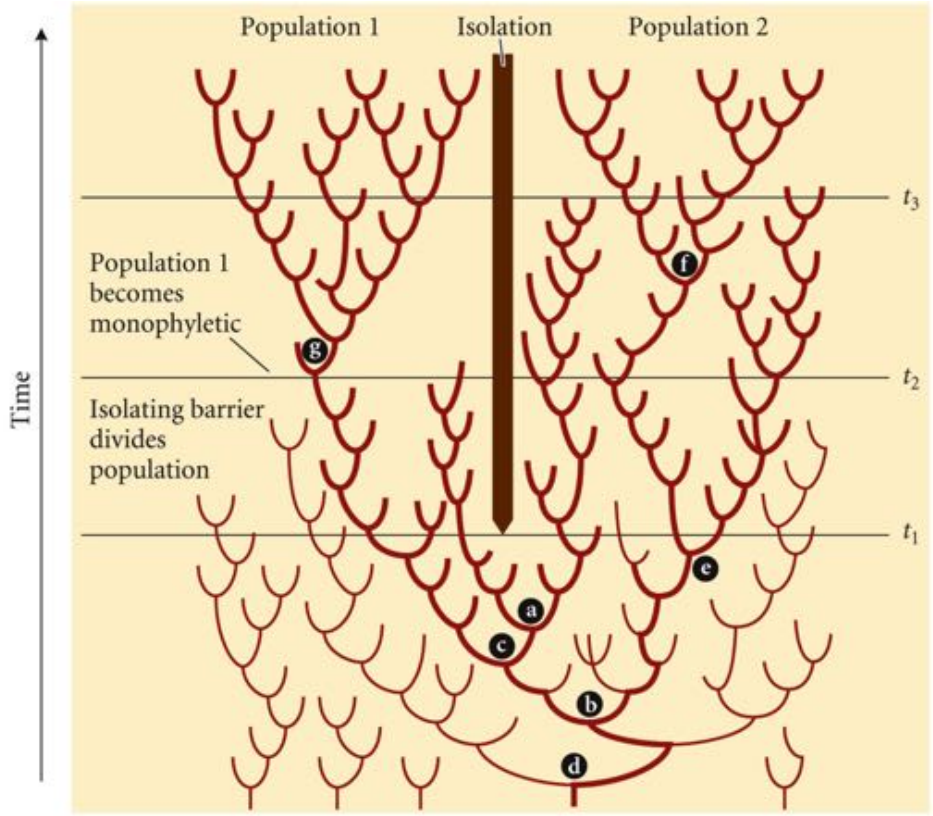
Figure 9-2 Human Molecular Genetics, 3/e. (© Garland Science 2004)





Challenges for recently diverged stocks

- Recently isolated stocks may not exhibit divergence at neutral loci



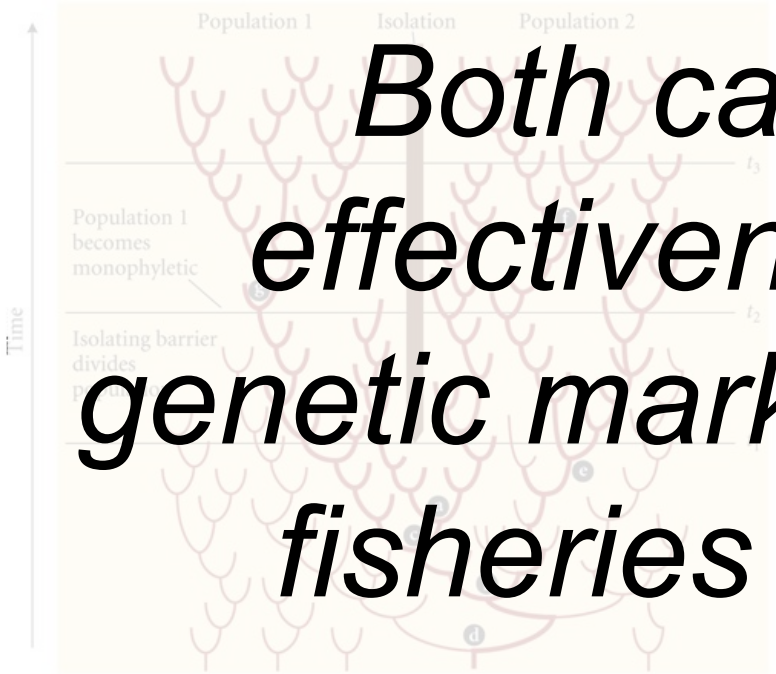
Challenges for recently diverged stocks

- Recently isolated stocks may not exhibit divergence at neutral loci
- Low levels of gene flow may persist

Nm is **>** 1 the allele frequencies in the subpopulations will remain homogenised (Wright 1931)

Challenges for recently diverged stocks

- Recently isolated stocks may not exhibit divergence at neutral loci
- Low levels of gene flow may persist



Both cases limit the effectiveness of neutral genetic markers for informing fisheries management

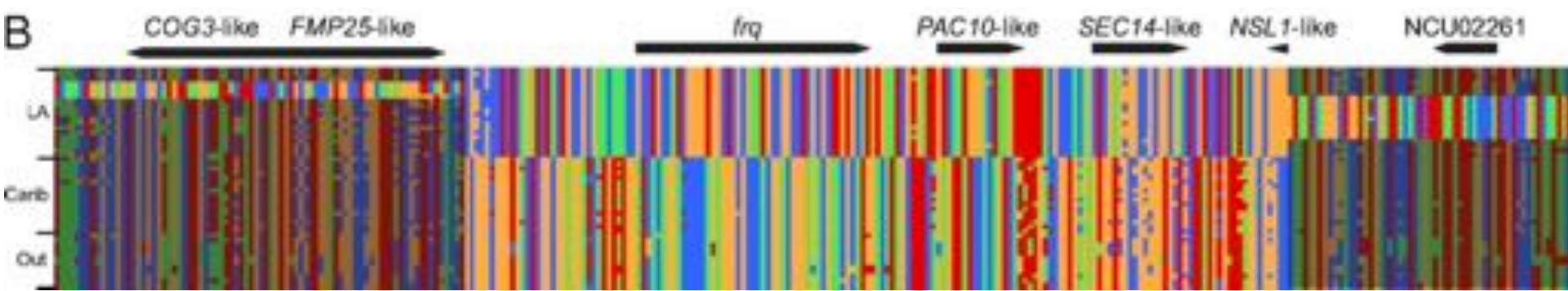
Challenges for recently diverged stocks

- Recently isolated stocks may not exhibit divergence at neutral loci
- Low levels of gene flow may persist

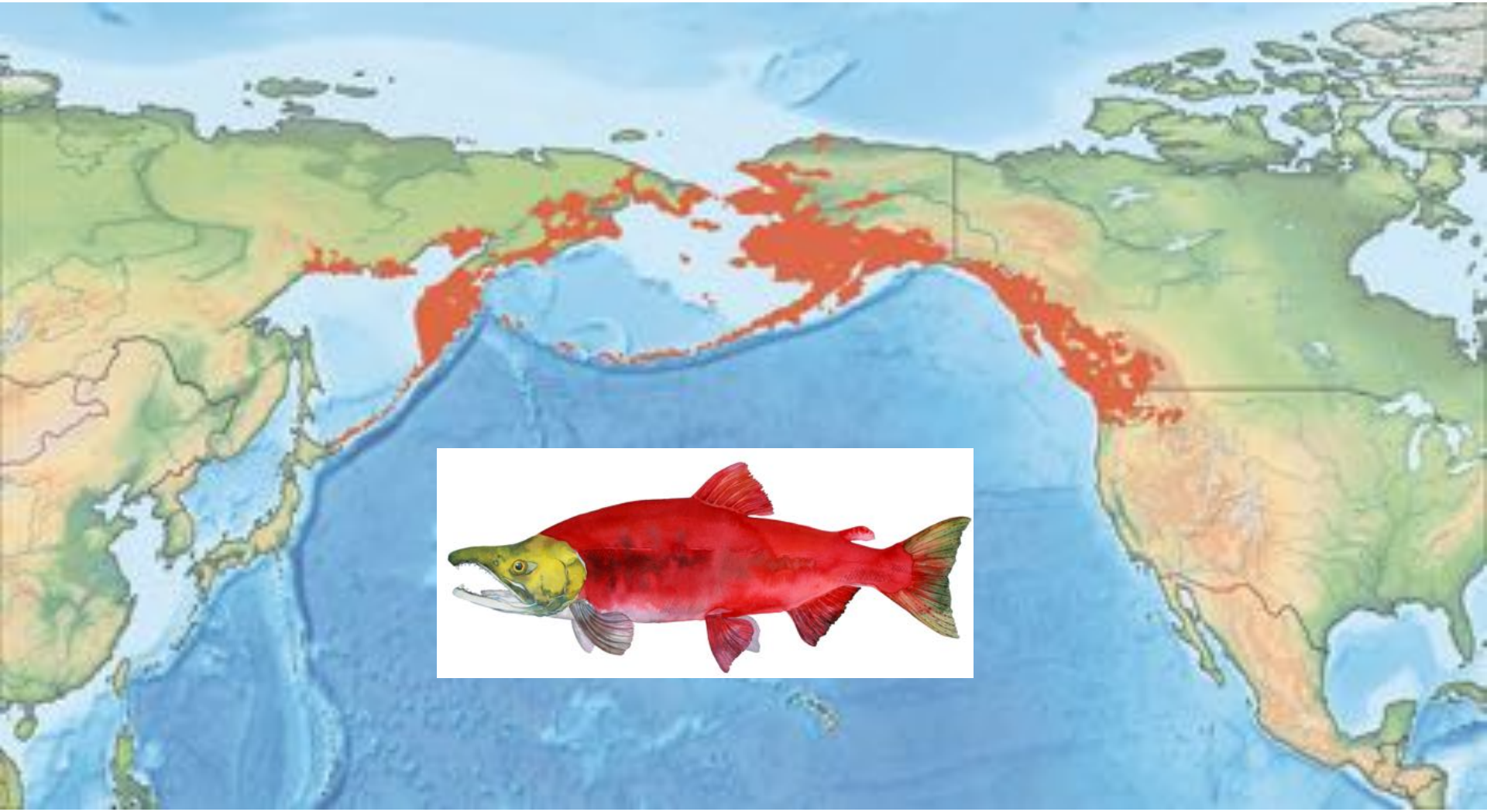
Loci influenced by selection may offer valuable population markers on more recent (ecological) time scales

Population genomics

- Extension of population genetics
- Transition from analyzing genotypic data at a handful of molecular markers to 1,000's to >100,000's across genome
- Discrimination between locus-specific & genome-wide effects

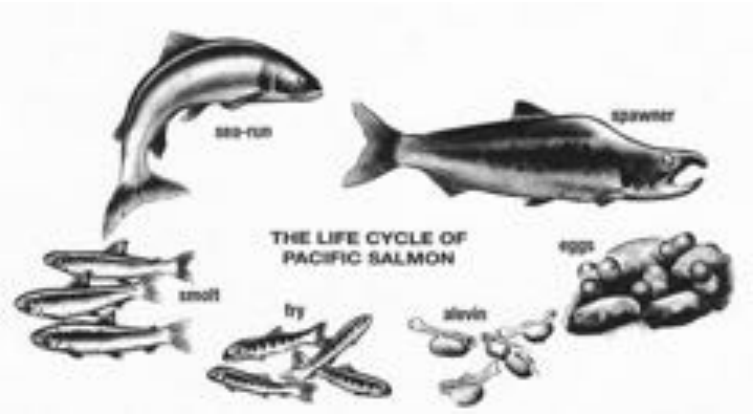


Sockeye salmon (*Oncorhynchus nerka*)



Sockeye salmon (*Oncorhynchus nerka*)

- Migratory ecotypes
  - Anadromous
  - Resident (kokanee)



Sockeye salmon (*Oncorhynchus nerka*)

- Migratory ecotypes
  - Anadromous
  - Resident (kokanee)

♀

♂

- Reproductive ecotypes
  - River/stream-spawning
  - Beach/shore-spawning

Sockeye salmon (*Oncorhynchus nerka*)

Ecotype divergence likely occurred since isolation <10,000 years before present

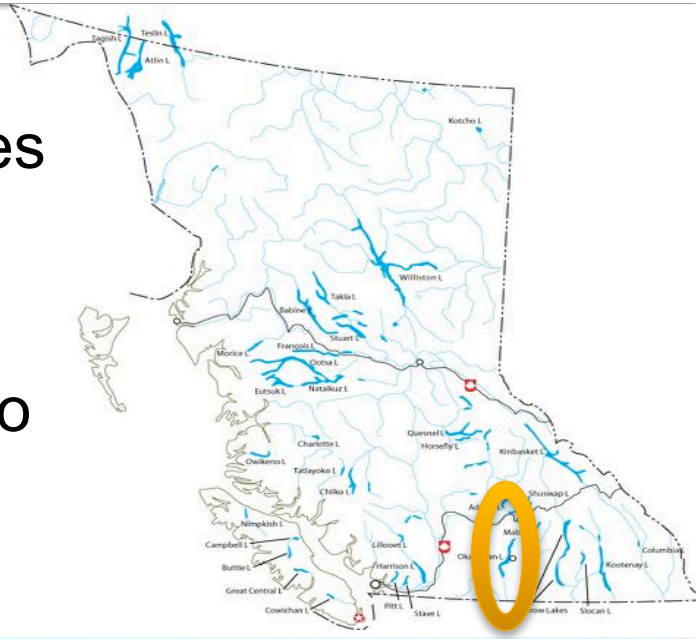
Research objectives

1. Is divergent selection driving differentiation between sockeye salmon migratory and reproductive ecotypes?

2. Does the use of outlier loci improve accuracy and cost-effectiveness relative to conventional approaches to genetics-based fisheries management?

Study system: Kokanee

- Okanagan Lake located between the Monashee & Cascade mountain ranges
  - spans 351 km^2, average depth 76 m
- Kokanee in Okanagan Lake exhibit two sympatric ecotypes



Reproductive ecotypes

STREAM SPAWNERS

- Larger body size
- Bright red/green colouration
- More pronounced sexual characteristics
- Peak spawning time early October
- Spawn in pairs, male mate defense

SHORE SPAWNERS

- Smaller body size
- Darker, more uniform colouration
- Less pronounced sexual characteristics
- Peak spawning time late October
- Spawn in schools

Reproductive ecotypes

STREAM SPAWNERS

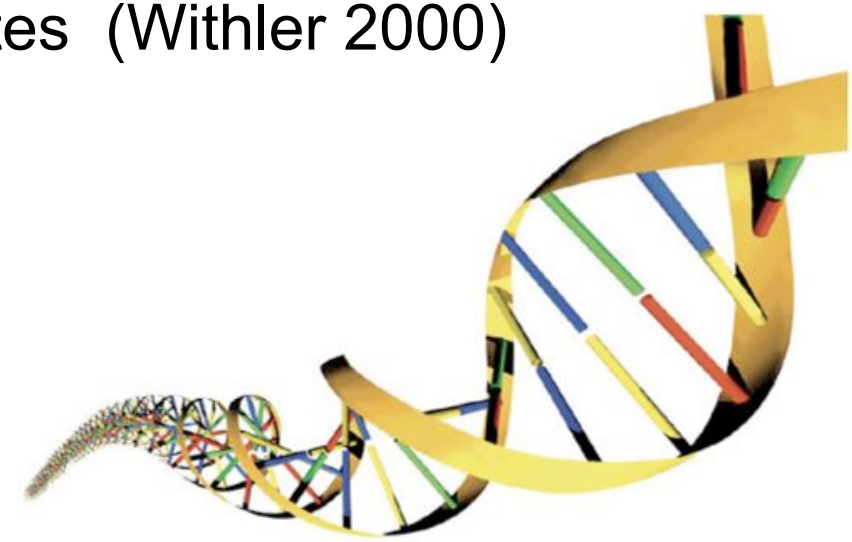
♀

♂

SHORE SPAWNERS

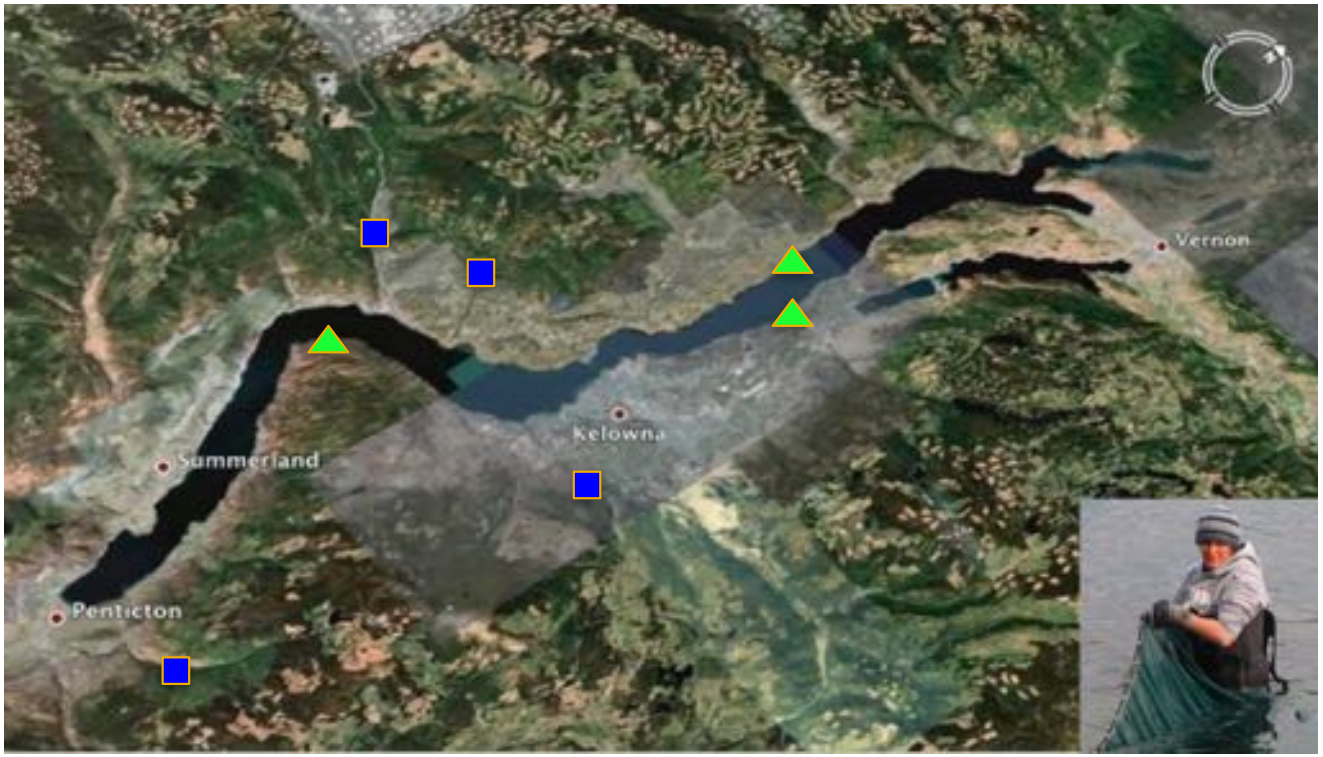
Previous genetic work

- Low levels of neutral genetic differentiation detected between ecotypes (Taylor *et al.* 1997, 2000)
- Low individual assignment probabilities to ecotype (71% and 76% accurate, Taylor *et al.* 2000)
- Unacceptable error rates in mixed composition analyses using microsatellites (Withler 2000)



Okanagan Lake kokanee

Reproductive ecotype divergence



▲ shore spawning sites
■ stream spawning sites

n = 138
year = 2007

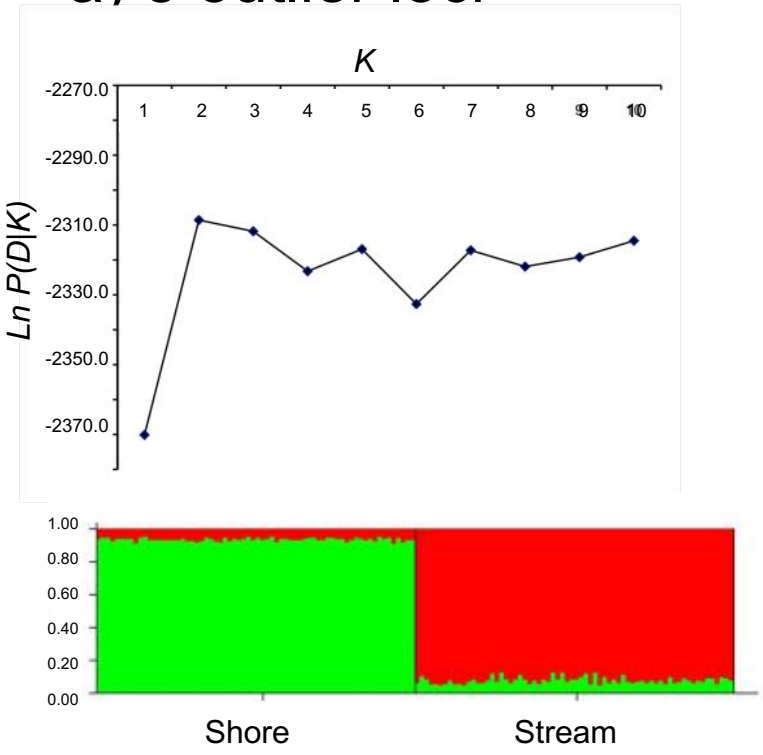
Russello et al. (2012) *Evol. Appl.*

Okanagan Lake kokanee

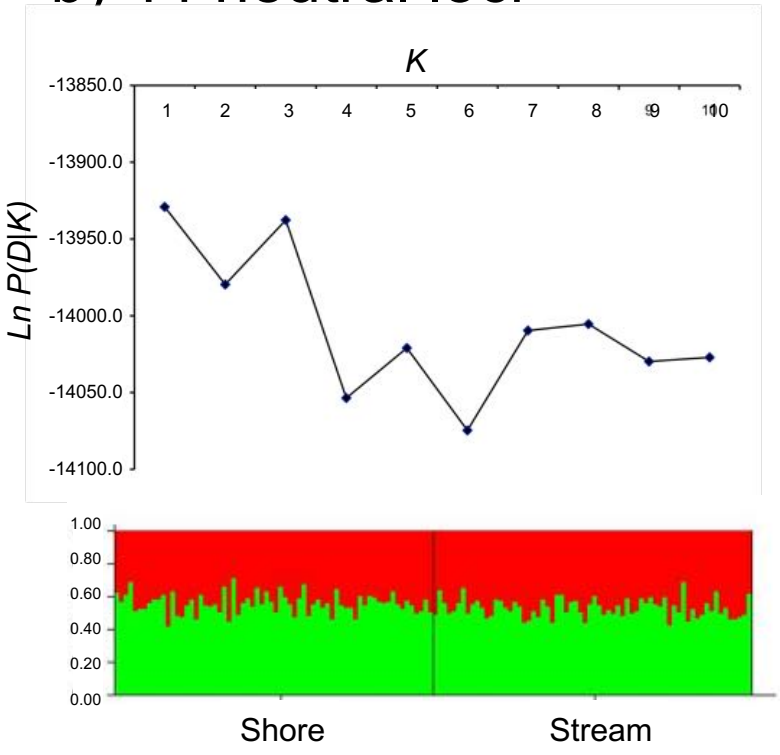
Reproductive ecotype divergence

Genotyped at 52 expressed sequence tag-linked microsatellites

a) 8 outlier loci



b) 44 neutral loci



Russello et al. (2012) *Evol. Appl.*

Okanagan Lake kokanee

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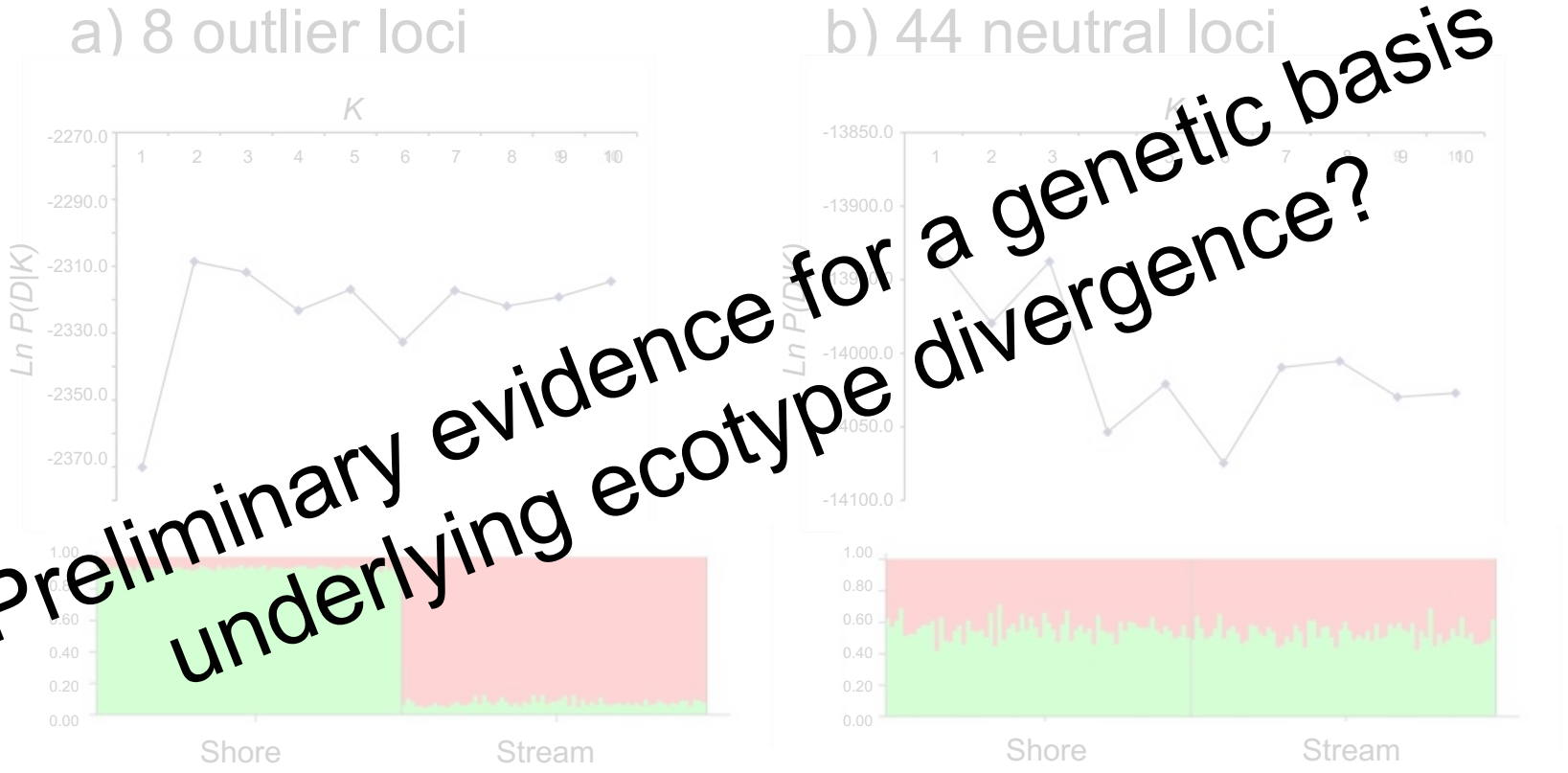


Preliminary evidence for a genetic basis underlying ecotype divergence?

Russello et al. (2012) *Evol. Appl.*

British Columbia-wide kokanee

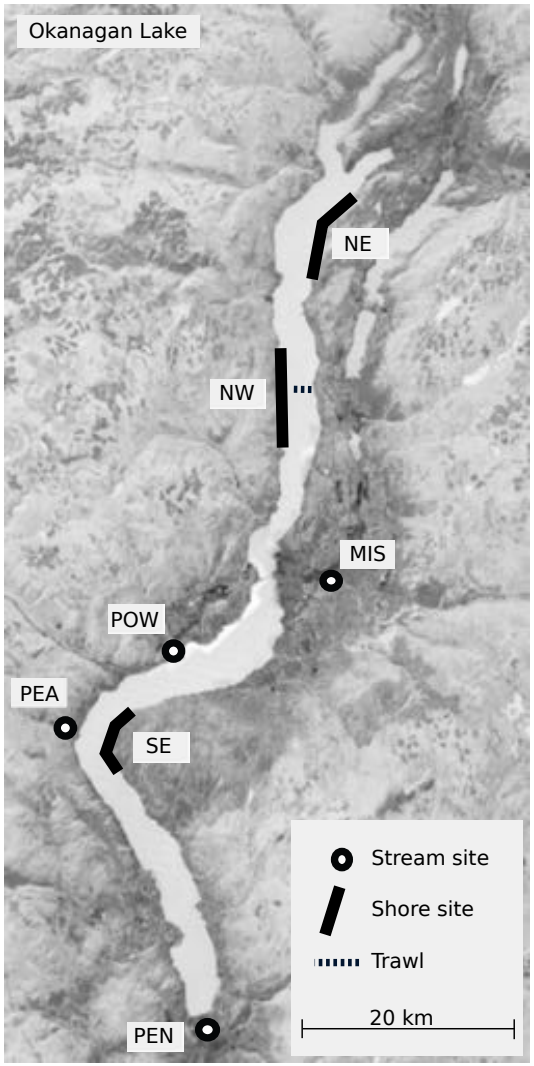
Reproductive ecotype divergence

No parallel patterns of divergence in a BC-wide sampling

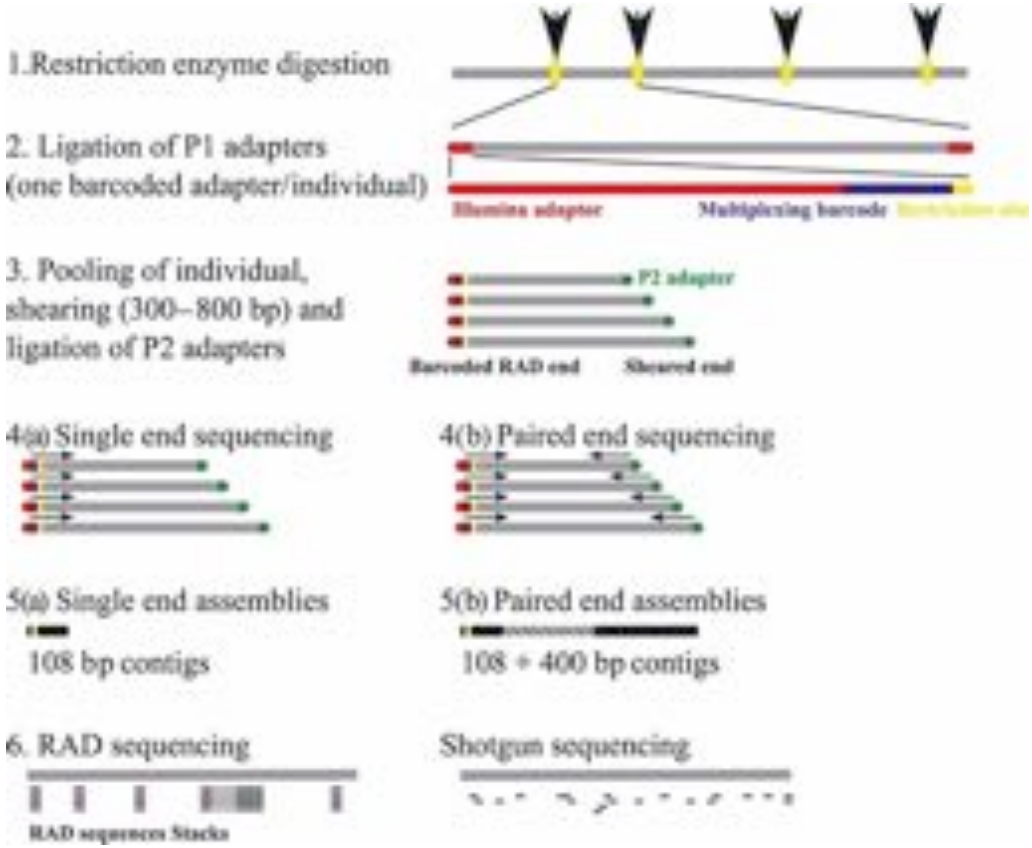
Frazer & Russello (2013) *J. Evol. Biol.*

Okanagan Lake kokanee

Reproductive ecotype divergence

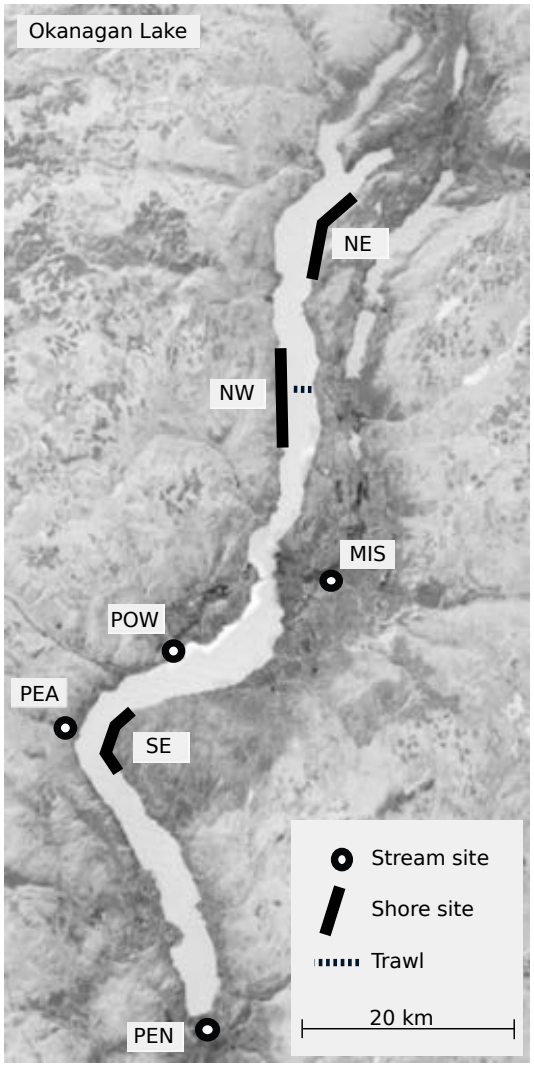


RADseq genotyped 5,996 SNPs

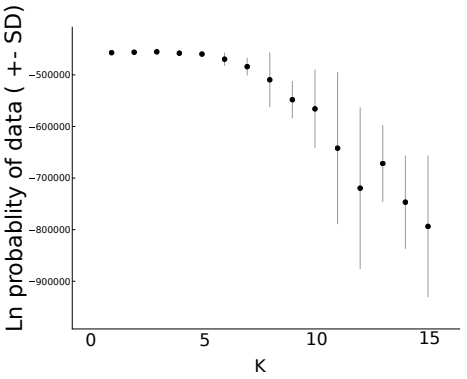


Okanagan Lake kokanee

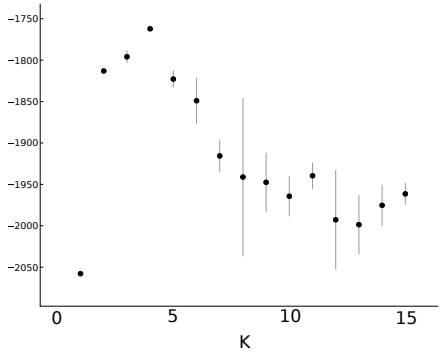
Reproductive ecotype divergence

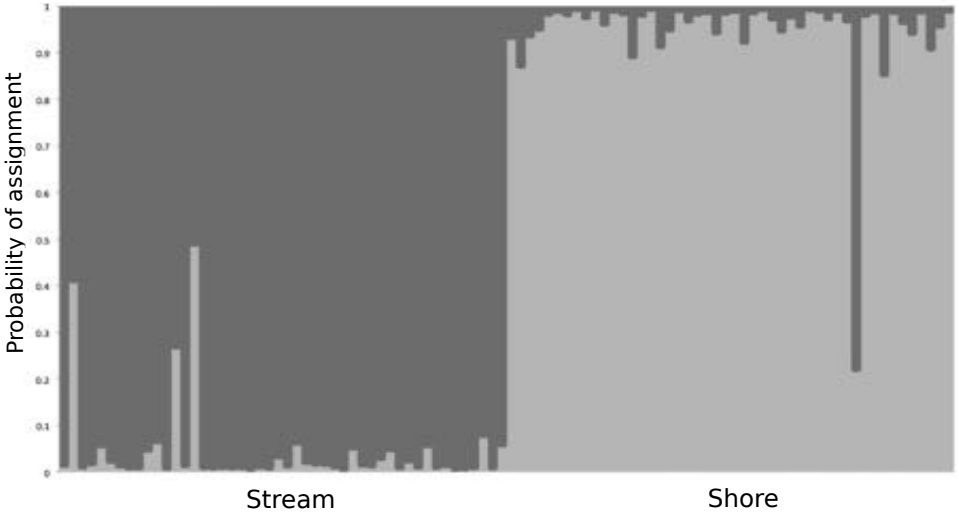


Neutral (n = 5,976)



Outlier (n = 20)

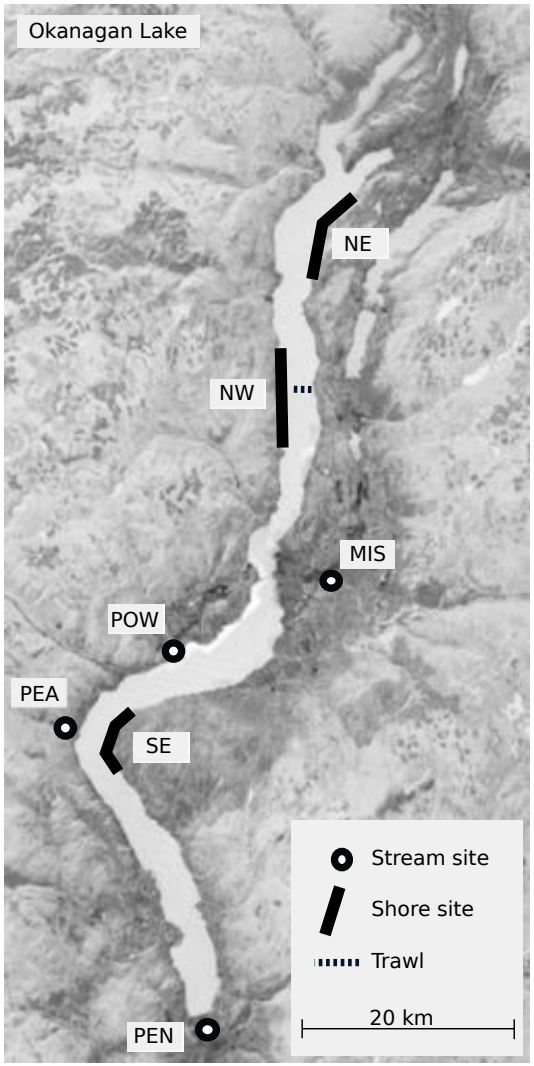




Lemay & Russello (2015) *Mol. Ecol.*

Okanagan Lake kokanee

Reproductive ecotype divergence

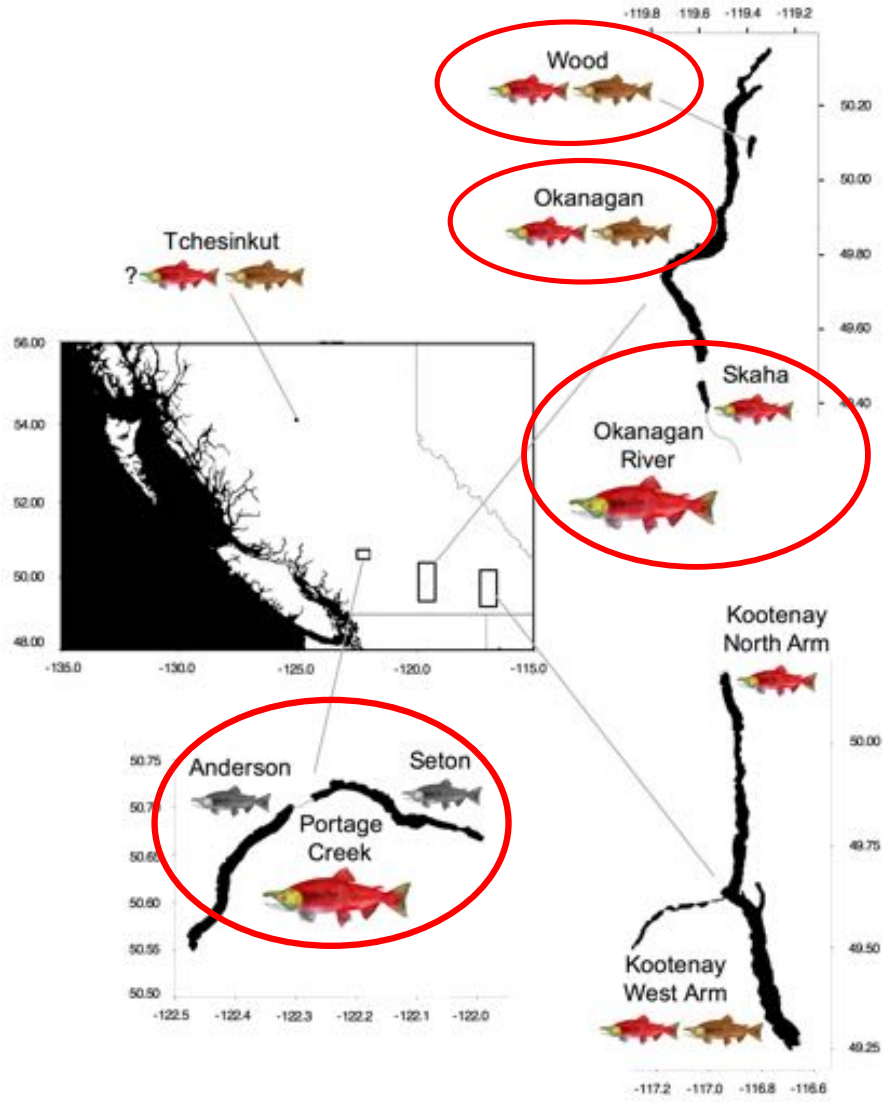


Data	Ecotype	Accuracy (± SD)
20 outlier loci	Stream	0.9999 (± 0.0007)
	Shore	0.9999 (± 0.0006)
20 neutral loci	Stream	0.8277 (± 0.0517)
	Shore	0.8400 (± 0.0592)
500 neutral loci	Stream	0.9413 (± 0.0168)
	Shore	0.9598 (± 0.0158)

Lemay & Russello (2015) *Mol. Ecol.*

British Columbia kokanee and sockeye

Reproductive ecotype divergence



RADseq genotyped 7,347 SNPs

126 outlier SNPs
shore-spawning kokanee x
stream-spawning kokanee

R68810 independently detected in 4 systems across 2 drainages

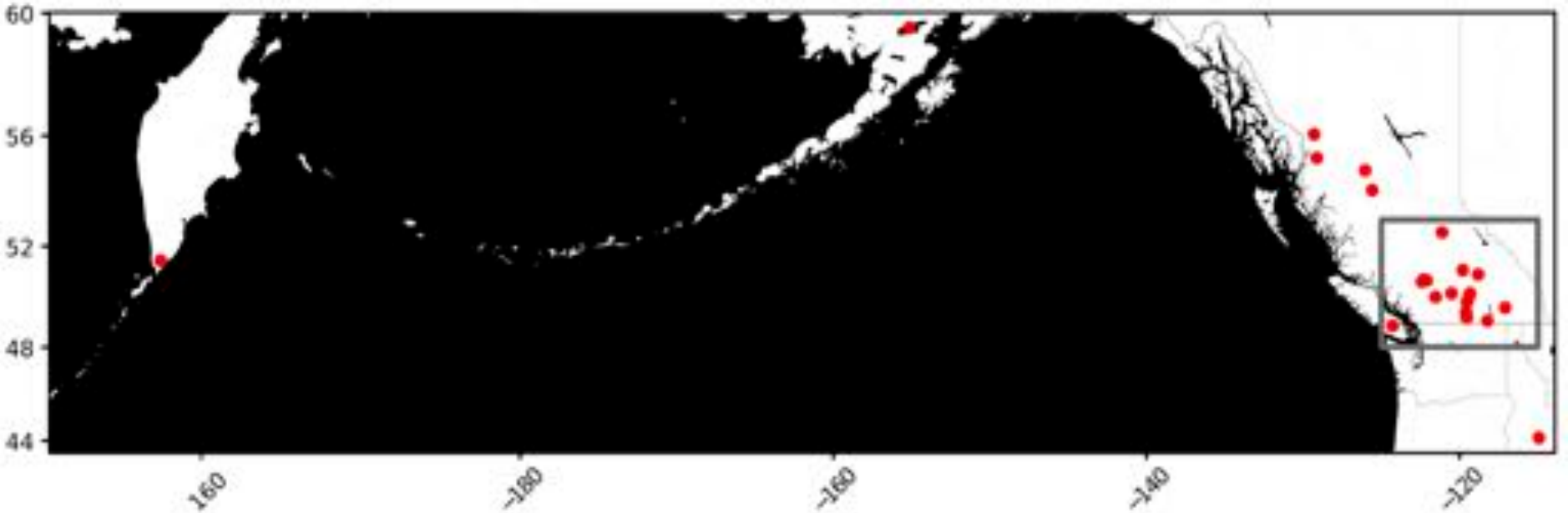
R68810 maps to leucine-rich repeat-containing protein-9 gene (LRRC9)

Veale & Russello (2017) *GBE*

Pan-Pacific kokanee and sockeye

Reproductive ecotype divergence

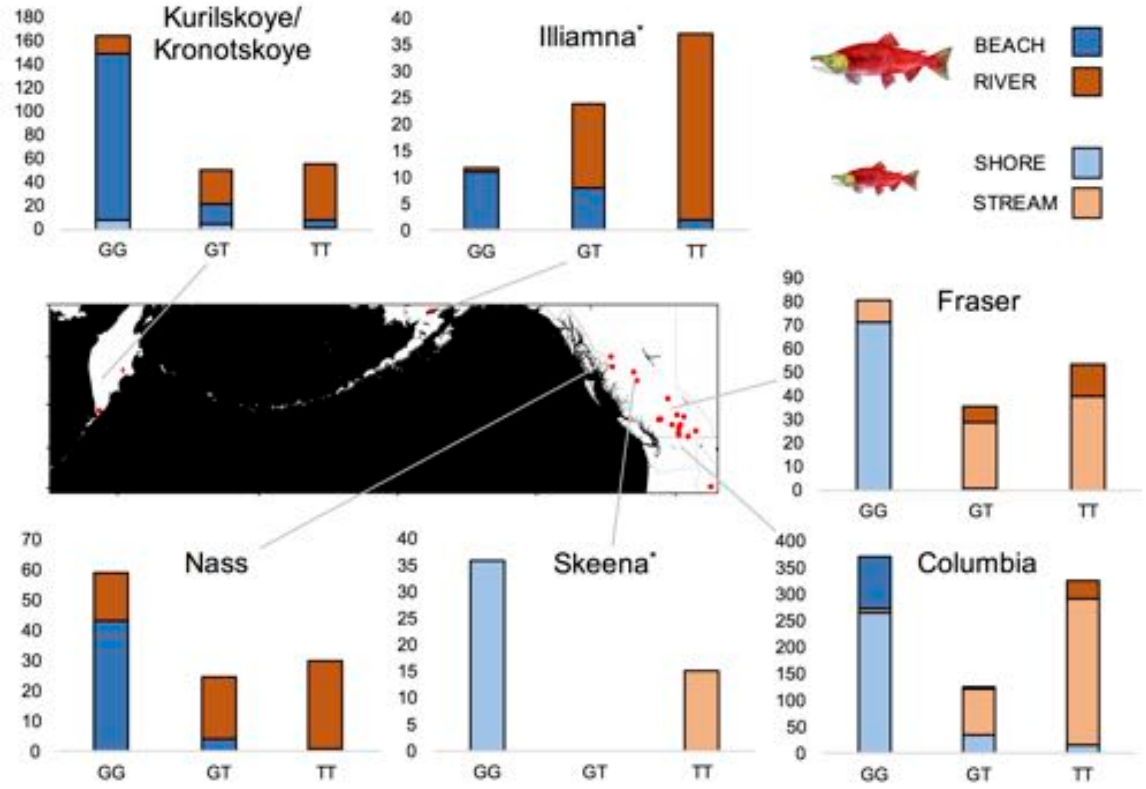
Developed a TaqMan® assay and genotyped 1519 sockeye/kokanee from 47 sites across pan-Pacific distribution



Veale & Russello (2017) *Sci. Rep.*

Pan-Pacific kokanee and sockeye

Reproductive ecotype divergence



Evidence for directional divergence across the natural range of *O. nerka* in Russia, Alaska and Canada

>99% correct assignment to reproductive ecotype

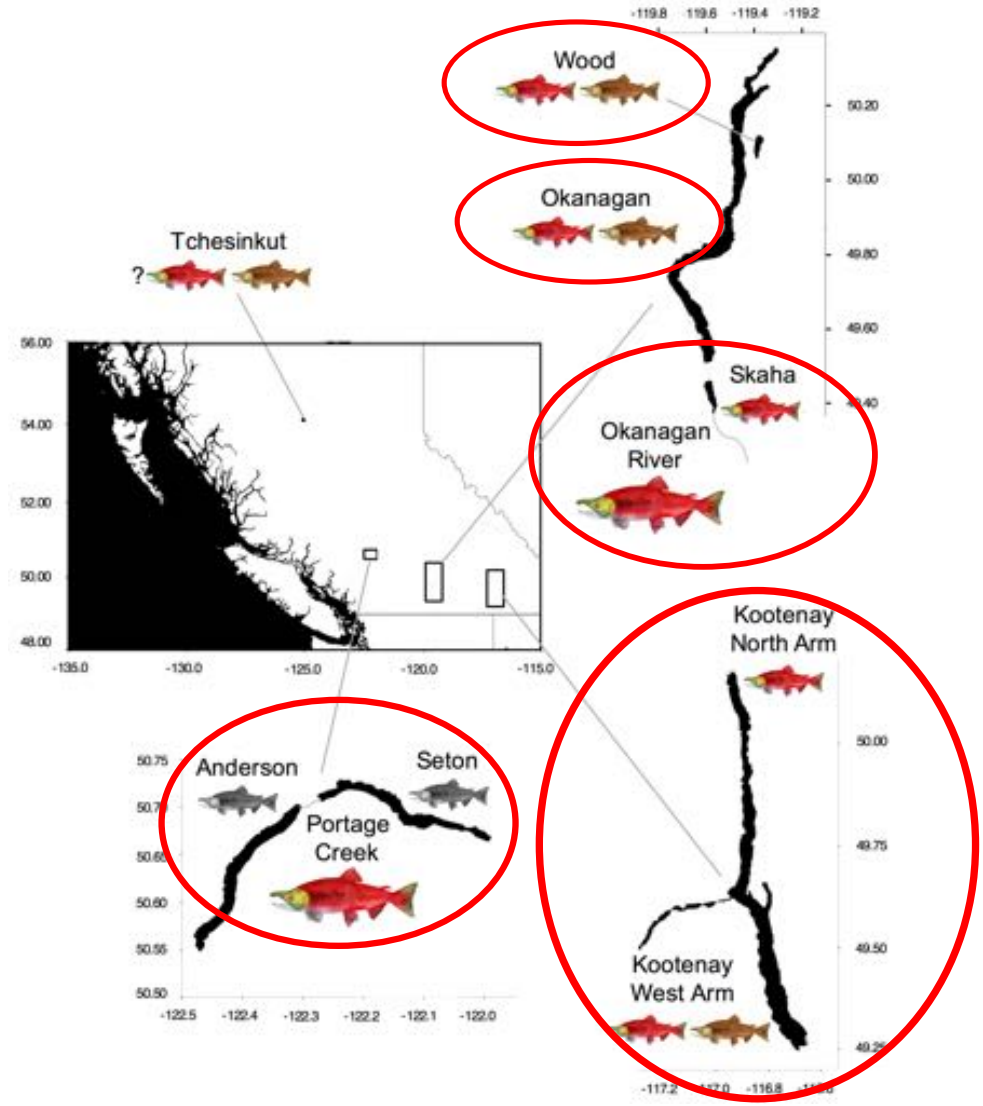
- GG = shore
- GT/TT = stream

G (shore) allele could be associated with loss of function, leading to a lack of spawning habitat preference

Veale & Russello (2017) *Sci. Rep.*

British Columbia kokanee and sockeye

Migratory ecotype divergence



RADseq genotyped 7,347 SNPs

219 outlier SNPs
anadromous x resident

75 of which independently detected in ≥ 2 comparisons

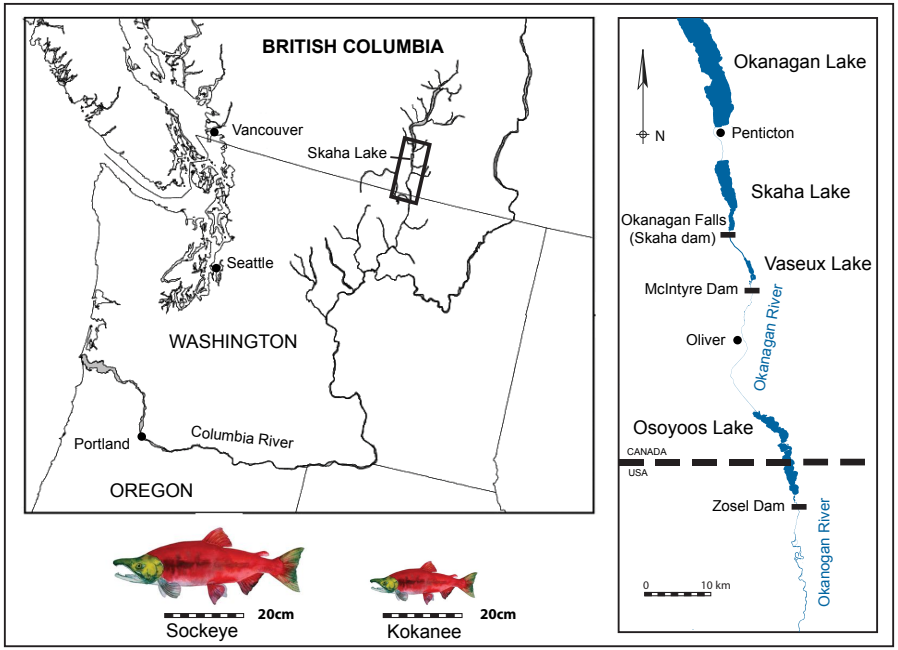
7 of which independently detected in ≥ 4 comparisons

Annotations identifying genes associated with development, environmental tolerance & immune response

Veale & Russello (2017) *GBE*

Monitoring sockeye reintroduction

Fisheries management applications



Hatchery conservation programs are increasingly being employed to reintroduce or maintain local populations

Sockeye salmon hatchery restocking in Skaha Lake began in 2004

Need for monitoring sockeye population establishment and introgression trends with the resident kokanee population

Veale & Russello (2016) *Evol. App.*

Monitoring sockeye reintroduction

Fisheries management applications

Genotyped samples from reference populations, annual trawl surveys and angler surveys collected over 8-year period at previously published and newly developed TaqMan assays based on our RADseq data (n = 35)

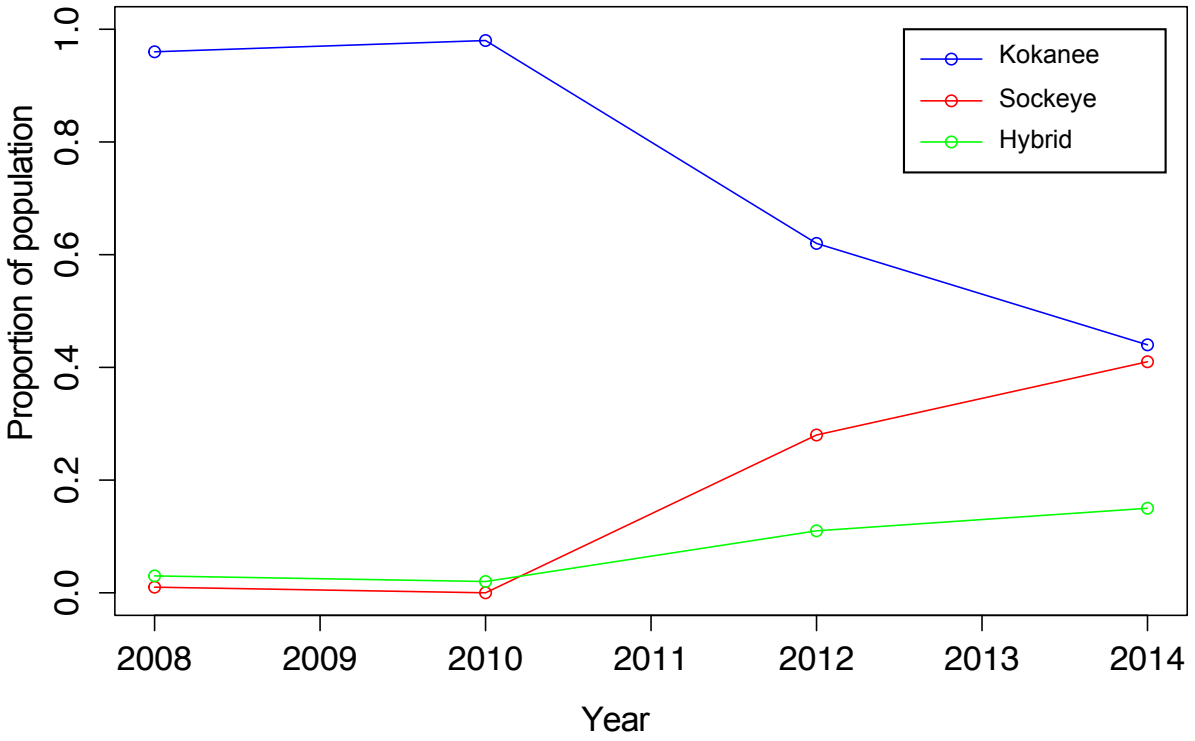
Sample Year	Sampling Period	Type	Age	Sample size
2003	September - October	Kokanee Reference	3+	130
2012	September - October	Sockeye Reference	3+	148
2008	September - October	Annual Trawl Survey	0	96
2010	September - October	Annual Trawl Survey	0	96
2012	September - October	Annual Trawl Survey	0	96
2014	September - October	Annual Trawl Survey	0	96
2013	September - October	Annual Trawl Survey	1 - 2	136
2015	September - October	Angler Survey	2 - 5	45

Veale & Russello (2016) *Evol. App.*

Monitoring sockeye reintroduction

Fisheries management applications

Low proportions of sockeye and hybrids detected in 2008 & 2010 age-0 samples; by 2012, 28% were sockeye, rising to 41% in 2014

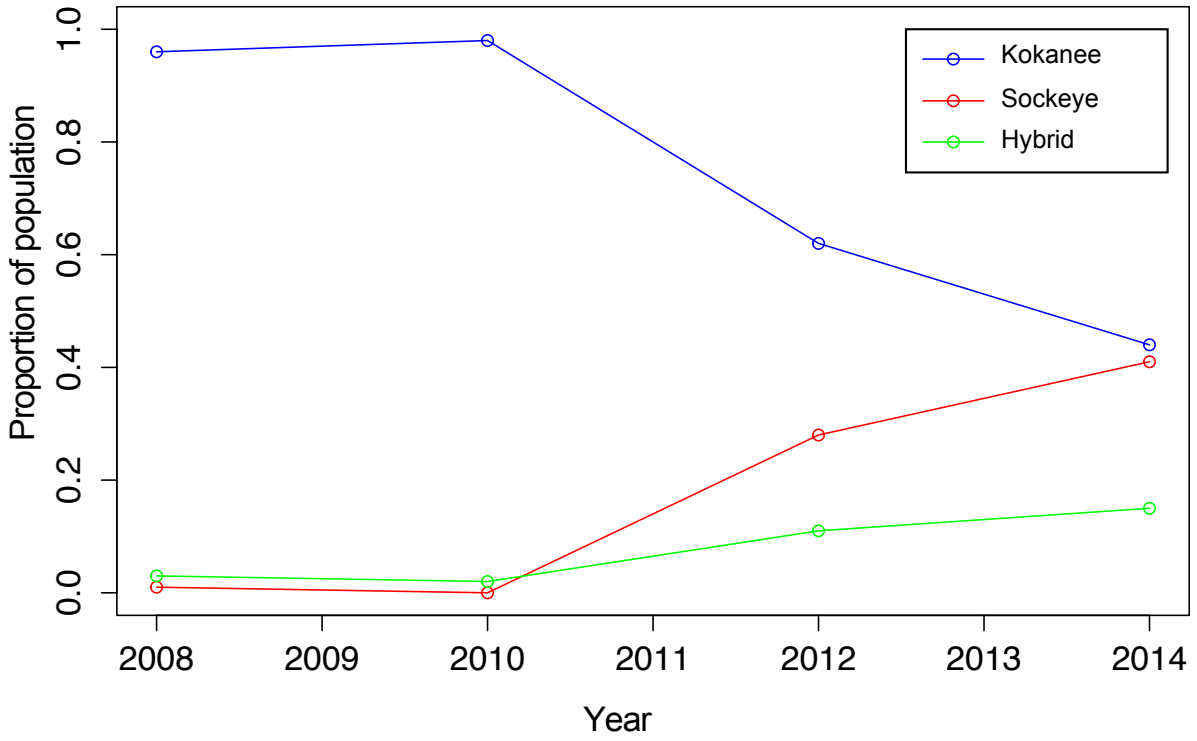


Veale & Russello (2016) *Evol. App.*

Monitoring sockeye reintroduction

Fisheries management applications

The number of hybrids detected rose proportionally with the increase in sockeye, and exhibited an intermediate phenotype.



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Monitoring sockeye reintroduction

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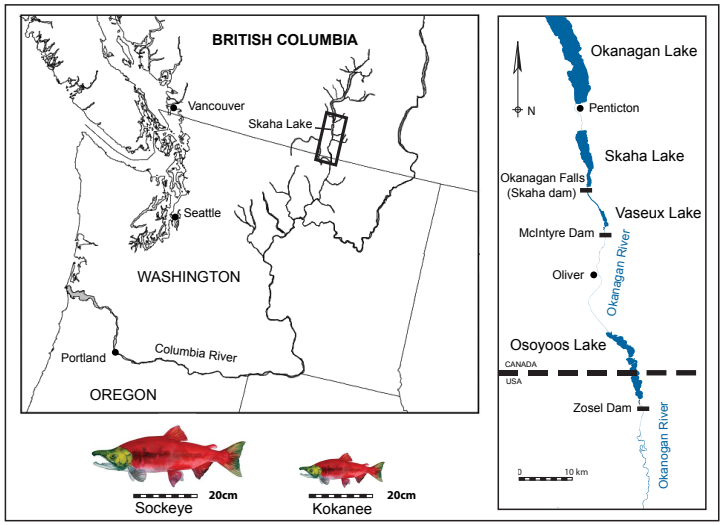
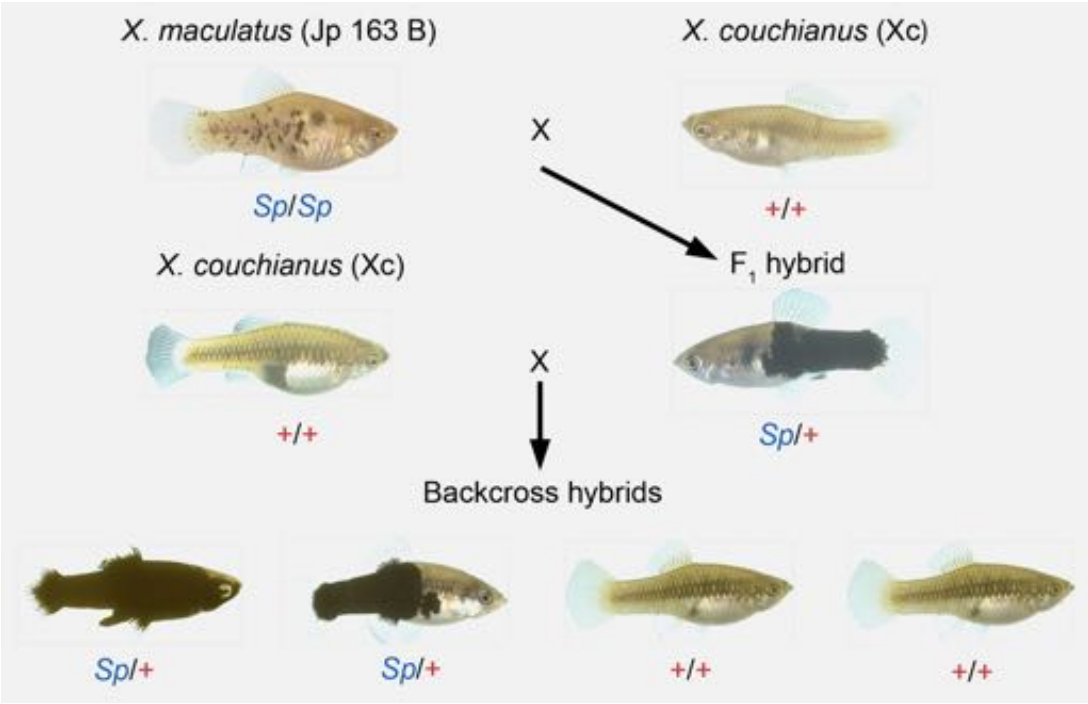
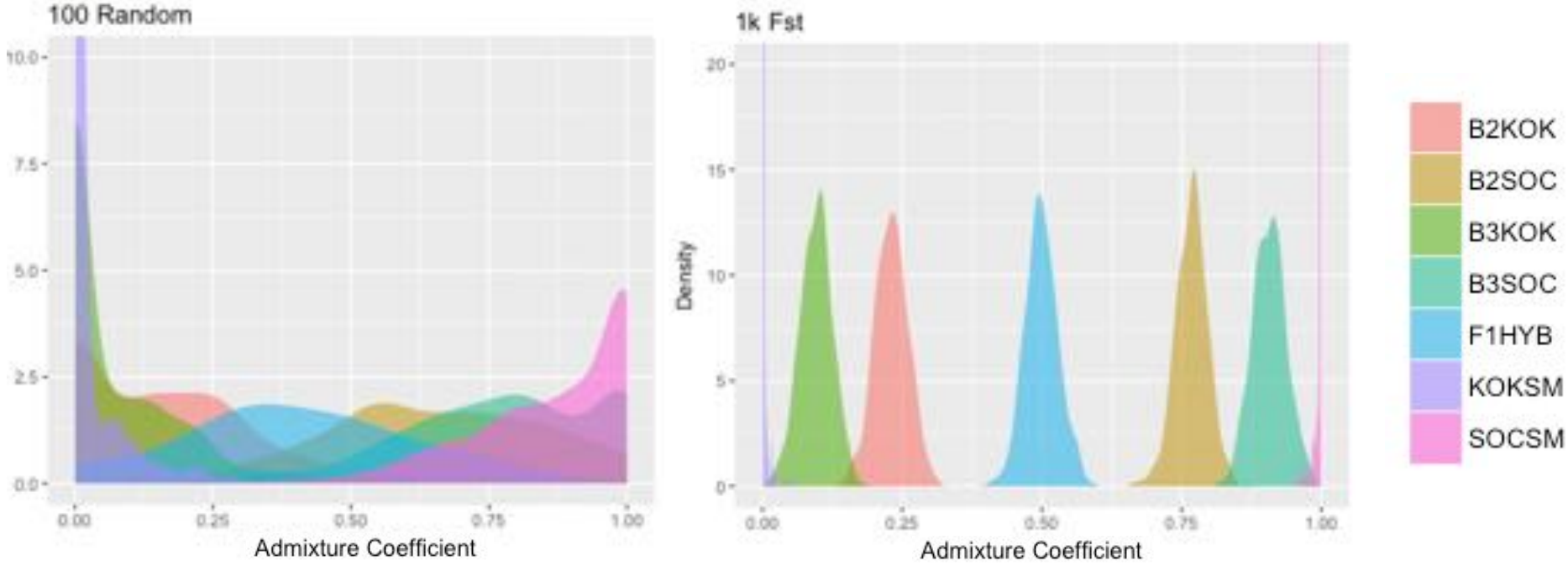




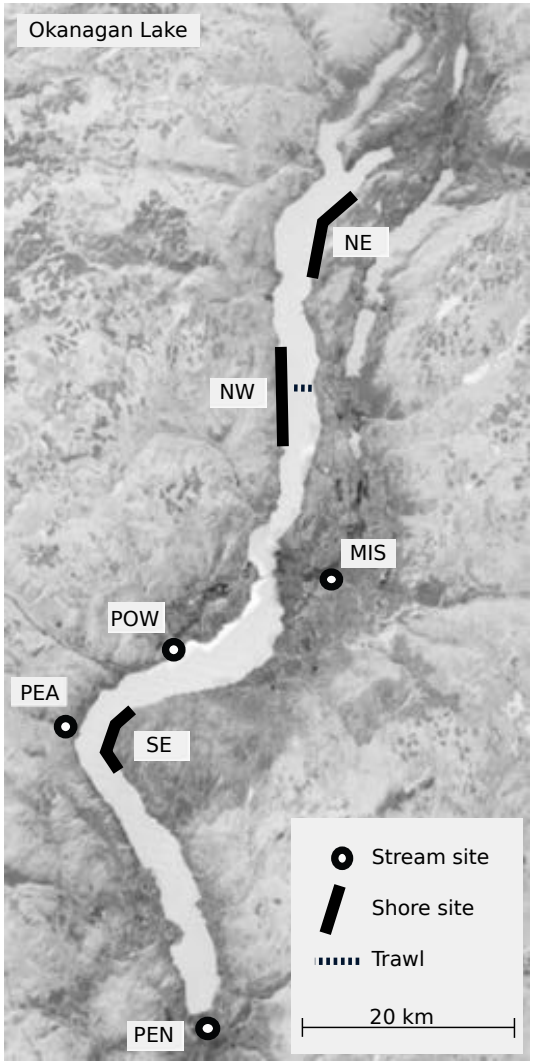
Monitoring sockeye reintroduction

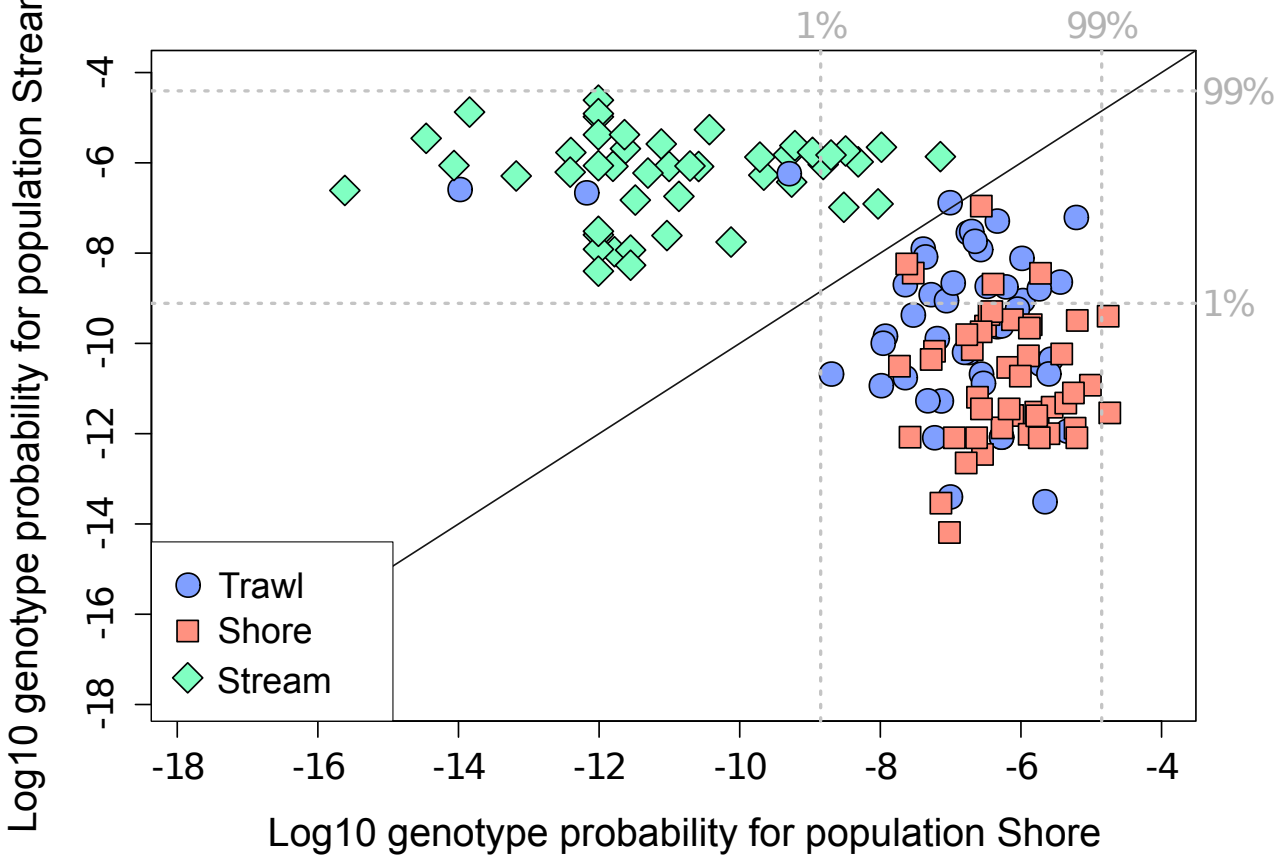
Fisheries management applications



Stock assessment

Fisheries management applications

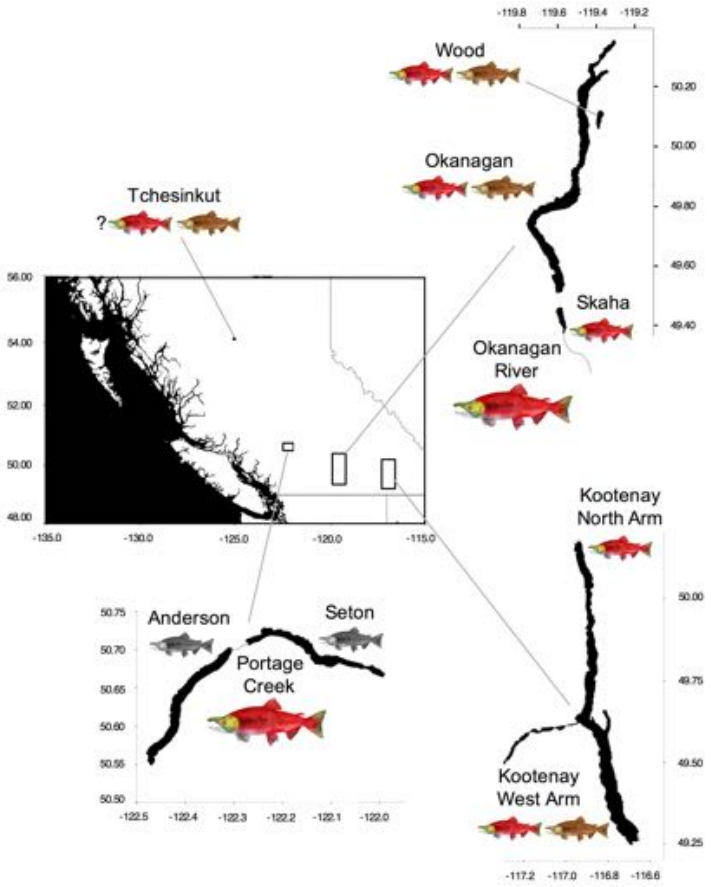


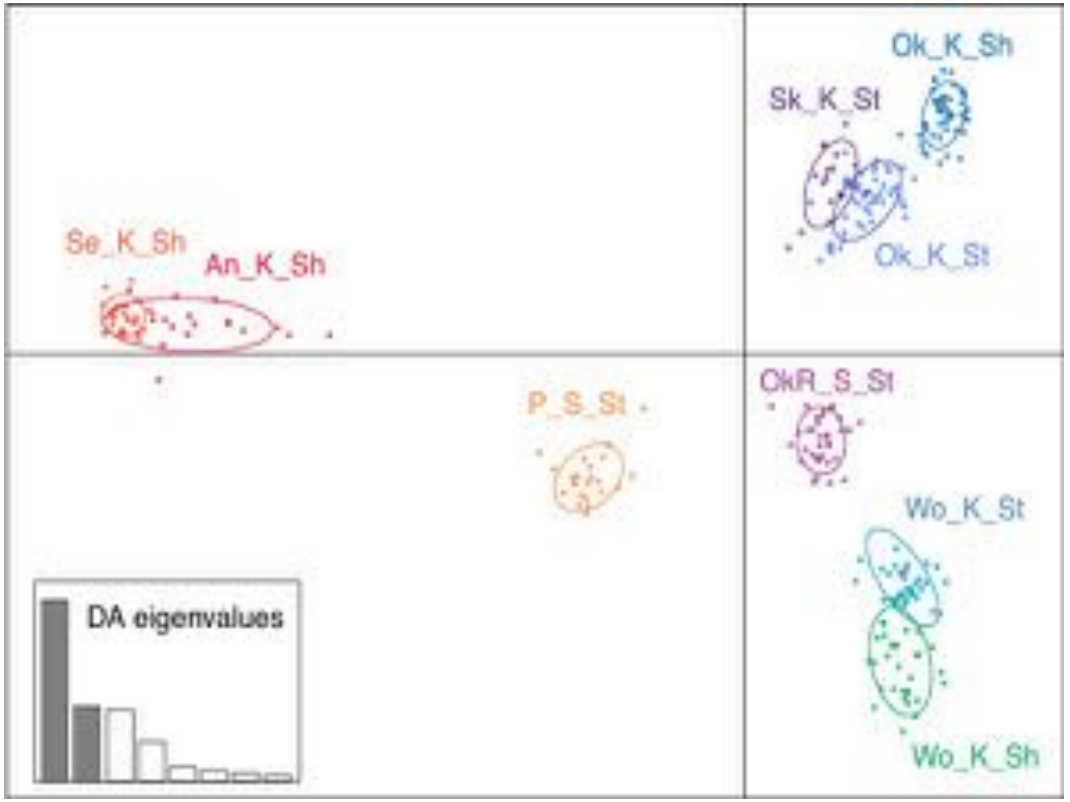


Lemay & Russello (2015) *Mol. Ecol.*

Stock assessment

Fisheries management applications

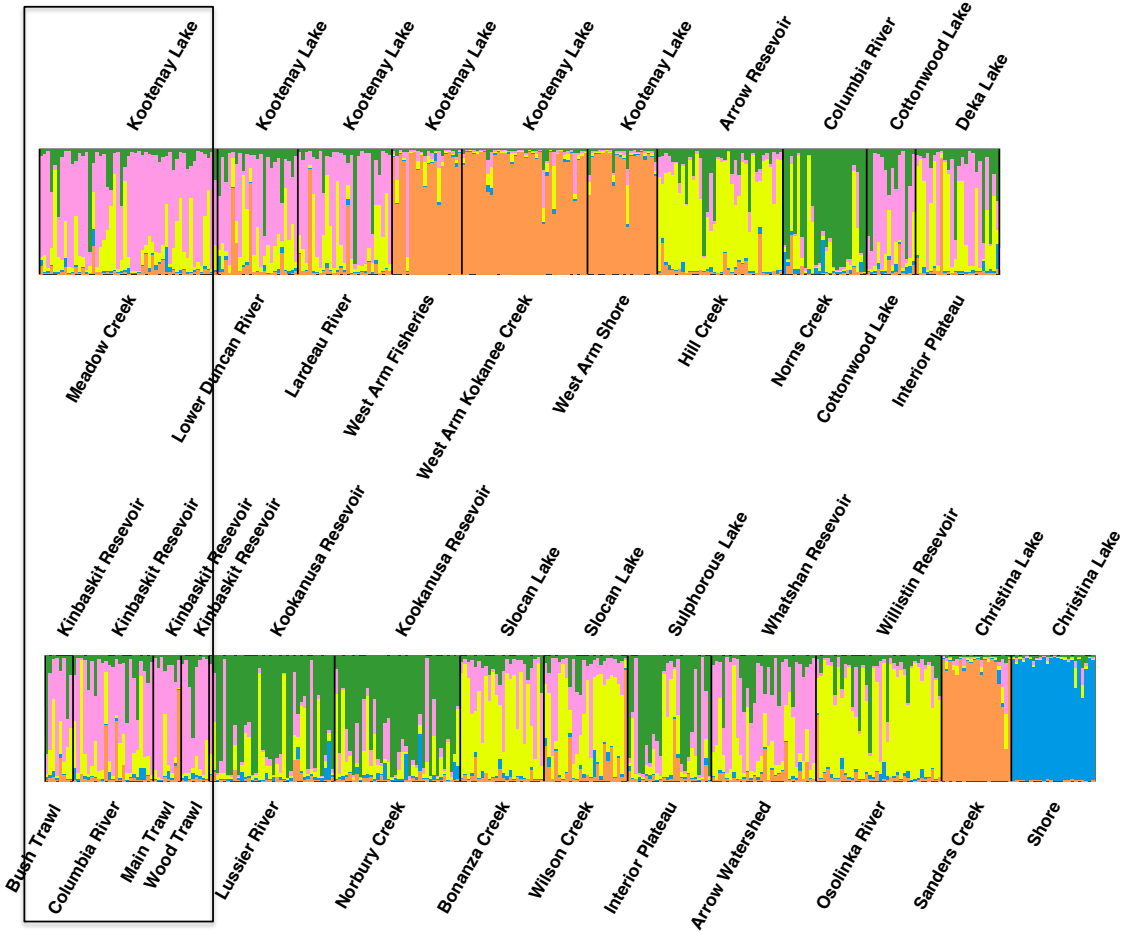




Veale & Russello (2017) *GBE*

Broodstock selection

Fisheries management applications



THANK YOU

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