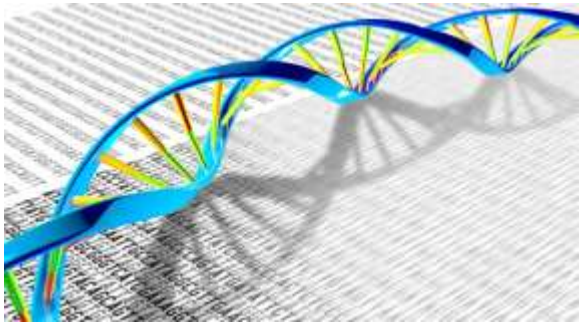
# IMPROVING OUR UNDERSTANDING OF CHINOOK SALMON BIOLOGY

RASMUS GABRIELSSON
JANE SYMONDS

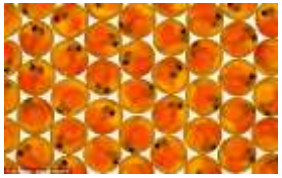


SALMON SYMPOSIUM, ASHBURTON, 11TH- 12TH NOV 2017

# Chinook salmon: fit for a lifetime

**Broodstock**

**Spawning**



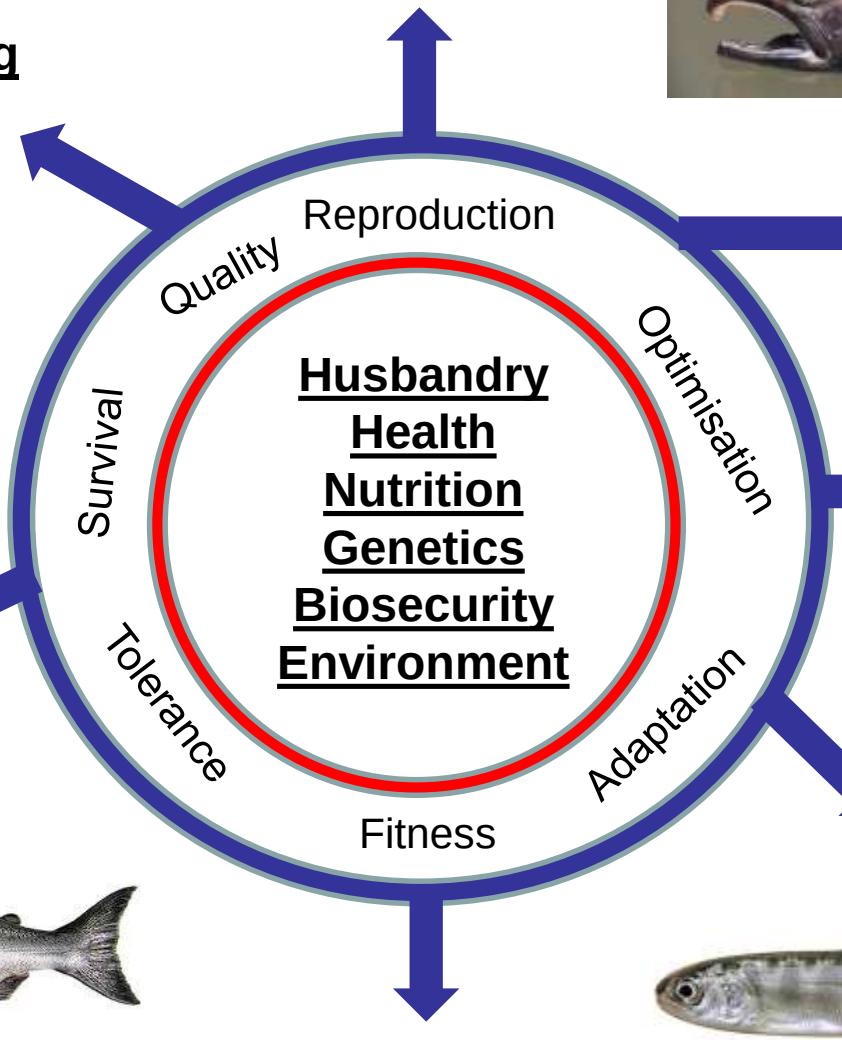
**Gametes**

**Alevins/Fry**

**Juveniles**

**Ocean**

**Smolt**



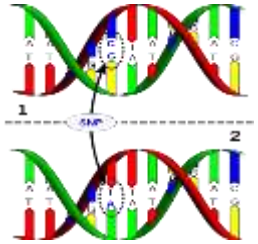
# OUR RESEARCH TAKES A MULTI-DISCIPLINARY APPROACH

Field & On-farm

Fish & trials

**Improved Performance**

Breeding

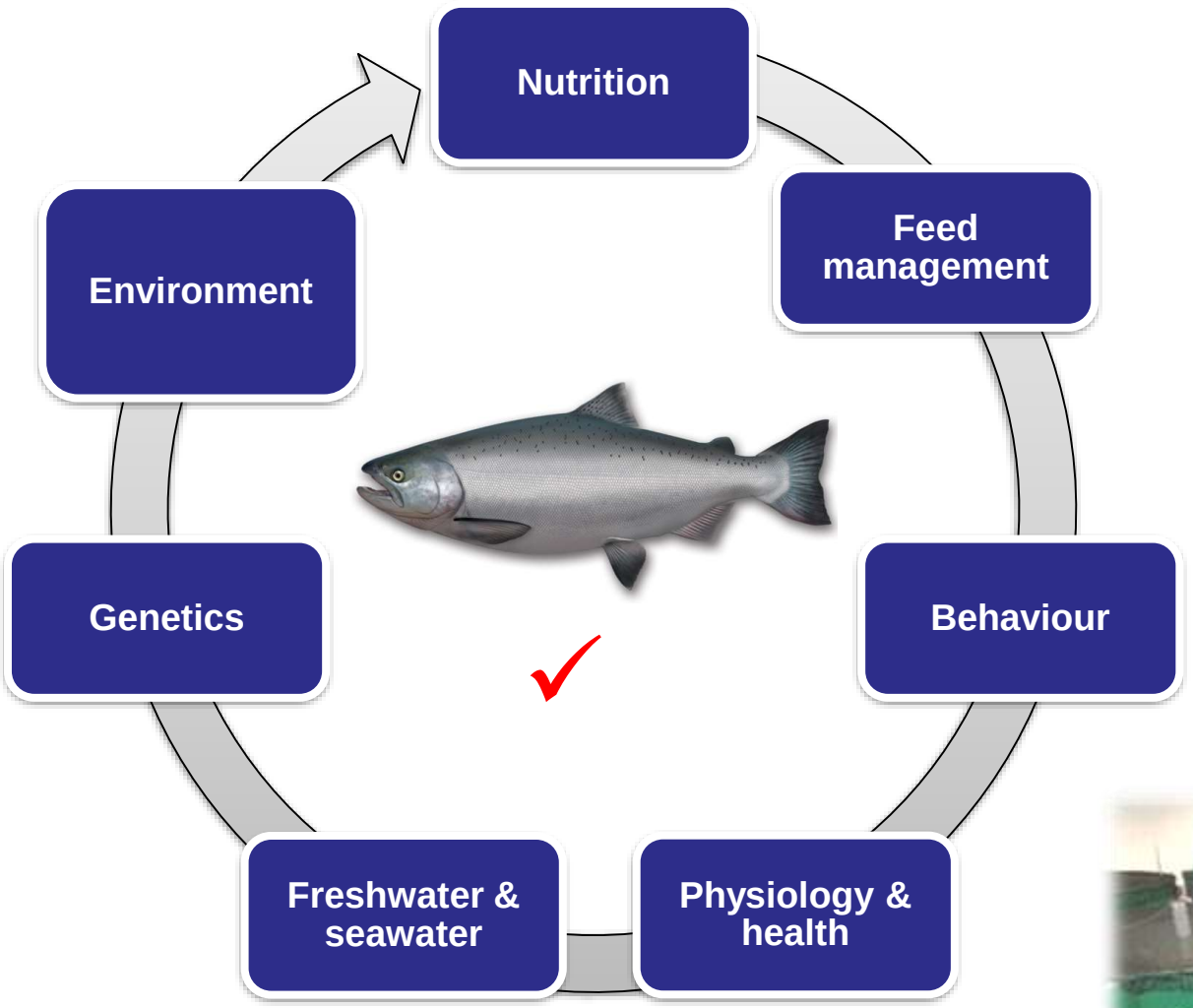


# CAWTHRON AQUACULTURE PARK - SALMON R&D FACILITY


Three recirculation systems:

- Freshwater and/or seawater
- 2 x 9 8,000 L tanks, 9 x 2,500 L tanks
- Full environment control
- Two to four temperatures at the same time

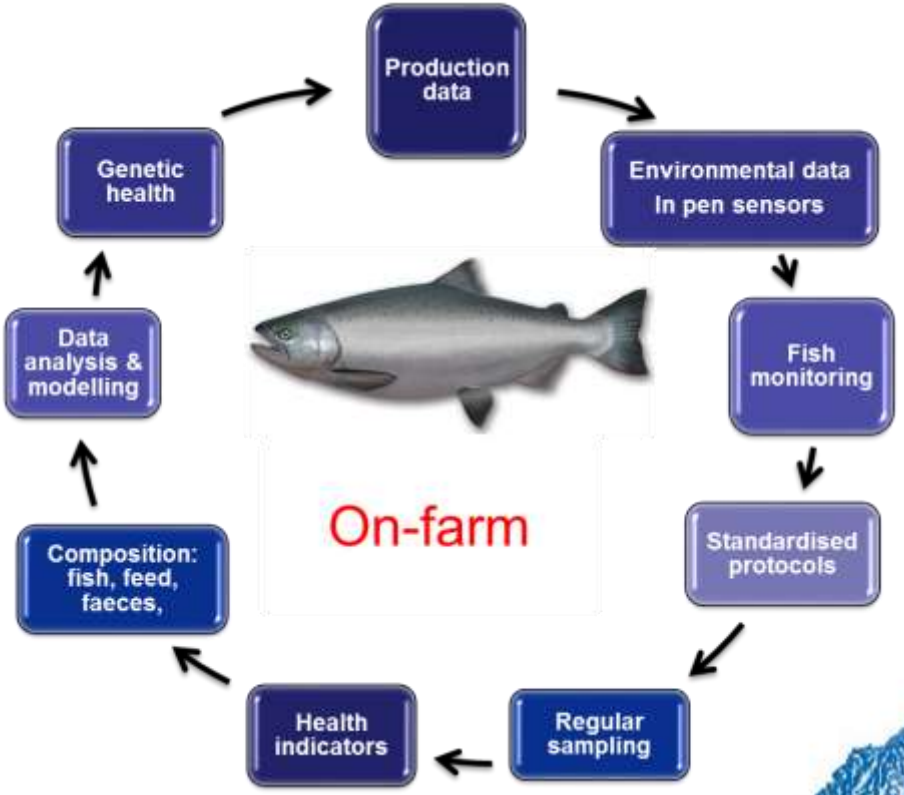
# TANK TRIALS

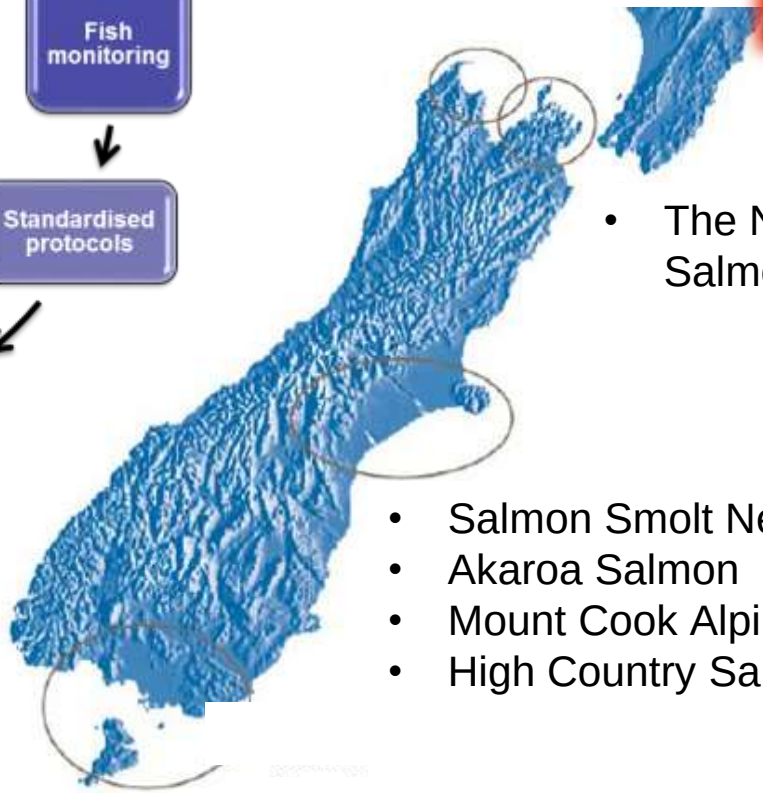



## JUVENILES TO ADULTS

CAWTHRON
The power of science®

# ON-FARM INVESTIGATION



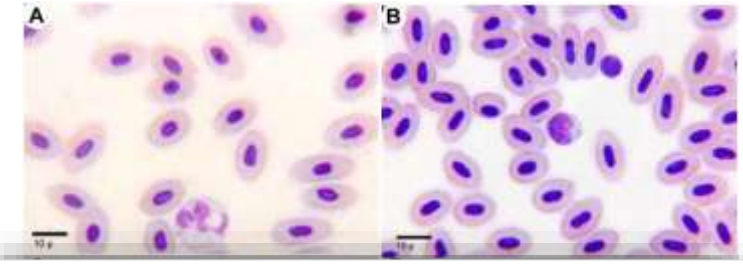
- The New Zealand King Salmon Co. Ltd.
- Salmon Smolt New Zealand
- Akaroa Salmon
- Mount Cook Alpine Salmon
- High Country Salmon
- Sanford Ltd.

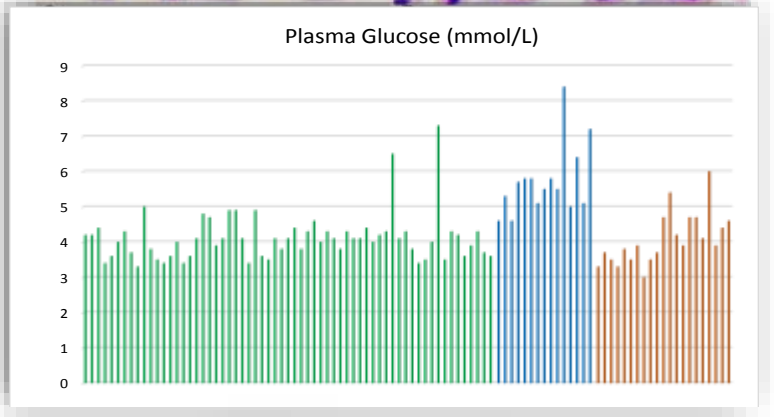
# MONITORING SALMON HEALTH

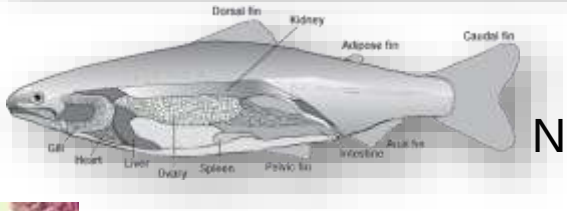
What's a good indicator?

- Dissection and necropsy
- Condition and composition
- Histology
- Plasma biochemistry
- Hematology (blood)
- Metabolites
- Stress & welfare
- Immune response
- Pathogen detection
- X-ray, skeletal health

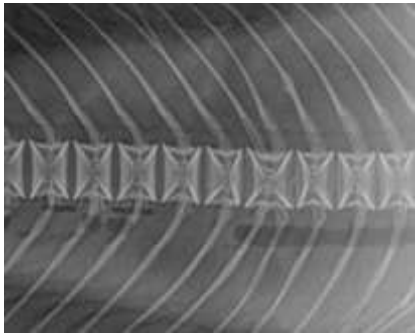
Blood cells

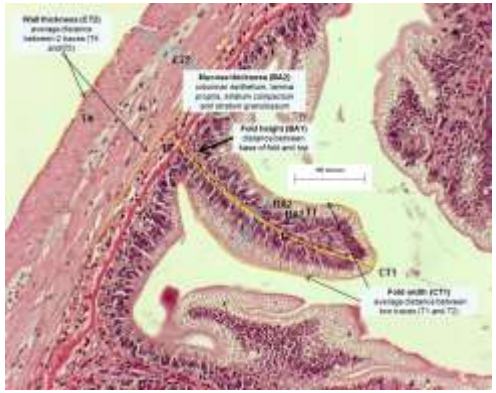



Necropsy

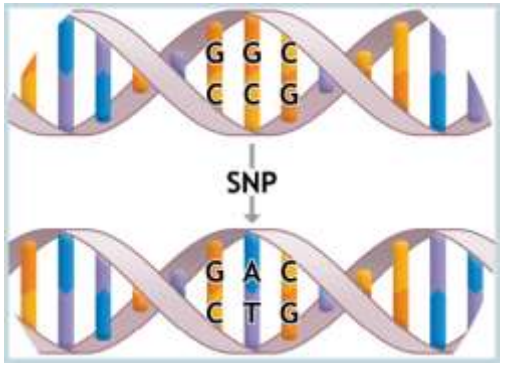




Gut health

## NEW TOOLS FOR MONITORING GENETIC HEALTH

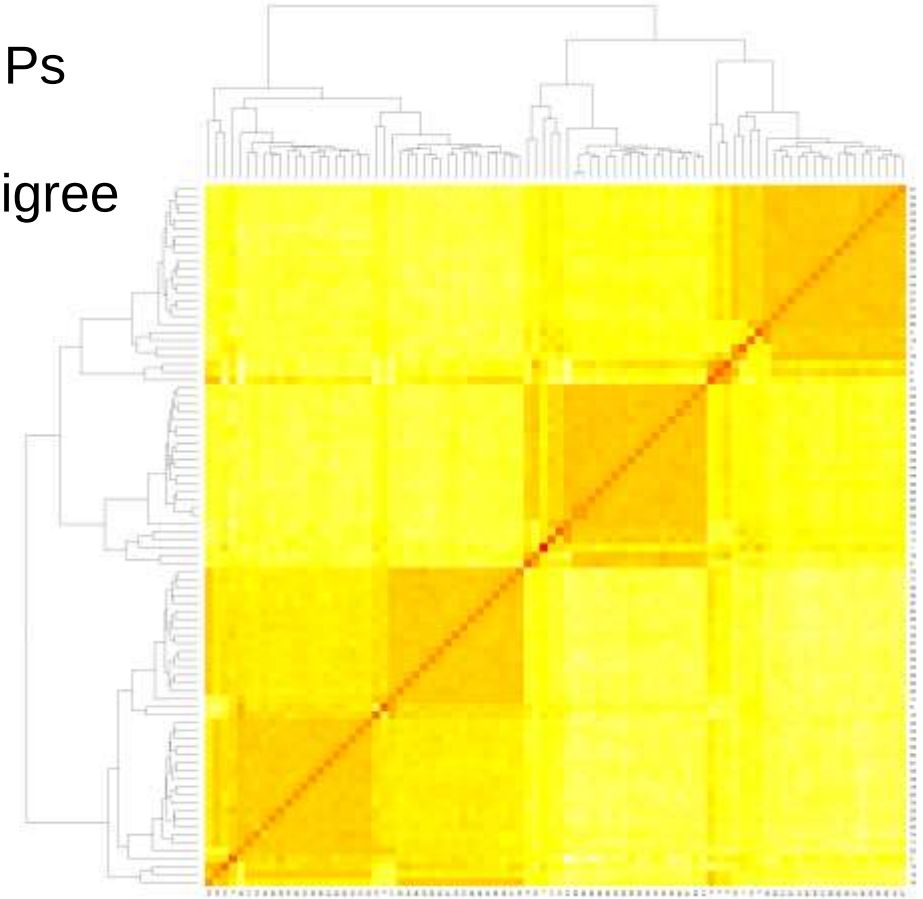
## SINGLE NUCLEOTIDE POLYMORPHISMS (SNPS)




- SNP = DNA base difference (e.g. C to T) in DNA sequence
- Very common, SNPs account for ~90% of all genetic variation
- SNPs reveal hidden variation not detected with other markers
- The ability to genotype thousands of SNPs rapidly in large numbers of samples – e.g. **Genotyping-By-Sequencing (GBS)**
- SNPs allow whole genome coverage and high levels of automation – high throughput and cost effective
- Sampling is straightforward – e.g. fin clip in ethanol

# DEVELOPING GBS FOR CHINOOK SALMON

- AgResearch developed GBS methodology for chinook salmon
- Generates >20,000 to 100,000 SNPs
- Utilised 20,000 SNPs to verify pedigree
- Farmed salmon, currently genotyping
  300 broodstock x 5 populations

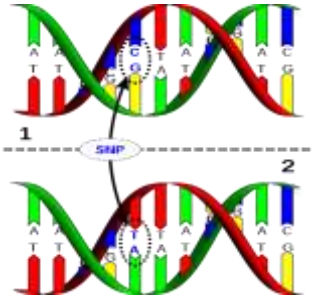


Data provided by Dr. Shannon Clark, AgResearch

agresearch

# GBS APPLICATIONS

- Population genetics
- Genetic diversity
- Relatedness
- Inbreeding management
- Pedigree assignment
- Broodstock management
- Selection




*Transactions of the American Fisheries Society* 140:783–807, 2011
© American Fisheries Society 2011
ISSN: 0002-8487 print / 1548-8659 online
DOI: 10.1080/00028487.2011.590092

SPECIAL SECTION: GENETIC ADAPTATION

## Resolving Adaptive and Demographic Divergence among Chinook Salmon Populations in the Columbia River Basin

**Andrew P. Matala,* Jon E. Hess, and Shawn R. Narum**
*Columbia River Inter-Tribal Fish Commission, Hagerman Fish Culture Experiment Station, 3059-F National Fish Hatchery Road, Hagerman, Idaho 83332, USA*

Biol Invasions (2015) 17:2989–2998
DOI 10.1007/s10530-015-0928-x

CrossMark

ORIGINAL PAPER

## The invasion of an Atlantic Ocean river basin in Patagonia by Chinook salmon: new insights from SNPs

**Javier E. Ciancio · Carla Riva Rossi · Miguel Pascual · Eric Anderson · John Carlos Garza**

Evolutionary Applications
Open Access
Evolutionary Applications ISSN 1752-4571

ORIGINAL ARTICLE

## Detection and mapping of QTL for temperature tolerance and body size in Chinook salmon (*Oncorhynchus tshawytscha*) using genotyping by sequencing

Meredith V. Everett* and James E. Seeb

School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA, USA
* Present address: Northwest Fisheries Science Center, National Oceanic and Atmospheric Administration, 2725 Montlake Blvd East, Seattle, WA, 98112, USA

CAWTHRON
The power of science®

# WHY IS GBS RELEVANT TO WILD NZ CHINOOK SALMON?

- Can be used to better understand how chinook salmon populations in NZ differ and have potentially adapted and diverged since they were introduced. Building on the work done in the 1990's by Unwin, Quinn and Kinnison, but uses higher resolution DNA markers.

- Can determine the "genetic health" of NZ chinook salmon populations by estimating genetic diversity, inbreeding levels and relatedness

- Can provide tools for broodstock management:
  - Reduced risk of inbreeding
  - Ensuring genetic variation is maintained
  - Parentage assignment - ability to monitor success of hatchery releases

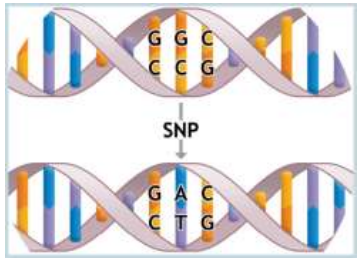
CAWTHRON
The power of science®

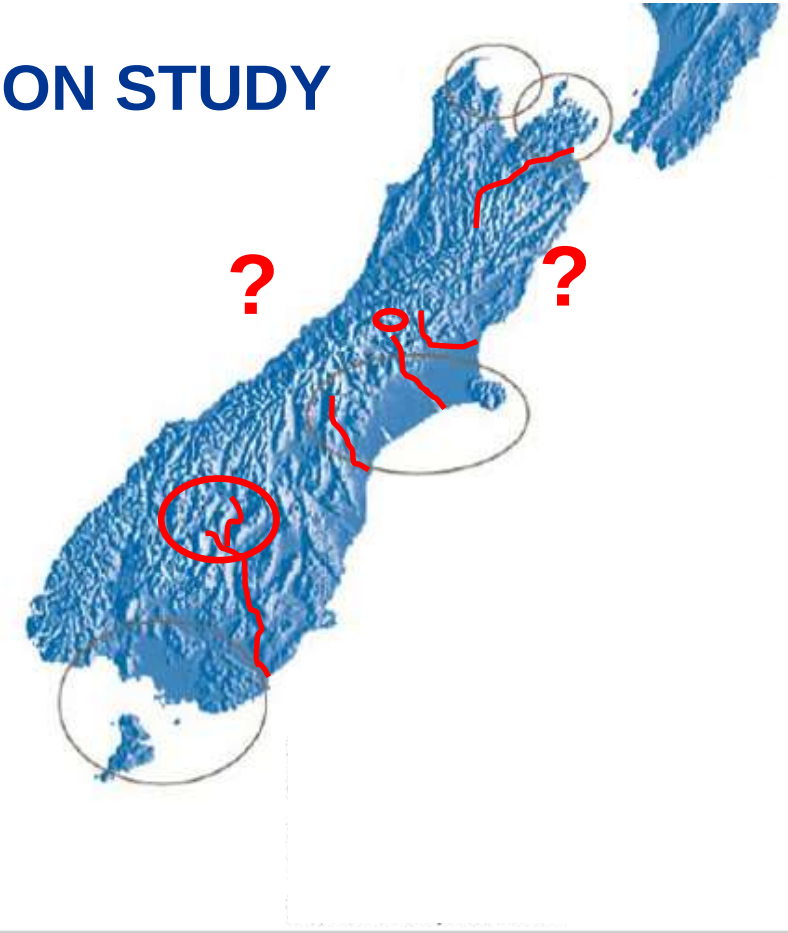
# PROJECT PROPOSAL

- Use GBS to characterize the population genetics of NZ wild chinook salmons
- Collect 50 samples from spawning individuals from at least 5 different populations for analysis
- Collaboration with: Fish & Game, Cawthron, AgResearch and University of Victoria
- University of Victoria: work with population geneticist Dr Peter Ritchie and establish a MSc student project to help
- Samples from 10 frozen heads tested – good DNA
- 100+ wild fish collected. Preliminary results expected in early 2018

CAWTHRON
The power of science®

# POPULATION GENOMICS:
# GBS WILD CHINOOK SALMON STUDY

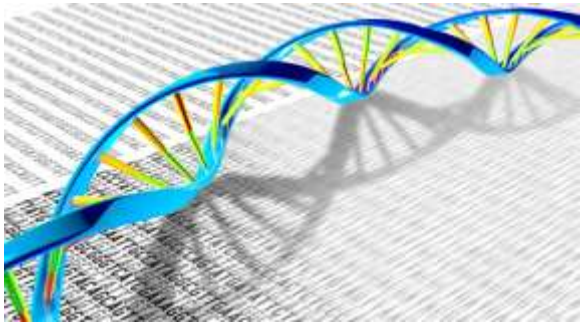



Possible sampling locations:

- Wairau R,
- Waimakariri R,
- Rakaia R (including Lake Coldridge perhaps?),
- Rangitata R,
- Waitaki R,
- Clutha R (incl landlocked salmon from the Southern Lakes)

CAWTHRON
The power of science®



# QUESTIONS?