

# Skeena River Aggregate Coho Salmon Estimator

Final Report  
March 2020

PSC NF-2019-I-44

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## Abstract

The number of coho salmon (*Oncorhynchus kisutch*) in the Skeena River, British Columbia, is unknown. In 2019, funding was received from the Pacific Salmon Commission's Northern Endowment Fund to estimate the Skeena River coho salmon aggregate population using genetic techniques. We used a genetic mark-recapture technique and adopted modifications to the Lincoln-Peterson mark-recapture estimator ( $N=M/p$ ) in combination with the SNP-based genetic baseline to create the first watershed-wide escapement estimate for Skeena River coho salmon. In a traditional mark-recapture scheme, individuals are captured and marked ( $M$ ) upon river entry. The proportion of marked to unmarked individuals ( $p$ ) is then estimated on the spawning grounds. In our scenario, the typical mark-recapture experiment is reversed: the first sampling occasion, when individuals are traditionally marked ( $M$ ), occurs when a single population is identified as genetically distinct, and the second sampling occasion occurs when the proportion ( $p$ ) of the "marked" population is determined (recaptured) in a mixed stock fishery in the lower Skeena River. In 2019, we estimated escapement of 19,957 coho salmon to the genetically distinct (marked) upriver population. The proportion ( $p$ ) of the "marked" population present in the lower Skeena River test fishery was estimated as 30%, yielding an abundance estimate of 65,104 coho salmon.

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## Introduction

Funding for this project was provided by the Pacific Salmon Commission's Northern Endowment Fund (NEF) to estimate coho salmon (*Oncorhynchus kisutch*) abundance in the Skeena River in 2019. This report presents the initial genetic information from samples collected at the Tyee Test Fishery, preliminary estimate of the coho salmon return to the Skeena River, and population supplementation to the current coho salmon ("coho") baseline. Costs to the NEF consisted of the genetic analyses, labor, and genetic tissue collection. All other costs to the project were already funded by the Office of Wet'suwet'en and Fisheries & Oceans Canada.

The primary objective of this study was to generate a watershed-wide estimate of the coho return to the Skeena River. Coho escapement estimates for the Skeena River are measured with an index that is comprised of the mark-recapture estimate for the Bulkley River (above Witsset Canyon), partial weir counts for the Babine, Kitwanga and Slangeesh Rivers, and visual estimates for various small populations throughout the Skeena River watershed. The Bulkley River is considered the index stream for this experiment, and hypothesized to comprise over 20% of Skeena River coho aggregate.

Two components, the Tyee Test Fishery and the Witsset Canyon (formally Moricetown Canyon) mark-recapture (MR) program, contribute data needed to produce a Skeena River watershed-wide estimate of coho. These programs are currently funded by Fisheries and Oceans Canada, the Province of British Columbia, and the Office of Wet'suwet'en.

The Skeena River Tyee Test Fishery ("Tyee") is located in the lower Skeena River (Figure 1.). This program was developed in 1955 specifically to provide daily estimates of sockeye and pink salmon escapements through the commercial fishery, but also provides relative abundance and timing for all other species (Chinook, coho and chum salmon and steelhead trout). A major assumption of the general operation of Tyee is that it allows the collection of unbiased sub-samples for all returning populations of salmonid species as they pass through the lower Skeena River above the Ecstall River.

The Witsset Canyon MR program is located at the Witsset Canyon on the Bulkley River northwest of Smithers, British Columbia (Figure 1.). In operation since 1998, the MR program was developed to provide escapement estimates of sockeye salmon, coho salmon, and steelhead trout returning to the Bulkley River above Witsset Canyon. In the context of this experiment, the Bulkley River coho population is considered the "index" population and is genetically distinguishable from all other coho populations within the Skeena River watershed.

## Objective

The main objectives of the project as identified in the Detailed Proposal include:

- Create an escapement estimator for the Skeena River aggregate using genetic tools
- Supplement current genetic baseline with additional coho populations

The project met these objectives as explained in further detail below.



## Methods

### Tyee Test Fishery

The Tyee Test Fishery (“Tyee”) is located on the north side of the Skeena River just upstream of the confluence with the Ecstall River (Figure 1). The Tyee is standardized to focus on providing in-season indication of sockeye salmon (*Oncorhynchus nerka*) abundance, but also monitors the relative abundance of other salmon species including coho (Cox-Rodgers and Jantz, 1993; Jantz et al. 1990). From mid-June through late September, a multi-panel gill net with varying mesh size is deployed in standard locations. A full description of the test fishery is outlined in Kadowaki, 1977.

Coho captured at Tyee are sampled for scales (age & genotyping), nose-fork length, eye orbit to hypural length, and sex is determined. These primary data are collected using standardized procedures outlined in literature such as MacLellan (1999). Scales are forwarded to the Fisheries & Oceans Canada, Fish Ageing Laboratory and Molecular Genetics Laboratory (MGL) at the Pacific Biological Station for processing.

To estimate stock composition of coho captured at Tyee, tissue samples were genotyped by staff scientists at DFO’s MGL using a panel of 302 SNP markers described in Beacham et al. 2017. The laboratory procedures for genotyping SNP loci are well-established (Campbell et al. 2015). The genotypes of the individuals captured at the “mixed stock” fishery (“Tyee”) are compared against the Skeena River genetic baseline that currently contains 21 distinct coho populations. The software RUBIUS (Moran and Anderson 2018), which employs Bayesian inference from a conditional genetic stock identification model, is used to estimate the population of origin.

### Witset Canyon Mark-Recapture

To estimate escapement of coho above Witset Canyon on the Bulkley River ( $\hat{N}_b$ ), we used the closed population “pooled” or “simple” Lincoln-Peterson model with the Chapman adjustment to account for low numbers of recaptures (Seber, 1982).

$$\hat{N}_b = \left( \frac{(M + 1)(C + 1)}{R + 1} \right) - 1$$

During the first sampling occasion ( $M$ ), individuals are captured immediately downstream of Witset Canyon using a beach seine and at the upstream end of the Witset Canyon using dip nets. FLOY tags with individual identification are used for temporary marks and caudal fin hole punches for secondary permanent marks. During the second sampling occasion, fish are captured and examined ( $C$ ) for marks 12 km upstream of Witset Canyon at the adult fish trapping facility located on Toboggan Creek (Figure 1). Marked individuals identified during the second sampling occasion are considered recaptures ( $R$ ).

The variance  $Var(\hat{N}_b)$  is estimated by:

$$Var(\hat{N}_b) = \frac{(M + 1)(C + 1)(M - R)(C - R)}{(R + 1)^2(R + 2)}$$

### Escapement Estimate

To estimate escapement of the Skeena River coho aggregate population, we used a modified Lincoln Peterson mark-recapture estimator in conjunction with the relative mixed-stock proportions estimated at Tyee and the MR program at Witset Canyon. In a traditional mark-recapture scheme ( $\hat{N} = M/\hat{p}$ ) individuals are captured and marked ( $M$ ) upon river entry. The proportion of marked to unmarked individuals ( $\hat{p}$ ) is

then estimated on the spawning grounds. In our scenario, the typical mark-recapture experiment is reversed and therefore modified;  $\hat{N}_s$  represents the escapement estimate of the Skeena River aggregate coho population.

$$\hat{N}_s = \frac{\hat{N}_b}{\hat{p}_b}$$

The first sampling occasion, when individuals are traditionally marked ( $M$ ), occurs when a single population is identified as genetically distinct (Bulkley River) and abundance is estimated ( $\hat{N}_b$ ); the second sampling occasion occurs when the proportion ( $\hat{p}$ ) of the Bulkley River is determined (recaptured) in a mixed stock fishery (“Tyee”) in the lower Skeena River ( $\hat{p}_b$ ).

Variance for the Skeena River aggregate coho escapement is estimated as the quotient of two independent variables, where  $cv$  represents the coefficient of variation:

$$Var(\hat{N}_s) = \hat{N}_s^2 \left( \left( \frac{Var(\hat{N}_b)}{\hat{N}_b^2} \right) + \left( \frac{Var(\hat{p}_b)}{\hat{p}_b^2} \right) \right)$$

Or

$$Var(\hat{N}_s) = \hat{N}_s^2 (cv^2(\hat{N}_b) + cv^2(\hat{p}_b))$$

### Genetic Baseline

The current Skeena River genetic baseline represents 21 distinct coho populations. To supplement the baseline and increase confidence in self assignment tests, an additional seven distinct populations were targeted for sampling. These seven populations have varying population sizes within the Middle Skeena River Conservation Unit (CO-33) and Upper Skeena River Conservation Unit (CO-34) and include the Babine, Bear, Kispiox, Kitsegukla, Shegunia, Suskwa, and Telkwa Rivers. A target of 100 tissue samples were pursued for each of the seven additional populations. Samples are currently being genotyped and will be added to the genetic baseline.

Adult coho were collected by weir, beach seine and angling. Adult coho capture techniques depend on the location, terrain, access, and hydrologic characteristics at the sampling location. Juvenile coho were sampled from populations where access to adult coho was unreliable. Juvenile coho were captured and sampled using gee traps and electroshocking. A potential source of error is that juvenile coho may move into tributaries to feed during their downstream migration from the Skeena Rivers. To reduce the likelihood of sampling juvenile coho originating from other systems, juvenile coho were collected from each target stream 2 to 3 km above its confluence.

Sex, nose-fork length (mm) and location (UTMs) was recorded for each sampled adult coho. Weight (g), nose-fork length (mm) and location (UTMs) was recorded for each sampled juvenile coho. Tissue was stored on Whatman sheets provided by Fisheries and Oceans Canada MGL following standardized protocols. All tissue samples were processed by the MGL using techniques described in Beacham et al. 2017.

## Results

### Tyee Test Fishery

The Tyee Test Fishery operated from June 10 to September 26 in 2019, and coho were captured from July 8 through September 25. A total of 283 coho were encountered and 176 sampled for size, sex and genetic tissue. Of the 176 samples submitted for analysis, 175 were successfully genotyped as coho, one fish was assigned as a steelhead trout and removed from the analysis.

The Skeena River baseline used for sample analysis ( $n=175$ ) included representation from 21 populations. The proportion of samples assigned to the Bulkley River above Witset Canyon was estimated at 30.6%. The Upper Skeena CU contributed 29.7%, followed by the Lower Skeena CU at 23.1% and Middle Skeena CU (excluding the Bulkley River) at 16.6%.

### Witset Canyon Mark-Recapture

The Witset Canyon MR program operated from July 2 through October 11, 2019. Coho were captured from July 23 through October 8. A total of 678 coho were marked and released ( $M$ ). At the adult fish trapping facility located on Toboggan Creek, 1,484 fish were examined for marks ( $C$ ), with 47 recorded as recaptures ( $R$ ). The 2019 escapement of coho to the Bulkley River above the Witset Canyon was estimated at 19,957 individuals ( $\pm 5,289$  fish;  $CV = 13.5\%$ ).

### Escapement Estimate

We estimated an escapement of 19,957 ( $\hat{N}_b$ ) coho to the genetically distinct (marked) upriver population. The proportion ( $\hat{p}_b$ ) of the “marked” population present at Tyee was estimated as 30.6%. The escapement for the Skeena River coho aggregate was estimated at 65,104 individuals ( $\pm 38,619$  fish;  $CV = 30\%$ ).

### Genetic Baseline

In total, 833 coho tissue samples were submitted to supplement the current genetic baseline. Adult coho tissue was collected on the Kispiox River ( $n=93$ ) and Babine River ( $n=100$ ). Juvenile coho tissue was collected on the Kitsegukla River ( $n=151$ ), Shegunia River ( $n=112$ ), Suskwa River ( $n=217$ ), and Telkwa River ( $n=160$ ). Populations where juvenile coho tissue was collected were “over-sampled” ( $>100$  samples) to account for the probability of related individuals. Individuals considered related are treated as duplicates and will not be added to the genetic baseline. At the time of this report, results for the genetic baseline supplementation are not yet available.



## Discussion

The findings presented in this report are preliminary. We estimated an escapement of 65,104 coho (CV = 30%) to the Skeena River aggregate. This does not meet precision standards set by McElhany et al. (2000) of a CV less than 15%. With an acceptable CV associated with the Witset Canyon escapement estimate (13.2%), the elevated uncertainty must have been introduced by the Tyee mixed stock analysis results (CV= 27%). An increased sample size accompanied by a more robust genetic baseline should improve estimates for the Tyee mixed stock analysis. The results for the updated genetic baseline were not available during the time of writing this report.

Additional analyses are required to develop final estimates for the aggregate Skeena River coho population as well as the major component stocks and conservation units. Results were developed in 2019 using the current genetic baseline from 21 coho salmon spawning populations, however this baseline does not fully represent all distinct populations within the Skeena River watershed. Use of a genetic mark-recapture technique for the applications described in this study, requires accurate assignment of individuals to their population of origin. Incorrect or missing assignments can introduce a greater level of uncertainty to the escapement estimate. Evidence of this error is observed in the Tyee coho mixed stock analysis (CV= 27%), and can be associated with the “incomplete” genetic baseline as well as the low number of coho sampled at the Tyee ( $n= 176$ ). Previous research estimates that a sample size of 100-400 is sufficient to estimate a genetic stock proportion with a standard deviation of less than 7% (Decovich et al. 2010). A standard deviation of 8.3% was estimated in the Tyee mixed stock analysis for individuals assigned to the Bulkley River. Therefore, it is more likely the elevated error is associated with an incomplete genetic baseline and not an artifact of sample size.

Our escapement estimate of coho above Witset Canyon met precision standards with a CV of 13.2%, and could be improved by increasing the number of deployed tags and through more precise estimate of recaptures. Historically, a tag loss rate of 5% was applied before calculating the escapement estimate (Barry Finnegan, *pers. comm.*). In 2019, we also applied tag loss rate of 5%. With tagged fish receiving permanent marks (e.g., caudal fin hole punch), the actual tag loss rate can be estimated if all fish captured at the Toboggan Creek adult counting facility were examined. Fish with caudal fin hole punches present without FLOY tags are considered recaptures, and will yield a tag loss rate for fish returning to Toboggan Creek. Assuming the Toboggan Creek coho population represents a given proportion of Bulkley River coho, this approach then allows us to create an estimate of annual tag loss. Fishery removals at Witset Canyon are not taken into account for the 2019 estimate. The inclusion of catch estimates will require exact counts currently not available for this report.

In 2019, a total of 833 coho tissue samples from seven populations (Babine, Kispiox, Kitsegulka, Shegunia, Suskwa, and Telkwa Rivers) were collected and are currently being added to the genetic baseline. We were successful in collecting our target sample sizes from all but one population, the Bear River. This remote, fly-in only river presented unforeseen challenges that will be addressed in the proceeding field seasons.

## Measure of Success

Quantifiable objectives of the project used to evaluate success include:

- An escapement estimate for the 2019 Skeena River aggregate coho population with a CV <15%.

Even though the precision standards were not met, this project is considered a success as an escapement estimate (and associated variance) was created for the Skeena River aggregate coho population providing mixed-stock fisheries managers with the additional information to make informed decisions.

- Collection of  $\geq 100$  genetic tissue samples for each target coho population for inclusion into the genetic baseline.

The target sample size was met for five of the six populations plus an additional non-target population (Babine River) resulting in the inclusion of six new populations into the genetic baseline.

## Recommendations

This project has been approved for continuation for a second year by the Northern Endowment Fund. The technique used to estimate escapement for the Skeena River coho aggregate population will be improved through the following additional work:

1. Reanalyzing the 2019 escapement estimate once the six additional populations are included in the baseline.
2. Complete a robust baseline for all distinct populations of coho in the Skeena River watershed.
3. Determine at what resolution we can determine stock composition or CU proportions in the Tye sub-sample.
4. Increase the sample size of coho at the Tye by sampling all fish encountered.
5. Reduce error associated with the Witset Canyon MR program by tagging all coho encountered.
6. Reduce error associated with the Witset Canyon MR program by examining all fish encountered at the Toboggan Creek adult counting facility for permanent marks.
7. Include catch accounting for all Skeena River terminal fisheries in the final results.

## Budget Summary

Expenditures of the Northern Endowment Funds amounted to \$61,735 CAN and matched the budgeted amount. The remaining \$30,735 is anticipated to be released once the final report is accepted by the Pacific Salmon Commission. The summary of fund expenditures in relation to budgeted amounts is as follows:

Description	Budget (PSC)	Expenditure	Balance
Wages and Salaries	41,055.00	41,055.00	0.00
Contract Services	13,500.00	13,500.00	0.00
Travel	5,000.00	5,203.11	-203.11
Supplies and materials	2,180.00	1,976.89	203.11
Capital Equipment	0.00	0.00	0.00
Indirect costs	0.00	0.00	0.00
<b>Total</b>	<b>61,735.00</b>	<b>61,735.00</b>	<b>0.00</b>

## Acknowledgements

This project is a result of collaboration among many stakeholders. Fisheries and Oceans Canada provided funds to run the Tyee Test Fishery and supplement the Witsset Canyon mark-recapture program. The Tyee Test Fishery was run by Richard Kristmanson and staff with support from Fisheries and Oceans Canada field technicians for biological sampling. Technicians from the Office of Wet'suwet'en conducted the mark-recapture program at Witsset Canyon. The Toboggan Creek adult fish counting facility was ran by staff from the Salmon Creek Salmon Enhancement Society with support from Fisheries and Oceans Canada. The MGL at the Pacific Biological Station, provided the genetic analysis. Improvements to the genetic baseline were supported by staff from the Gitksan Watershed Authorities and Skeena Fisheries Commission.

## Literature Cited

- Beacham, T.D., Wallace, C., MacConnachie, C., Jonsen, K., McIntosh, B., Candy, J.R., Devlin, R.H., and Withler, R. R., 2017. Population and individual identification of Coho salmon in British Columbia through parentage-based tagging and genetic stock identification: an alternative to coded-wire tags. *Canadian Journal of Fisheries and Aquatic Sciences*: 74(9).
- Campbell, N. R., Harmon, S. A., and Narum, S. R., 2015. Genotyping-in-Thousands by sequencing (GT-seq): A cost effective SNP genotyping method based on custom amplicon sequencing. *Molecular ecology resources*: 15(4):855-867.
- Cox-Rogers, S., and Jantz, L., 1993. Recent trends in the catchability of sockeye salmon in the Skeena River gillnet fishery, and impacts on escapement estimation. *Can. Manusc. Rep. Fish and Aquatic Science*: 2219 (19).
- Decovich, N. A., Templin, W. D., and Evenson, D. F., 2010. Genetic stock identification of Chinook Salmon harvest on the Yukon River 2008. Alaska Department of Fish and Game, Fishery Data Series 10-20, Anchorage.
- Kadowaki, R., 1977. The Skeena river gillnet test fishery, 1955 to 1976. In-house document. Department of Fisheries and Oceans.
- Jantz, L., Kadowaki, R., and Spilsted, B., 1990. Skeena River salmon test fishery, 1987. *Canadian Data Report of Fisheries and Aquatic Sciences* 804.
- MacLellan, S. E., 1999. Guide for sampling structures used in age determination of Pacific salmon. Fisheries and Oceans Canada, Stock Assessment Branch, Pacific Biological Station, Nanaimo, British Columbia.
- McElhany, P., Ruckelshaus, M. H., Ford, M. J., Wainwright, T. C., and Bjorkstedt, E. P., 2000. Viable salmonid populations and the recovery of evolutionarily significant units. *US Dept. Commer. NOAA Tech. Memo. NMFS-NWFSC*, 42, 156.

Moran, B.M, and Anderson, E.C., 2018. Bayesian inference from the conditional genetic stock identification model. *Canadian Journal of Fisheries and Aquatic Sciences*. 76(4).

Seber, G. A. F., 1982. *The estimation of animal abundance*.