

# TRENDS IN SIZE-AT-AGE, SEX RATIOS, AND AGE-AT-RETURN IN HATCHERY AND WILD CHINOOK SALMON ACROSS BC

## DATA REPORT



Photo credit: Eiko Jones

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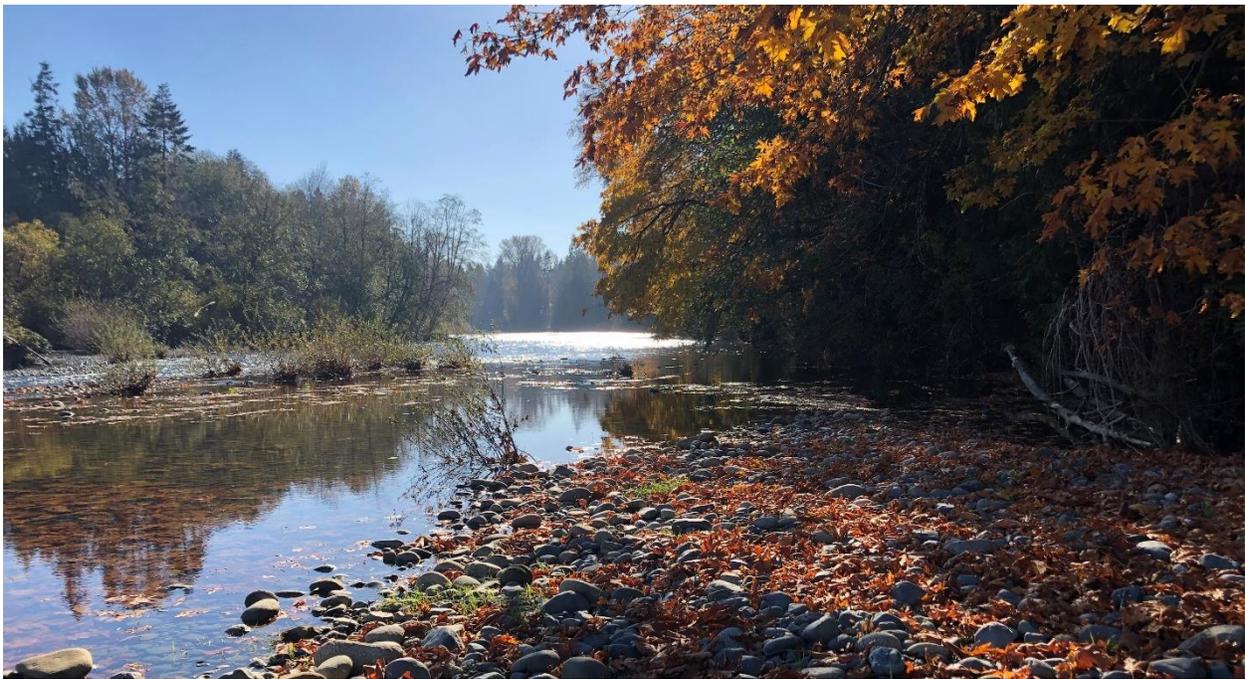
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## INTRODUCTION

This report contains a breakdown of the datasets included in the Chinook Biodatabase used in the biodata component of the PSF Comprehensive Review. The Chinook Biodatabase was used to identify biological and demographic trends for BC Chinook salmon stocks, specifically size-at-age, age composition and sex composition. As such, escapement records that offered data on postorbital-hypural length (POHL), age, sex and 'Stock of origin' were used. Our main questions were as follows:

1. Has mean age and age proportions of Chinook salmon changed over time?
2. Has mean size and size-at-age changed over time in Chinook salmon?
3. Has the sex composition changed over time in Chinook salmon?
4. What systems have enough data to analysis for these questions?

We note that the data that we had access to include mostly hatchery dominated Chinook populations, primarily over the time frame 1996–2020, with some additional pre-1996 data for Robertson Creek and Chilliwack River.

While DFO, through the Salmon Enhancement Program (SEP) and Stock Assessment Division (StAD), has compiled a significant portion of the most current data, a number of local Chinook Biodatabases still remain unaccounted for. This includes data from a number of non-EnPro hatchery facilities and historical data that are yet to be assessed, standardized and incorporated. As such, a large portion of the current project involved the procurement, assessment and standardization of data from unaccounted stocks and historical files.

This data report aims to provide an in-depth description of the variables of interest, sources and main characteristics of the datasets included, and standardizations conducted to harmonize them into a single contiguous database.



Photo credit: Mitch Miller

## VARIABLES OF INTEREST

### Year

Referring to sample year (or run year), this was the main time variable used and was readily available for all datasets. In some instances, the full date of sampling was included, sometimes in a variety of formats, which required some data manipulation and cleaning to extract sample year.

### Stock

This refers to the natal stock from which the sampled fish originated. It was the main spatial unit used in this study. In the datasets we used, stock could be represented using either the 'sample site' or 'stock of origin', with the latter extracted from CWT and/or thermal mark information.

### Sex

The biological sex of individuals, which for most individuals was assessed through external examination conducted in the field. Some individuals were internally examined as well.

Photo credit: Nicole Christiansen



## Ocean age

Age was represented in our study using ocean age, or the number of years an individual spent at sea. While Gilbert-rich age (G-R age) is the most common age format used for salmonids, and provides information regarding time spent in freshwater, ocean age was preferred for the following reasons. First, we were most interested in the effects of hatchery enhancement on growth and time spent in the marine phase contributes significantly more to overall growth than the freshwater phase due to higher productivity levels. Second, ocean age helped simplify the myriad G-R age classes resulting from variation in freshwater age across individuals (Table 1).

**Table 1.** Gilbert-rich ages in the Biodatabase, their equivalent ages and respective ocean age class.

Gilbert-rich age	Equivalent age	Ocean age
21	21	Ocean-1
32	21	Ocean-1
43	21	Ocean-1
31	31	Ocean-2
42	31	Ocean-2
53	31	Ocean-2
41	41	Ocean-3
52	41	Ocean-3
63	41	Ocean-3
51	51	Ocean-4
62	51	Ocean-4
73	51	Ocean-4
61	61	Ocean-5
72	61	Ocean-5
71	71	Ocean-6

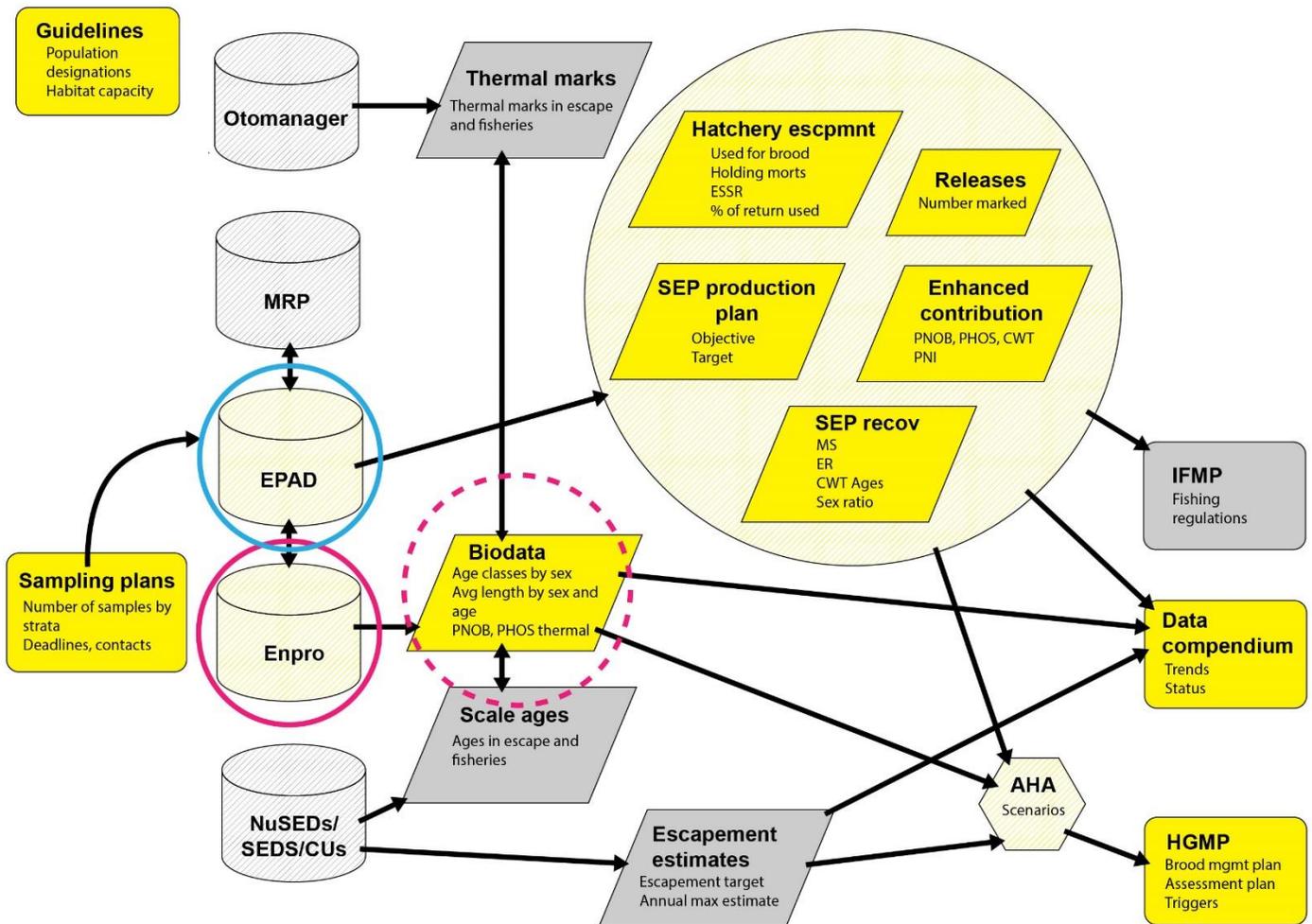
## Post-orbital hypural length (POHL)

POHL is a standardized measure of length used for biosampling in salmonids and is taken as the length from just behind the eye opening to the end of the hypural plate. It is used instead of fork length, which is less reliable due to morphological changes that occur for salmonids during spawning.

# OVERVIEW OF DATASETS USED

## THE SEP ENPRO AND EPAD DATABASES

EnPro and EPAD form critical components of the SEP/StAD data ecosystem, acting as starting points for the raw biosamples and enumerations collected according to facility sampling plans. These data eventually feed into other important data systems and assessment programs (Figure 1). They formed the foundation of the data used in our study.



**Figure 1.** An overview of the SEP data ecosystem showing the relative locations of EnPro (magenta), biodata (dashed magenta) and EPAD (blue). Adapted from materials shared by SEP staff.

## EnPro and the Stock Assessment Biodatabase

EnPro is a hatchery operations management database and reporting tool that focuses on collecting hatchery data for individual salmon such as adult escapement enumeration and sampling, inventory transactions, feeding rates, growth rates, marking and tagging activities, juvenile releases, among others. EnPro contains data from just over 70 Chinook salmon stocks in BC. EnPro was implemented by the SEP in 1998.

The SEP coordinates the collection of data for EnPro from a number of sources, including southern BC escapement and broodstock data (from 1996 to 2019). Data are collected through river and hatchery enumeration and sampling, in collaboration with DFO Stock Assessment Division (StAD), SEP Major Operations, the Public Involvement Program (PIP), and the Community Economic Development Program (CEDP), which includes community and First Nations-run hatcheries. The Stock Assessment Biodatabase (henceforth referred to as 'the Biodatabase') is a collection of biodata that is subsequently exported, formatted, reviewed and updated for analytical purposes, and is currently maintained by South Coast StAD, DFO.

EnPro provides critical data to meet reporting requirements of the Pacific Salmon Treaty (PST), including annual stock reconstructions and CTC modeling exercises. EnPro also supports the management of hatchery operations; data collection methods (i.e. brood collection and sampling methods) feeding into EnPro are not designed to provide biodata that meet the very strict criteria necessary for the PSF's analytical assessment of biological trends. Therefore, the data were thoroughly assessed for their analytical utility for this particular project using metadata on the variables collected and notes on sampling design taken from transcripts of PSF and DFO interviews with hatchery managers, as well as copies of sampling plans for most hatcheries from recent years.

## EPADS

The EPADS is a regional summary stock aimed at tracking activities for SEP related to planning, assessment and fulfillment of the International Fisheries Management Plan (IFMP), such as targeted and actual production totals; escapement of enhanced stocks, CWT and fin-clip expansions for enhanced catch, and enhanced contribution to escapement and brood; and marine survival. EPADS has return estimates for over 130 stocks.

The EPADS came into service in 2010, integrating several historical databases (Production, Targets, Mark Plan, Escapement and Biostandards) into one stock and came into service in 2010. Because the EPADS reports estimates on returns, it does not contain POHL data for individual fish. However, it provides a comprehensive estimate of total returns, including hatchery removals and natural spawners, compared to the Biodatabase. Therefore, the EPADS was used to produce stock-specific age and sex composition trends.

The EPADS reports a number of return estimates which we used in our analyses:

#### Total river returns

These are combined totals of natural origin and enhanced returns reported by sex and sample sites. They are the most complete return estimates in terms of numbers, but do not contain age data. As such, we used them for sex compositions only.

#### Observed, Estimated and Expanded returns

The observed, estimated, and expanded returns are raw and corrected estimates of CWT recoveries. The observed (raw) returns are based on counts of tagged fish. The estimated returns are the observed numbers corrected to account for tagged fish that were not counted. The expanded returns include a further correction to account for untagged hatchery fish. These counts are only meant to account for hatchery origin fish and are not as complete as the total river returns. However, they include age and are used to calculate age compositions. Though we calculated age compositions with all three indices, we only reported those calculated using the 'estimated' returns as they represent a reasonable middle ground between raw and corrected values.

#### Data issues

As with biosampling, returns are estimated at hatcheries, biasing counts toward hatchery-enhanced stocks. However, unlike biosampling, counts are conducted with the intention of scientific assessment in mind and present fewer issues. As such, while they meet some of the necessary criteria to be used in some of our analyses, they still contain issues that prevent us from answering our main question.

#### *Data only collected from hatchery enhanced streams*

The EPADS database does not cover any wild stocks. However, it contains data for a few minimally enhanced stocks such as Harrison River and Kitsumkalum River. While there were not enough stocks to assess the effect of enhancement as a factor in our trends analysis, the few minimally enhanced stocks present were used as qualitative references for comparison in our results.

#### *Inability to determine 'Stock of origin' for non-CWT records*

Stock of origin was determined from 'Estimated returns' using data in the variable 'Release site', derived from CWTs. This variable was not available for the more complete 'River returns' as they also included untagged natural-origin fish. For our analyses, 'Stock of origin' for the 'River returns' were assumed to be their sample site.

## KITIMAT RIVER HATCHERY BIODATA

Not all hatcheries have the infrastructure or the operational capacity to report biosample data directly into SEP databases such as EnPro. Since the Biodatabase is compiled using EnPro and PADs data, the data from these hatcheries are not included in EnPro. The PSF team has been able to procure and incorporate a small portion of these valuable datasets.

Kitimat River hatchery is one example, where biosample data exist but is not included in the Biodatabase as it was not entered into EnPro. Members of the PSF team reached out to the hatchery and SEP assessment bios and data was provided that spanned from 1991–2019. These records contained information on sex, age and POHL, making it a valuable dataset. These data were provided by Sarah Bouwmeester (Operations Manager of Kitimat River Hatchery, DFO, 2021).

## NECHAKO RIVER - NECHAKO FISHERY CONSERVATION PROGRAM (NFCP) & DFO

The NFCP was originally established to conduct broad scale monitoring of native of Chinook and sockeye salmon populations in the Nechako River. These monitoring projects were aimed at supporting the conservation goal of the 1987 Settlement Agreement, which was created in response to concerns about the impacts of the construction of the Kennedy Dam on native salmon populations.

Escapement samples in these programs were taken from both the Nechako River and nearby Stuart River, with the latter being used as a baseline comparison for the former. Sampling in the Stuart was discontinued as trends from the Nechako River showed no obvious departures from or anomalies compared to those from the Stuart River. Presently these data are collected and collated by the stock assessment division (StAD) of DFO. The dataset used in this analysis was provided by Mark Potyrala (Resource Manager, DFO, 2021).

## REGIONAL MARK INFORMATION STOCK (RMIS)

RMIS<sup>1</sup> is a collection of databases for coded wire tag releases, recoveries and locations. They are maintained and updated by the Regional Mark Processing Center (RMPC) which services international, state, federal, and tribal fisheries organizations involved in marking anadromous salmonids throughout the Pacific region. RMIS contains records of releases and recoveries by WT, which, when combined, can provide information on sex, age, POHL and stock, among other variables. These tags tend to be recovered by commercial and recreational fisheries.

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<sup>1</sup> Available online at: [www.rmhc.org](http://www.rmhc.org)

## DATA CHARACTERISTICS AND ANALYTICAL CONSIDERATIONS

Here we provide a brief description of the characteristics of the data within each dataset and specific analytical considerations made as a result. Potential issues are outlined as well, but details about changes made to address these issues are provided in the following section.

### THE SEP ENPRO AND EPAD DATABASES

The Biodatabase and the EPADS provided the most complete record of Chinook salmon returns and escapement samples for BC respectively. However, through conversations with DFO staff and our review of sampling plans, a number of important data limitations were identified, and subsequently addressed. Additional datasets were sourced to help supplement the existing database, and some assumptions were made to deal with unavoidable, systemic issues. Here we describe these limitations, solutions suggested, and their implementation in detail.

#### *Data are not available for all species of Pacific salmon*

We focused on Chinook salmon in our report because data availability and quality varied greatly across species. Biodata for Chinook were the most complete and accurate, having undergone significant QAQC by SEP and StAD staff (Jeffery Till, Stock Assessment, DFO). Biodata for coho and chum salmon have been compiled by SEP, but were still undergoing QAQC. Pink and sockeye salmon biodata are collected by SEP, but are not compiled in one location and had to be sourced from the facilities responsible. Sockeye salmon biodata were requested for the Fraser, Pinkut and Fulton Rivers. Biodata for all three were provided by either DFO stock assessment or SEP staff, though only Fraser River data contained all variables of interest. However, these data were not ultimately analyzed to avoid duplication of current work by the Pacific Salmon Commission on a review of Fraser River sockeye biological trends (Steve Latham, Pacific Salmon Commission, personal communication). Data collected from Pinkut and Fulton Rivers for recent years were not aged, although some effort was made to explore data starting in the 60s. Due to these limitations, our analyses were limited to Chinook salmon.

#### *Data only collected for hatchery enhanced streams*

We extensively solicited information from DFO and SEP staff, both retired and active, to identify wild stocks with size and age data. Unfortunately, we were not able to identify any systems, other than the Nechako and Stuart Rivers which are described above.

Due to the rarity of long-term data for fully wild stocks, we also sought data from 'minimally enhanced' stocks (stocks with PNI > 0.9) via the respective DFO stock assessment biologists. While data for the Harrison River were present in the original SEP biodata, we were specifically interested in the data used for a recent review of climate effects on Fraser River Chinook salmon (Xu et al., 2020) However, due to capacity issues, these requests remain unfulfilled.

We also requested raw data size and age data for Kitsumkalum Chinook from North Coast Stock Assessment following the official publication of Winther et al. (2021)<sup>2</sup>, unfortunately the data could not be shared.

Our final database did not contain a sufficient number of wild stocks to conduct statistical comparisons of wild and enhanced stocks. Instead, we used the few wild and minimally enhanced stocks as qualitative references for understanding trends in enhanced stocks.

*Data from non-EnPro hatcheries not included*

Not all hatcheries submit their biodata to EnPro and are therefore they are not included in the Biodatabase. For example, we obtained Kitimat River hatchery data directly from the hatchery and SEP assessment biologists.

*Data for fewer variables collected at smaller hatcheries*

Data from smaller hatcheries tended to be less complete, so data from these hatcheries were only used to assess trends for mean size, despite the potential confounding influence of age and sex on these trends.

*Available historical data not yet incorporated*

EnPro was put into service in 1996, but biodata was originally maintained in the 'Framework' system, with records from as early as 1970. These are currently archived in MS Excel format, but are yet to be formally incorporated with the SEP EnPro biodata. Because this pre-1996 time period represents a significant period in the development of salmon fisheries, these data were included for a few major stocks, specifically Robertson Creek and Chilliwack River hatcheries. Historical data from Robertson Creek and Chilliwack River hatcheries were provided by DFO (Brock Ramshow, Cheryl Lynch, SEP, 2021) and compiled and processed by PSF staff during the course of this review.

*Inability to determine 'Stock of origin' for records without CWTs or thermal marks*

In the EnPro Biodatabase, stock of origin can only be determined using information coded in CWTs and thermal marks. However, because these methods can only be implemented for hatchery-origin fish, 'Stock of origin' cannot be identified for wild fish and some untagged hatchery fish. As such, we dropped samples that did not have stock of origin, to remove any uncertainty in biological trends that may be introduced by samples from strays from other populations. This resulted in exclusion of a large portion of samples from the Biodatabase as a result, including any untagged wild samples.

In some cases, this issue was unavoidable. Because juveniles from wild stocks, such as Nechako and Stuart Rivers are typically not tagged with CWTs, 'Stock of origin' for escapement samples cannot be verified. In addition, we were not able to match release records for pre-1996 data

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<sup>2</sup> Winther, I., Vélez-Espino, L.A., Brown, G.S. and Wor, C. 2021. Assessment of Kitsumkalum River Chinook salmon with revised escapement estimates 1984 to 2020. Can. Manuscr. Rep. Fish. Aquat. Sci. 3217: ix + 131 p.

to tie CWTs in samples from escapement to their release site. In these cases, the 'Stock of origin' of samples from escapement was assumed to be the location where the sample was taken.

#### *No coverage of terminal fisheries samples*

EnPro primarily contains hatchery production data, biosample data of hatchery production, and biosamples of natural spawners, and the Biodatabase is a reflection of this. As such samples from fishery catches were sought from the DFO Mark Recovery Program (MRP). However, due to issues with data access we looked to the Regional Mark Information System (RMIS), which allows public access to coastwide CWT records to which MRP contributes. RMIS is a database for releases and CWT recoveries with locations, and is maintained and updated by the Regional Mark Processing Center (RMPC) which services international, state, federal, and tribal fisheries organizations involved in marking anadromous salmonids throughout the Pacific Northwest region (Regional Mark Processing Center (RMPC), 2022). Like the EnPro database, records from the RMIS database contained information on sex, age length and stock of origin, among other variables. These tag recoveries include catch sample and tag recovery records from escapement, commercial and recreational fisheries. There may be bias in these samples as fisheries recoveries may be representative of the individuals targeted by these sectors, typically the larger and older fish. Escapement samples were excluded as they were likely already present in the Biodatabase.

#### *Stratification in sampling for males, females and jacks (1 year old males)*

Upon reviewing hatchery/stock-specific sampling plans, we determined that the vast majority of hatcheries conducted biosampling on a set number of males and females and jacks. As such, in many cases the EnPro biodata could not be reliably used to assess age and sex compositions. For these demographic trends, return estimates from EPADS were used because they were a more representative of the population.

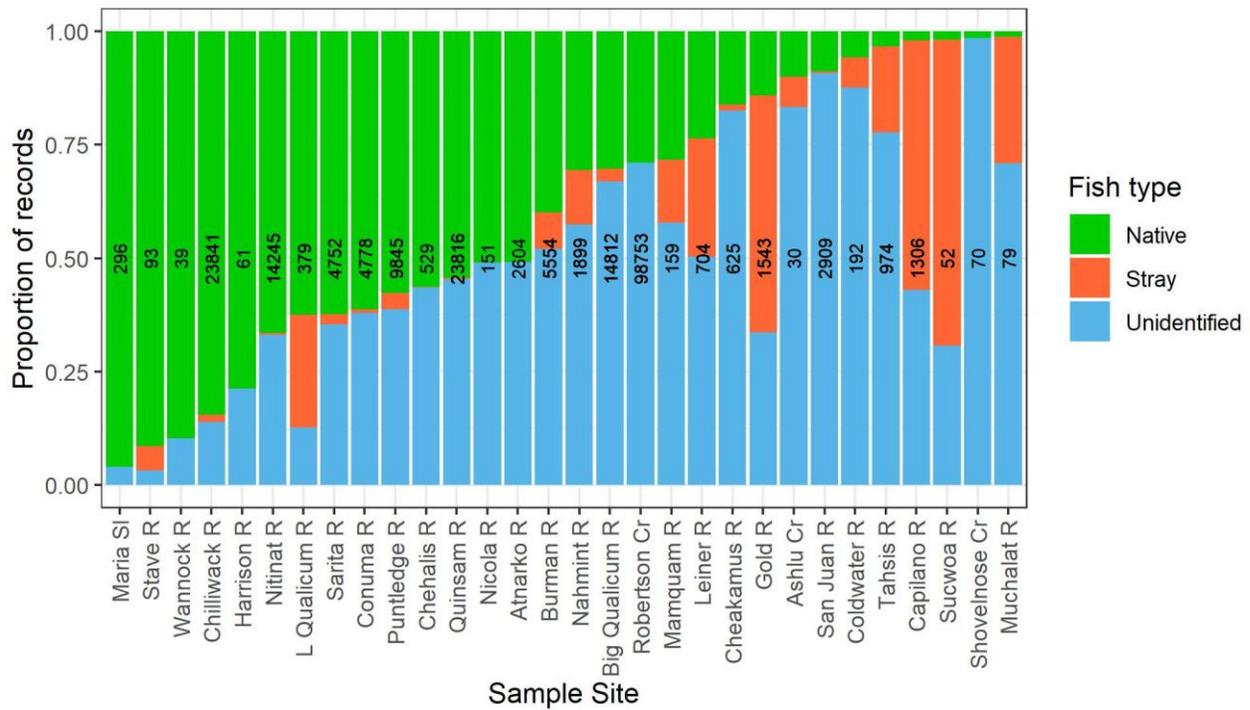
### **Differentiating between records from wild and hatchery salmon**

In most cases, CWT tagging is conducted on hatchery releases, and as such wild escapement samples should simply be all untagged samples. However, because CWT tagging is quite time and effort intensive, not all hatchery juveniles are tagged prior to being released. As such, it is impossible to separate untagged wild and untagged hatchery samples to reliably make comparisons of biological trends between hatchery and wild salmon. In addition, there is a lack of coverage of wild systems, which would ideally act as experimental controls, against which trends from streams with greater hatchery influence would be compared.

### **Stock**

'Stock of Origin' and 'Sample Site' were both available for EnPro, though 'Stock of origin' was only available for hatchery fish as wild fish are not tagged as juveniles, although in some cases Genetic Stock ID may have been incorporated into the EnPro Biodatabase. As such any trends produced with 'Stock of Origin' used for this variable will represented the biological characteristics of enhanced fish only. Trends for both enhanced and wild fish can be obtained

if 'Sample Site' is used as the spatial unit for non-CWT samples. An important distinction between 'Stock of Origin' and 'Sample Site' exists in that the former is impacted by straying, a phenomenon where some salmon do not return to spawn in streams other than their natal stream, and thus does not always accurately represent an individual's natal stream. However, because only a portion of hatchery releases are tagged, and few wild juvenile tagging programs exist, these biodata records were either excluded or, for stocks containing no CWT records, 'Stock of Origin' was assumed to be 'Sample Site'. Depending on the degree of straying, this assumption may introduce some uncertainty in the isolation of stock-specific signals in biological and demographic trends. Chinook, however, exhibit the lowest straying rates of all Pacific salmon species. Further, the value of including wild salmon in these trends may be worth the added uncertainty from non-native escapement samples. On the other hand, straying in some stocks may be too great to provide useful trends for native populations (Figure 2).



**Figure 2.** The proportion of EnPro escapement records across sample sites belonging to native, stray and unidentified salmon. Numbers in the plot are the total escapement samples taken at each sample site between 1997–2018. The groups are defined by the release site (stock of origin) of the sampled fish, extracted from CWTs and thermal marks. Native fish (green) are those whose CWTs match with their 'Sample Site', while strays (red) are those that do not. Unidentified fish (blue) are untagged wild and hatchery fish collected at sample sites and for whom a release site could not be determined and may be either native or stray. Though 'Stock of Origin' is consistent with most sample sites, higher prevalence of strays in a few stocks presents a significant issue for the use of 'Sample Site' for unidentified fish.

For escapement samples that do not have CWTs associated, thermal marks can provide information on origin stock. These marks provide the advantage of being applied to entire release lines of production. At different stages of hatchery rearing, temperature is varied according to very strict regimes to produce specific banding patterns on the otoliths of developing juvenile salmon. These banding patterns are associated with specific hatcheries and release timings to help determine origin stock upon the subsequent recovery of the fish as an escapement sample. However, if these regimes are not strictly controlled during hatchery rearing, banding patterns may sometimes be erroneous or unclear, introducing some degree of uncertainty in the determination of origin stock. As such, wherever both CWTs and thermal marks are present for escapement records, CWTs were prioritized.

### **Rules for enumerations and biological sampling affect the utility of EnPro and EPAD for certain analyses**

Some important characteristics of the EnPro and EPAD databases were inferred from sampling plans obtained for the 2005 and 2020/21 seasons. These were provided by Cheryl Lynch (South Coast Planning and Assessment Biologist, DFO), Angus Straight (Lower Fraser Planning and Assessment Biologist, SEP), Brock Ramshaw (Lead Biologist, SEP), Paul Welch (BC Interior and Coasts Planning and Assessment Biologist, SEP). Sampling plans specify how enumerations and biological sampling should be conducted at the hatchery level and the consistency of rules can vary across hatcheries. These sampling plans were reviewed and the relevant rules summarized (Tables S1a – S4c in the Supplementary Information section below).

Generally, plans mandate the enumeration of all fish handled, by sex, mark status/type and sample location. Rules about biological samples on the other hand can vary substantially across hatchery facilities. The majority of hatcheries specify set numbers of males, females and/or jacks from which POHL and age samples should be taken, while others do not mandate the taking of age samples and a few encourage the sampling of all fish handled. Rules about the numbers of males, females and/or jacks to be sampled can be specific to strata of interest to the hatchery such as sample location, mark type/status and run timing.

'River Returns' in the EPAD database are the most complete enumerations of Chinook returns, but are only given by sex, which is readily assessed in the field. This, however, comes at the cost of age data, which are present in the less complete, but still quite comprehensive 'Obs-Est-Exp' returns. Because age in the 'Obs-Est-Exp' returns is determined from CWTs, they are not restricted by rules for biological sampling.

Size-at-age and size-by-sex trends are not susceptible to the stratification by sex and jacks present in the sampling plans. Thus, biological samples for POHL by age and sex in the EnPro database were used to construct them. Conversely, sex and age composition trends are affected by stratification in sampling and the more complete enumerations in the 'River Returns' and 'Obs-Est-Exp' returns were used for their construction.

There may also be cases where biological sampling is not always conducted randomly, with some anecdotal reports of stratification in sampling regime across age and sex. As such, some age composition trends may contain bias depending on the extent of stratification across stocks. The strongest analysis potential lies with size-at-age by sex, as sampling stratification would not interfere with results, however mis-aged fish will present challenges and appropriate size filters by age may constrain the number of age-sex combinations in systems with low samples sizes. Stratification of samples from the Biodatabase into age and sex for analysis presents its own challenges due to the reduction of sample size that occurs when data are blocked using multiple variables. As such, some analyses are conducted on unstratified samples where warranted.

### Lingering issues with age data

Age data are only present when CWT sampling or scale and/or otolith sampling are specified in the sampling plans of individual hatcheries. There were a few issues with the EnPro age data that required validation using age data from a separate age dataset from PADs. Age data in EnPro were cross-checked with Gilbert-rich (G-R age) ages from PADs to produce a separate age column referred to as 'Resolved Age'. As this is an ongoing effort at SEP, some issues still remain and required attention. Further, errors specific to biodata from Cowichan River were shared with us by SEP staff as well as the specific fixes required.

### Non-EnPro historical biodata

Some of the historical data not yet incorporated into EnPro were made available for these analyses, specifically for Robertson Creek, Chilliwack River and Quinsam River. These data contain all of our variables of interest, but are given in a variety of formats that required some degree of standardization. See sections Data Manipulation: Robertson Creek Hatchery and Data Manipulation: Chilliwack River Hatchery for further details on the standardization of these datasets. Further, because these data have not undergone the usual QAQC by SEP staff, there may be further underlying issues, the resolution of which may require closer examination beyond the scope of this project.

## KITIMAT RIVER HATCHERY DATABASE

Just like other hatcheries under SEP, the Kitimat River Hatchery conducts data collection in accordance with regional sampling plans established at the beginning of each season. Sampling plans for 2005 do not specify any biological sampling for age (scales or otoliths), though those for 2021 do. This was corroborated by the raw data originally received, where in years prior to 2008, only CWT age was available. From 2008 onward, scale ages were present in the data suggesting that sampling plans were changed to include biological sampling for age. While total age should not be different between ages estimated from hard parts and CWTs, records prior to 2008 did not include estimates of freshwater age usually provided by scales and otoliths.

## NECHAKO & STUART RIVER - NECHAKO FISHERIES CONSERVATION PROGRAM & STAD-DFO

As stated previously, data from the Nechako & Stuart Rivers were collected specifically to monitor the condition of the Chinook salmon populations native to that stock. As such, they likely meet the requirements to produce statistically robust analyses. In addition, the Nechako and Stuart Rivers contain salmon populations that are unaffected by any hatchery enhancement and as such may act as a benchmark for wild trends in the biology and demography of salmon runs in that area and with similar life-histories.

### REGIONAL MARK INFORMATION STOCK (RMIS)

RMIS is generally used to provide estimates of returns for regional coordination of salmon management across the Pacific Northwest. RMIS samples are for CWT fish only, and as such can only represent trends from hatchery enhanced fish. In addition, because samples provided by RMIS are recovered by recreational and commercial fisheries, they are likely to represent the larger and older individuals targeted by these sectors. Age data in RMIS have to be derived from CWTs by taking the difference between recovery and release years. As stated for the Kitimat River Hatchery data, CWT ages give a relatively accurate estimate of saltwater age, but provide no information on freshwater age. This was estimated in a manner similar to that use for CWT ages in the EnPro data, using data provided by release records on the specific life stage of release.



Photo credit: Eiko Jones

## DATA MANIPULATION, CLEANING AND STANDARDIZATION

Different manipulations were required to clean the different datasets of erroneous data and harmonize the different datasets into one continuous source. In addition, some of the variables used in this study were not included in the original databases and had to be estimated. Here we provide a detailed description of manipulations conducted to standardize the datasets and provide continuity among them.

### GENERAL ADJUSTMENTS

#### Ocean Age

Not all records contained G-R age, but instead total age, taken from CWTs. In these cases, ocean age was calculated from G-R age by taking the difference between total age and freshwater age. Freshwater age was either interpreted from data about juvenile stage at release or assumed as one (Table 2). Individuals in the latter category that have spent more than year in freshwater would tend to be smaller than their assumed G-R age group.

**Table 2.** Freshwater age assumed based on data on freshwater stage at release.

Release stage code	Release stage	Database	Freshwater age
"1"	Smolt	EnPro	1
"2"	Yearling	EnPro	2
"S"	Smolt	RMIS	1
"Y"	Yearling	RMIS	2
"F"	Fry	RMIS	1
"P"	Parr	RMIS	1
"E"	Egg	RMIS	1
"NA"	No data	Robertson Cr Historical; Chilliwack River Historical	1

## Sex

Sex was available for all datasets, though in a variety of formats that needed to be standardized. Where they were present as coded entries, they were easily translatable using metadata documents available for each database. Jacks, or male fish that have only spent one year at sea, were sometimes included under sex in some databases and these were adjusted to reflect their biological sex for clarity (Table 3).

**Table 3.** The original entries under sex used in different databases and the final sex designated in our Biodatabase.

Sex (Raw)	Database	Sex (Clean)
"male"	EnPro	Male
"M"	Nechako River - DFO; Robertson Cr Historical	Male
"m"	Nechako River - DFO; Robertson Cr Historical Robertson Cr Historical;	Male
"1"	Chilliwack River Historical Robertson Cr Historical;	Male
"3"	Chilliwack River Historical	Male
"J"	Robertson Cr Historical data	Male
"female"	EnPro	Female
"F"	Nechako River - DFO; Robertson Cr Historical	Female
"f"	Nechako River - DFO Robertson Cr Historical;	Female
"2"	Chilliwack River Historical	Female
" "	All	NA

## Post-orbital hypural length (POHL)

Generally, POHL was given in millimeters (mm), but in some data were given in centimeters (cm) and were converted.

# ENPRO

## Stock

“Stock of Origin” (referring to release site) was primarily used, and was estimated by SEP staff by cross referencing CWT codes and thermal mark data with their respective hatchery glossaries. If thermal marks and CWTs provided differing release sites, the origin stock specified by CWT glossaries was preferentially used due to known issues with thermal marking. Because not all fish sampled had CWTs or were thermally marked, using release site exclusively will exclude some records, specifically those for untagged hatchery fish and all wild fish. As stated before, sample site (SITE\_RIVER\_ LOCATION in the database) can be used to help fill these gaps, but carries important trade-offs. An alternate version of ‘Stock’ including sample site was thus created to test the effects of these trade-offs on biological trends. For this alternate version of ‘Stock’, sample site was only used for those records without entries for release site.

Finally, all stock names were standardized, with some stocks combined for simplicity due to the relatedness of their stocks.

## Ocean Age

G-R age was represented by several columns in the EnPro biodata and needed to be combined before ocean age could be designated:

1. The RESOLVED\_AGE and AGE\_GR (from PADs) columns were cleaned and combined, with any non-age or text entries converted to ‘NA’. Gaps in RESOLVED\_AGE were filled with corresponding entries from AGE\_GR.
2. Following this, G-R age was reconstructed for records still lacking age estimates by combining total age, calculated as the difference between the YEAR and BROOD\_YEAR columns, with freshwater age given by juvenile stage at release from EnPro: SMOLT OR YEARLING. Any non-numeric or text entries were first converted to NA. After this, all records where this variable indicated ‘1’, where juveniles were released as smolts, were assumed to have spent a single year in freshwater before moving into their saltwater phase. If ‘2’ was indicated, then juveniles were released as yearlings (one year old juveniles) and would likely have had two freshwater years (Table 2).
3. The supplemented RESOLVED\_AGE was then combined with reconstructed G-R age. Where records had entries for both variables, the reconstructed G-R age was preferentially used. This final combined G-R age was then translated to ocean age (Table 1).

Through the QAQC process, entries in the Biodatabase were flagged for specific issues to be addressed in the future. This was pertinent in the case of RESOLVED\_AGE for the Cowichan River Assessment, where error codes during specific sampling seasons needed to be replaced by their correct age entries. Under the guidance of SEP staff, these changes were made.

To estimate ocean age where only BROOD\_YEAR was available, CWT age was used as total age and freshwater age was assumed to be one year.

Finally, corrections were made to ocean age considering that jacks (returning male Ocean-1 fish) are typically considered to be male fish <500mm. Any male Ocean-1 fish >500mm were assumed to be Ocean-2.

## EPAD

Because EPAD only contains estimates of returns, it can only be used to calculate demographic trends of age and sex composition. On the other hand, because these return estimates are not as restricted by biosampling restrictions as the EnPro biodata, demographic trends from EPAD are a much more comprehensive and representative. As stated previously, river return estimates are only given by sex and can only be used for sex compositions. On the other hand, observed, estimated and expanded estimates are given by sex and age and can be used for both sex and age compositions.

### Stock

For river return estimates, sample site was used for stock. On the other hand, the observed, estimated and expanded return estimates were based only on tagged fish which had release site extracted from CWTs.

### Ocean age

Age in the observed, estimated and expanded return estimates were CWT age and not estimates from scales and/or otoliths. Since no data for juvenile stage at release were available, freshwater age was assumed to be 1 when calculating ocean age.

### Sex

Sex was available for estimates from river returns and observed, estimated and expanded returns. In addition to 'males' and 'females', sex for river returns included counts for 'jacks'. These were incorporated into their respective sex categories before sex compositions were calculated.

## SEP HISTORICAL DATA - ROBERTSON CREEK

Historical data were provided as zipped files containing separate spreadsheets for individual years and sampling location. These spreadsheets had a relatively consistent format in terms of variable names and standardization, but were sometimes ordered differently or contained/were missing unique columns. As such, they required a substantial manual effort to carefully collate them into a single unified data frame.

## Stock

Although many of these historical escapement samples have CWT tag codes, the CWT glossaries available to us do not apply to the time period of releases covered by the historical data. As such, sample site was taken as stock for these data.

## Ocean age

As before, ocean age was estimated as the difference between total age and freshwater age given by G-R age, reported in the data as 'scale age' (S\_AGE C 9). Ocean age for records without scale age data was estimated using 'CWT age' (CWT\_AGE C 9). This variable required some cleaning as entries took a variety of formats. Numerical entries gave either CWT age or brood year, with the latter used to calculate CWT age using sample year. Some non-numerical entries contained CWT age, which were extracted and, along with those from numerical entries, were used to estimate ocean age. Once again, freshwater age was assumed to be 1 to calculate ocean age from CWT age. Ocean age was then corrected using length with male fish <500mm assumed to be in the 'Ocean-1' age class, and male fish in the 'Ocean-1' age class >500mm moved to the 'Ocean-2' age class. Jacks (returning male Ocean-1 fish) were identified as any male fish <500mm. Any male Ocean-1 fish >500mm were assumed to be Ocean-2.

## Sex

Sex (SEX C 9) was entered as a number code in historical data, and was translated using documentation on biosample codes provided by SEP staff. Male fish were coded '1' or 'M' and females were coded '2' or 'F'.

## Post-orbital hypural length (POHL)

Length required some standardization to maintain consistency with other datasets. First, length (LENGTH C 9) was measured using a number of methods and those recorded as POHL needed to be selected. 'Length method' (LM C 9) in the historical data provided the specific method used to measure length for each escapement sample. SEP documentation on biosample codes indicated that records with '1' or 'POH' under 'LM C 9' contained lengths measured as POHL. Length frequencies by age class indicated that some lengths were recorded in cm. These entries, associated with samples taken between 1990-1994, were converted to mm.

## SEP HISTORICAL DATA - CHILLIWACK RIVER

As with Robertson Cr, historical data for Chilliwack River were provided as zipped files containing separate spreadsheets for individual years and sampling location. While spreadsheets had relatively consistent variable names, some were missing or contained unique variables. In addition, data entries under our variables of interest required some standardization. As such, they required a substantial manual effort to carefully collate them into a single unified data frame.

## Stock

Although many of these historical escapement samples have CWT tag codes, the CWT glossaries available to us do not apply to the time period of releases covered by the historical data. As such, sample site was taken as stock for these data.

## Ocean age

As before, ocean age was estimated as the difference between total age and freshwater age given by G-R age, reported in the data as 'scale age' (S\_AGE C 9) in these datasets. Further, ocean age for entries without a 'scale age' was estimated from 'CWT age' (CWT\_AGE C 9), which, in contrast to Robertson Cr, was given in either total age or G-R age. Where only total age was given, freshwater age was assumed to be 1. Jacks (returning male Ocean-1 fish) were identified as any male fish <500mm. Any male Ocean-1 fish >500mm were assumed to be Ocean-2.

## Sex

Sex was entered as a number code in historical data, and was translated using documentation on biosample codes provided by SEP staff. Male fish were coded '1' and '3' (Jacks), and females were coded '2'.

## Post-orbital hypural length (POHL)

Length data from Chilliwack River were reported in a similar manner to Robertson Cr, but all entries were recorded in POHL as indicated by the 'length method' (LM C 9) column.

# KITIMAT RIVER HATCHERY

## Stock

For the small portion of data with CWT tag codes, stock was assumed to be the release site associated with these codes. For all other samples, sample site was instead used to represent stock.

## Ocean age

As before, ocean age was estimated by taking the difference between total age and freshwater age given by G-R age. Because data prior to 2008 only contain CWT ages, freshwater age was set to one for these data, assuming that these individuals over-wintered in freshwater for a single year. Jacks (returning male Ocean-1 fish) were identified as any male fish <500mm. Any male Ocean-1 fish >500mm are assumed to be Ocean-2.

## Sex

All entries were standardized for consistency.

# NECHAKO RIVER

## Stock

Because the Nechako and Stuart Rivers were unenhanced, escapement samples do not have CWTs to identify release site. Thus, stock was assumed to be the sample site.

## Ocean age

As before, ocean age was estimated as the difference between total age and freshwater age given by G-R age estimated from scales and otoliths.

## Sex

All entries for sex were standardized for consistency.

# RMIS

RMIS data were available as separate databases of juvenile releases and adult recoveries that needed to first be combined using CWT tag codes.

## Stock

Because all RMIS records were from fish with CWTs, release data, including release site, were available for all records. As such, stock was assumed to be release site. Stock labels required some formatting, while some stocks were combined to maintain consistency with previous datasets.

## Ocean age

The RMIS database did not provide any age data and G-R age had to be estimated. Both release year (brood\_year) and juvenile stage at release (release stage) were available for all records and were used to estimate total age and freshwater age. Juvenile stage at release was coded, though documentation was available in the help pages of the RMIS website (Table 2). As before, ocean age was taken as the difference between total age and freshwater age provided by the G-R age estimates.

Photo credit: Nicole Christiansen



Size corrections were also applied to male fish within the “Ocean-1” and “-2” age classes, where all individuals <500mm were put in the former class and those >500mm were included with the latter. Upon plotting size distributions of the data in total, discrepancies were observed with the Ocean-6 age class, specifically regarding its overall size range in relation to other age classes (Figure 3). In addition, there were only 19 data points across all stocks and years. As such it was excluded from the database.

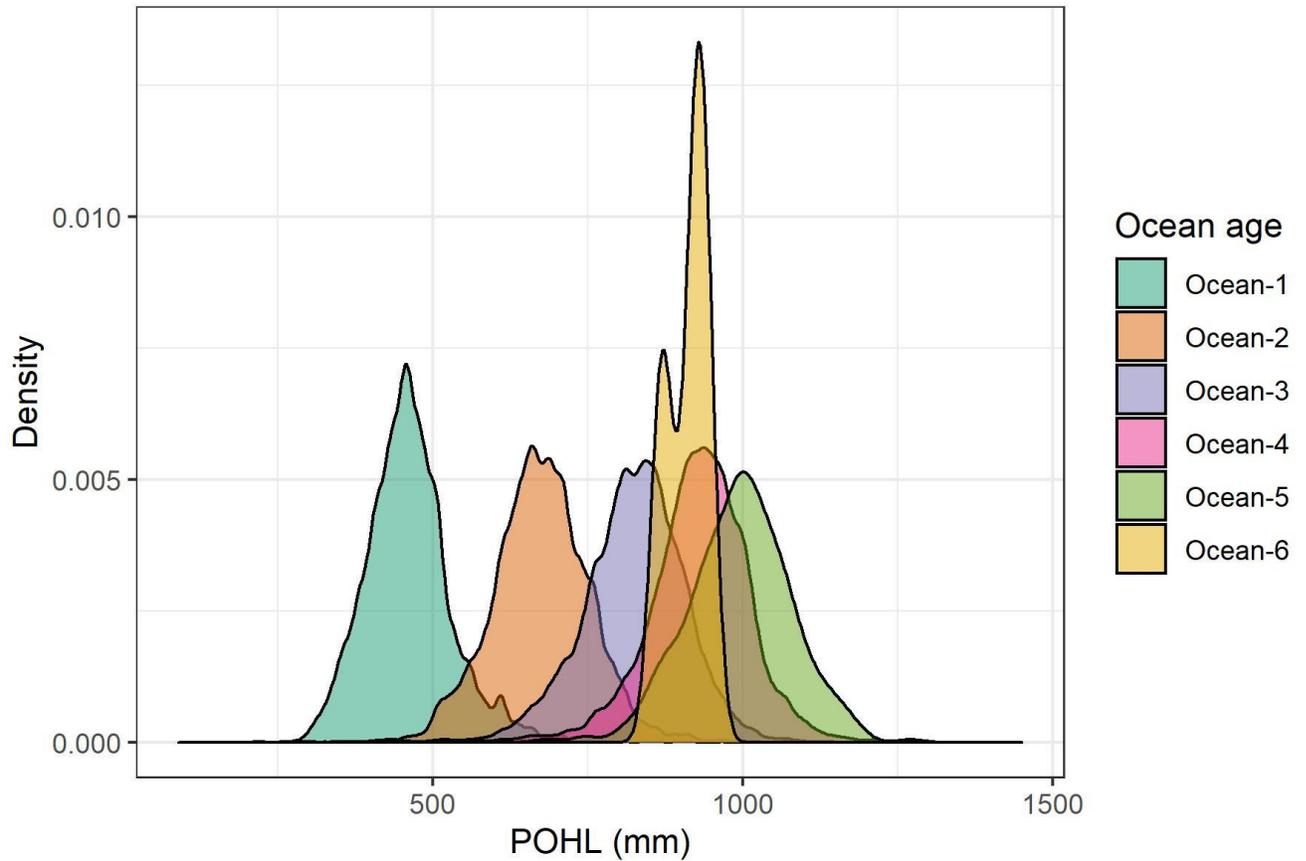


Figure 3. Size distributions of age classes in RMIS showing discrepancies associated with the dropped Ocean-6 age class.

### Sex

Sex data were available for the vast majority of data, coded as “M” and “F”. These were converted to remain consistent with the rest of the data.

## SUPPLEMENTARY INFORMATION

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**Table SI 1.** A summary of biosampling requirements specified for different hatchery facilities' sampling plans from 2005. These were used to determine the utility of biodata for size-at-age/-by-sex, and age/sex compositions.

Stock	Jacks (n)	Males (n)	Females (n)	Males (p)	Females (p)	Comments	Size-at-age	Size-by-sex	Age comps	Sex comps
Atnarko R										
Big Qualicum R	125	NA	NA	0.5	0.5	Adults: 125 tagged 500 unmarked jacks: 25 tagged 100 unmarked	Y	Y	Y, rm jacks	N
Burman R										
Capilano R	Sampling not required						NA	NA	NA	NA
Chehalis R	25	NA	NA	0.5	0.5	Adults: 125 tagged jacks: Tagged only	Y	Y	Y, rm jacks	N
Chilliwack R (Fall white)	NA	NA	NA	NA	NA	Swim-ins and seined fish: 100 untagged adults 50 untagged jacks 50 CWT fish (mixed adults and jacks) Deadpitch: 800 fish (random mix of adults, jacks, tagged and untagged)	Y	Y	Y, rm jacks	Y
Chilliwack R (Summer red)	Sampling not required						NA	NA	NA	NA
Conuma R	25	NA	NA	0.5	0.5	Adults: 125 marked Sample over entire length of run	Y	Y	Y, rm jacks	N
Cowichan R	50	NA	NA	0.5	0.5	Adults: 125 marked 125 unmarked jacks: 25 marked 25 unmarked	Y	Y	Y, rm jacks	N
Kitimat R	25	NA	NA	0.5	0.5	Adults: 125 tagged	Y	Y	Y, rm jacks	N
Nanaimo R	50	NA	NA	NA	NA	Use first set fish only; Adults: 125 fall run 50 first lake representative mix of males/females & marked/unmarked Jacks: 25 fall run 25 first lake representative mix of marked/unmarked	Y	Y	Y, rm jacks	Y
Nitinat R	NA	NA	NA	NA	NA	If StAd requests scales: 400 males, 400 females 100 jacks; Otherwise: 125 adults, 1:1 M:F No age estimation Sampled over entire length of run	Y	Y	Y, rm jacks	N
Puntledge R	25	NA	NA	NA	NA	Adults: 125 tagged jacks: Tagged only No M:F ratio specified; Sampled over entire length of run	Y	Y	Y, rm jacks	Y
Quinsam R	See comment					Hatchery: 75 marked adults, 1:1 M:F 25 marked jacks 150 unmarked females 100 unmarked males deadpitch: 150 unmarked females 100 unmarked males; Sampled over entire length of run	Y	Y	Y, rm jacks	N
Robertson Cr	200	800	800	0.5	0.5	Samples taken 50:50 between swim-ins & deadpitch jacks <59cm; Sampled over entire length of run	Y	Y	Y, rm jacks	N
Sarita R	All	All	All	NA	NA	Length and sex only	Y	Y	Y	Y

**Table SI 2.** A summary of biosampling requirements specified for different hatchery facilities' sampling plans from 2020–21. These were used to determine the utility of biodata for size-at-age/-by-sex, and age/sex compositions.

Stock	Jacks (n)	Males (n)	Females (n)	Males (p)	Females (p)	Comments	Size-at-age	Age comps	Sex comps
Atnarko R	NA	Comment		NA	NA	Broodstock: Take POH from 125 adults from each of Upper and Lower Atnarko; No sex ratio specified	Y	Y	Y
Big Qualicum R	NA	100	100	0.5	0.5	Adults: Unmarked only Sampling is random for size	Y	Y	N
Burman R	NA	NA	NA	NA	NA	Samples taken from all removals; Numbers or sex ratios for removals not specified	Y	Y	Y
Capilano R	NA	NA	NA	NA	NA	POH: Collect from all ad-clipped returns; Numbers or ratios not specified	Y	Y	Y
Chehalis R	All	NA	NA	NA	NA	Sample 160 adults total; No sex ratio specified; Jack POH<50cm	Y	Y	Y
Chilliwack R	NA	NA	NA	NA	NA	No protocol specified	Y	Y	Y
Conuma R	Comment			0.5	0.5	Single peak: 150 males 150 females 25 jacks Multiple peaks: >50 Males >50 females >10 jacks at each early/mid/late peak	Y	Y, rm jacks	N
Cowichan R	25	NA	NA	NA	NA	Broodstock: 125 unmarked adults 25 unmarked jacks Deadpitch: 150 unmarked adults	Y	Y, rm jacks	Y
Kitimat R	NA	Comment				POH only: All hatchery removals POH and age: 100 unmarked males 100 unmarked females 25 marked males 25 marked females	Y	Y	N
Nanaimo R	50	125	125	0.5	0.5	1:1 ratio of marked: unmarked sampled	Y	Y, rm jacks	N
Nitinat R	50	400	400	0.5	0.5	Jacks: 25 from river seining, 25 from swim-ins	Y	Y, rm jacks	N
Puntledge R	25	NA	NA	0.5	0.5	Sample 125 unclipped adults	Y	Y, rm jacks	N
Quinsam R	Comment					Swim-ins: 75 marked adults, 1:1 M:F 25 marked jacks 150 unmarked females 100 unmarked males Deadpitch: From each of Quinsam and Campbell Rivers; 150 unmarked females 100 unmarked males	Y	Y, rm jacks	N
Robertson Cr	125	425	425	0.5	0.5	Marked: 400 males 400 females 100 jacks Unmarked: 25 males 25 females 25 jacks	Y	Y, rm jacks	N
Sarita R	NA	NA	NA	NA	NA	Samples taken from all removals and carcasses; Numbers or ratios for removals not specified	Y	Y	Y

**Table SI 3.** A summary of enumeration requirements specified in different hatchery facilities' sampling plans from 2005. These were used to determine the utility of return estimates for age and sex compositions.

Stock	Sex	Age (Scales)	Age (Otoliths)	Sex comps	Age comps
Atnarko R	NA	NA	NA		
B Qualicum R	Total handled by run, source, mk type	Marked sampling not required, StAD sampling: 250 unmarked males 250 unmarked females 100 unmarked jacks Sample throughout run	NA	Y	Y, rm jacks
Burman R	Total handled by source & mk type	Not required	Not required	Y	N
Capilano R	Total handled by source	Not required	NA	Y	N
Chehalis R	Total handled by source & mk type	Not required	NA	Y	N
Chilliwack R (Fall white)	Total handled by source & mk type	Swim-ins and seined fish: 100 untagged adults 50 untagged jacks 50 CWT fish (mixed adults and jacks) Deadpitch: 800 fish (random mix of adults, jacks, tagged and untagged)	Taken from scale-sampled fish	Y	Y, rm jacks
Chilliwack R (Summer red)	Total handled by source & mk type	Not required	NA	Y	N
Conuma R	Total handled by source & mk type	100 females 100 males (Either unmarked or random sample of marked/unmarked)	100 females 100 males 50 jacks (Random sample of marked/unmarked)	Y	Y, rm jacks
Cowichan R	Total handled by source & mk type	Adults: 125 marked 125 unmarked 1:1 M:F; Jacks: 25 marked 25 unmarked	NA	Y	Y, rm jacks
Kitimat R	Total handled by source & mk type	Not required	NA	Y	
Nanaimo R	Total handled by source & mk type	Use first set fish only; Adults: 125 fall run 50 first lake; Representative mix of males/females & marked/unmarked Jacks: 25 fall run 25 first lake; Representative mix of marked/unmarked	NA	Y	Y
Nitinat R	Total handled by source & mk type River seining: sample throughout run	If StAd requests scales: River seine: 400 males, 400 females 100 jacks Swim-ins: 100 (from otolith samples) Sampled over entire length of run	Numbers to be determined by StAD	Y	Y
Puntledge R	Total handled by source & mk type	Not required	Not required	Y	N
Sarita R	Total handled by source & mk type	Not required	NA	Y	N

**Table SI 4.** A summary of enumeration requirements specified in different hatchery facilities' sampling plans from 2020–21. These were used to determine the utility of return estimates for age and sex compositions.

Stock	Sex	Scales	Otoliths	Sex comps	Age comps
Atnarko R	Total by source and mark status	Not specified	Not specified	Y	N
Big Qualicum R	Total by source and mark status	100 unmarked males 100 unmarked females Sample randomly throughout the run	Not specified	Y	Y
Burman R	Total by source and mark status	All removals sampled	All removals sampled	Y	Y
Capilano R	Total by source and mark status	Not specified	Not specified	Y	N
Chehalis R	Total by source	160 adults All jacks Jack POH<50cm Samples taken randomly	160 adults All jacks Jack POH<50cm Samples taken randomly	Y	Y
Chilliwack R (Fall white)	Total by source and mark status	Not specified	Not specified	Y	N
Chilliwack R (Spring)	Weekly live counts of spawning and holding salmon	Sample any carcasses encountered	Not specified	Y	Y
Chilliwack R (Summer red)	Total by source and mark status	Not specified	Not specified	Y	N
Conuma R	Total by source and mark status	Single peak: 150 males 150 females 25 jacks Multiple peaks: >50 Males >50 females >10 jacks at each early/mid/late peak	Single peak: 150 males 150 females 25 jacks Multiple peaks: >50 Males >50 females >10 jacks at each early/mid/late peak	Y	Y, rm jacks
Cowichan R	Total by source and mark status	Broodstock: 125 unmarked adults 25 unmarked jacks Deadpitch: 150 unmarked adults	Broodstock: 125 unmarked adults 25 unmarked jacks Deadpitch: 150 unmarked adults	Y	Y, rm jacks
Kitimat R	Total by source and mark status	100 unmarked males 100 unmarked females ~50 marked males/females	Not specified	Y	N
Nanaimo R	Total by source	Adults: 125 marked 125 unmarked 1:1 M:F Jacks: 25 marked 25 unmarked	100 samples from each run	Y	Y
Nitinat R	Total by source and mark status	River seining: 400 males 400 females 25 jacks Swim-ins: 25 jacks	River seining: 400 males 400 females 25 jacks Swim-ins: 25 jacks	Y	Y, rm jacks
Puntledge R (Fall)	Total by source and mark status	125 unmarked adults 1:1 M:F 25 unclipped jacks	Not specified	Y	N
Puntledge R (Summer)	Total by source and mark status	125 unclipped adults 1:1 M:F 25 unclipped jacks	Not specified	Y	N
Quinsam R	Total by source and mark status	Swim-ins: 75 marked adults 1:1 M:F 25 marked jacks 150 unmarked females 100 unmarked males Deadpitch: 150 unmarked females 100 unmarked males	100 samples from deadpitch	Y	Y
Robertson Cr	Total by source and mark status	Swim-ins: 400 unmarked males 400 unmarked females 100 unmarked jacks 25 marked males 25 marked females 25 marked jacks Deadpitch: 400 unmarked females 400 unmarked males 100 unmarked jacks	Swim-ins: 50 unmarked males 50 unmarked females 25 unmarked jacks Deadpitch: 175 unmarked males 175 unmarked females 50 unmarked jacks All samples taken from scale-sampled fish	Y	Y, rm jacks
Sarita R	Total by source and mark status	All removals sampled	All removals sampled	Y	Y



Photo credit: Eiko Jones



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FOUNDATION**