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The Magnitude and Extent of Chinook Straying from Hatcheries in Southern British Columbia

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Foreword

This series documents the scientific basis for the evaluation of aquatic resources and ecosystems in Canada. As such, it addresses the issues of the day in the time frames required and the documents it contains are not intended as definitive statements on the subjects addressed but rather as progress reports on ongoing investigations.

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ABSTRACT

Hatchery produced salmon have provided significant socio-economic benefit as well as conservation value in some cases. However, high levels of hatchery production also have the potential to create ecological and genetic risks for natural populations. In this report, we focus on one of those risks, straying of hatchery-origin, ocean-type Chinook Salmon into non-natal rivers in southern British Columbia.

We compiled coded wire tag (CWT) and otolith thermal mark data to assess straying of first generation hatchery Chinook. The geographic scope included the west coast of Vancouver Island (WCVI), the east coast of Vancouver Island (ECVI), and the Fraser River.

First we reviewed ‘donor’ stray rates. Based on otolith thermal marks we estimated an average hatchery ‘donor’ stray rate to non-natal rivers of approximately 4%. The donor stray rate to non-natal Conservation Units was lower, at less than 2% across populations and years. Straying between geographic regions of WCVI and ECVI was negligible. Conuma Hatchery on the WCVI had a significant stray rate, which resulted in the greatest magnitude of strays to other rivers.

Even low stray rates from large hatcheries can result in significant interbreeding with non-natal populations leading to a homogenization of spawning populations. We identified the contribution of strayed, hatchery-origin spawners ($pHOS_{\text{stray}}$) in the escapement, as a key metric to assess the impact of hatchery strays on natural-origin populations and compared observed values to a 0.03 benchmark proposed for wild populations by Withler et al. (2018). Average $pHOS_{\text{stray}}$ was highest on the WCVI, with most strays originating from Conuma Hatchery. Lower values, mostly below the 0.03 benchmark were observed on the ECVI, and a negligible stray contribution was observed in Fraser River populations.

Genetic analysis of population composition from 1985–2015 indicated that the genetic variation within each of the three major WCVI hatchery populations remained relatively consistent from the late 1980s to 2015 (the last year of analysis). The same could not be said for most other spawning populations along the WCVI. Hatchery populations contributed significantly to natural spawners in the surrounding populations of the WCVI, which resulted in genetic homogenization. However, the analysis also showed that local population genetics are still visible in many WCVI rivers, which suggests there should be a rapid transition to managing hatchery abundance under a proportionate natural influence (*PNI*) framework. This would include increased use of mass marking to identify hatchery fish as well as marking techniques such as the use of parentage-based tags (or thermal marking) to assess and manage $pHOS_{\text{stray}}$.

Delineating the effect of environmental conditions and hatchery practices as causal factors influencing stray rate is difficult considering the multiple scales at which environmental factors act, and a dearth of local, fine-scale data. Local knowledge often provided logical explanations in understanding straying patterns. It is important that hatchery practices place an emphasis on imprinting and improved homing. In addition, monitoring both straying and key environmental conditions should become routine, especially in regions where there is considerable hatchery enhancement.

The Hatchery Scientific Review Group (HSRG 2017, 2020), Anderson et al. (2020), and Withler et al. (2018) all indicate a need for the adaptive and scientifically defensible management of hatcheries, with improved annual planning, clear objectives, monitoring, assessment, and review. We support this view, and provide as a starting point, a data compilation and profile for each assessed river/Chinook population. These profiles include trends and data with respect to donor straying and recipient impacts. We hope these profiles will facilitate collection of local knowledge and support future efforts in the management of straying and genetic diversity, one river at a time.

1. INTRODUCTION

1.1. CONTEXT

One objective of Canada's Policy for Conservation of Wild Pacific Salmon (WSP) is to safeguard the genetic diversity of wild Pacific salmon. The policy indicates that diversity should be managed at the level of the Conservation Unit (CU); genetically and/or geographically distinct aggregates of populations.

Fisheries and Oceans Canada (DFO) Salmonid Enhancement Program (SEP) hatcheries produce over 40 million juvenile Chinook Salmon for release annually in southern British Columbia (SBC; south of Cape Caution) under objectives of Conservation, Rebuilding, Harvest, Stewardship, or Assessment. These hatchery programs attempt to balance the significant fishery benefits from this production against fishery, ecological, and genetic risks. In this report we focus on one component of risk, associated with straying of hatchery-origin Chinook Salmon into non-natal spawning populations.

Although the majority of Chinook Salmon exhibit strong homing behaviour to their natal streams as returning adults, straying (i.e., adults returning to non-natal streams) is known to occur naturally in Chinook populations. To date, the magnitude of straying from hatchery production in SBC has not been assessed.

The purpose of this report is to collate and review the data for an evaluation of the magnitude and extent of straying in hatchery Chinook Salmon in SBC. An examination of the genetic effects of straying and implications for hatchery reform has been completed (Withler et al. 2018) and will inform discussion on the potential risks and impacts of straying in southern BC.

The specific objectives of this review are to:

1. Provide a working definition of what constitutes a Chinook "hatchery stray" and compile available sampling data for the purposes of assessing hatchery stock straying, including metadata about the sampling program (e.g., spatial coverage and sampling purpose);
2. Provide estimates of mean stray rates, the magnitude of straying, and spatial and temporal patterns of straying by stock and rearing strategy of Chinook from hatcheries in SBC, using:
   a. Available coded wire tag (CWT) recovery data;
   b. Available thermally marked otolith recovery data;
3. Where possible, provide annual estimates of the contribution of hatchery strays into recipient spawning populations of sampled rivers in SBC (i.e., produce annual estimates for the proportion of hatchery-origin fish on the spawning grounds (*pHOS*), proportion of natural-origin parents in the hatchery broodstock (*pNOB*), proportion of local hatchery-origin fish on the spawning grounds ($pHOS_{\text{local}}$), proportion of stray hatchery-origin fish on the spawning grounds ($pHOS_{\text{stray}}$), proportionate natural influence (*PNI*), using CWT and thermally marked otolith recovery data; and
4. To the extent possible, identify and discuss potential sources of bias and uncertainties associated with the estimates of hatchery straying on natural spawners.

1.2. REVIEW OF STRAY RATES IN PACIFIC SALMON

Anadromous Pacific salmon (*Oncorhynchus spp.*) have a life cycle that begins in freshwater, then includes extended periods in ocean rearing and migration, before returning as maturing adults to spawn in freshwater where they originated. Each species, WSP CU, and even finer scale populations or groups of populations may have developed specific characteristics such as spawning time, size, fecundity, developmental rates, maturation schedule, and ‘homing’ to their natal freshwater drainage (Ricker 1972). However, a variable but typically small proportion of returning adult salmon do not home to their natal river but instead ‘stray’, spawning in a non-natal watershed or river. The reasons for straying may be tied to environmental factors or to species-specific life history characteristics.

Taylor (1990), Milner and Bailey (1989), Waples et al. (2008), and Leider (1989) described the ability of salmon to colonize or recolonize habitat to impart resilience to demographic bottlenecks. Quinn (1984) and Hendry et al. (2004) suggested that species with a greater number of age-classes may stray less, as they buffer demographic bottlenecks through time rather than space (e.g., Pink Salmon will spatially stray more than Chinook Salmon which have multiple age classes).

Chinook Salmon (*O. tshawytscha*) have a lower stray rate than Pink, Chum, and some Coho Salmon (Keefer and Caudill, 2014); perhaps due to factors such as freshwater residence time for stream-type Chinook Salmon, or having multiple age classes, which can lead to temporal straying in ocean-type Chinook (Healey 1991). The larger number of southern BC Chinook CUs relative to Pink, Chum, and Coho in the same region is consistent with Healey (1991); see Appendix Table B1 for a list of Chinook CUs in southern BC.

Increased freshwater residency is associated with lower stray rates. Imprinting occurs at the egg, alevin, and fry stages, and during outmigration at the parr-smolt transformation (PST) when spikes in adrenal hormones stimulate memory formation from environmental and chemical stimuli (Hasler and Scholz 1983; Nevitt et al. 1994; Dittman and Quinn 1996). Chum Salmon (*O. keta*) and Pink Salmon (*O. gorbuscha*) have shorter freshwater residency times and migration distances compared to other Pacific salmon and as such, tend to have greater straying rates, with most reported values > 10% (Sharp et al. 1994; Tallman and Healey 1994). These species can also exploit a greater variety of spawning habitat compared to others in the genus (Healey 1991; Heard 1996), which likely decreases the fitness costs associated with straying (Keefer and Caudill 2014). Stray rates for Coho Salmon (*O. kisutch*) are variable, balancing high freshwater residency and a low number of age classes returning. Labelle (1992) found an average stray rate of ≈2% across all years amongst Coho stocks examined on southeast Vancouver Island. Other studies in the United States (US), show higher mean stray rates for Coho Salmon, between 7–17% (Pess 2009). Sockeye Salmon (*O. nerka*) tend to have a high fidelity for natal spawning sites (Stewart et al. 2004). Although investigations into straying for Sockeye Salmon remain sparse, a survey of available data reported straying rates at a mean value of 2.4% across studied populations (Keefer and Caudill 2014).

Most estimates of Chinook Salmon straying come from hatchery populations, primarily in the Columbia River system. In British Columbia, Candy and Beacham (2000) reported stray rates between 0.3–2.1% for ocean-type hatchery Chinook Salmon based on CWT analysis. Hard and Heard (1999) reported a 2% average stray rate for ocean type Chinook in Alaska. Most of these stray observations were recovered in rivers near, or tributaries within, the natal watershed. Keefer and Caudill (2014) provided a thorough review of studies and estimates of straying from the Columbia River Basin and the Pacific Northwest, reporting a mean of 3.4% for Chinook Salmon. Keefer and Caudill (2014) cited issues with many of these studies related to the location of release and varied definitions of straying to discount some of higher estimates; and warned that variation in hatchery management and environmental conditions likely created a bias for higher stray rates relative to what may be expected in natural populations. Westley et al. (2013) went further by controlling for specific factors in choosing CWT to use as the basis for estimating hatchery stray rates. They estimated ocean type Chinook stray rates of 5.2–18.6% with variation attributed to species-specific behavioral and endocrine factors during juvenile stages, as well as environmental factors affecting adult migration. Westley et al. (2013) also reported that ocean-type Chinook, having short freshwater residence times, consistently had higher stray rates than stream-type Chinook.

There is currently a dearth of studies that focus on straying in natural-origin Chinook. A key study by Ford et al. (2015) used a parentage analysis to measure stray rates among natural- and hatchery-origin spring run (stream type) Chinook Salmon, among tributaries of the Wenatchee River, Washington. These authors found substantial variation among tributaries but average stray rates were approximately 4% for natural-origin returns and 29% for hatchery-origin returns. Interestingly, all natural-origin strays recovered in this analysis had at least one hatchery-origin parent. In another study, Pearsons and O'Connor (2020) passive integrated transponder (PIT)-tagged summer-fall juvenile Chinook (sub-yearling ocean-type) in the Upper Columbia River over a period of 15 years. They reported stray rates of less than 1% at the basin scale (straying from the Upper to Lower or Middle reaches of the Columbia River), for natural-origin returning Chinook.

1.3. HATCHERY PROGRAMS IN SOUTHERN BC

Hatchery programs in SBC, coordinated by SEP, manage annual salmon production in hatcheries to fulfill one or more stated objectives of hatchery enhancement: harvest, assessment, conservation, rebuilding and stewardship/education. SEP facilities produce more than 380 million juvenile salmon each year, including 46 million Chinook, the majority of which are allotted to harvest programs.

SEP has constructed and operated a total of 23 major production hatcheries and spawning channels across BC since its inception. These facilities are separated into large-scale, production facilities—termed Major Operations (OPS), that primarily support harvest and assessment objectives, and Community Involvement Program (CIP) projects that tend to focus on rebuilding, stock assessment, and stewardship. CIP facilities are classified as either a Community and Economic Development Program (CEDP), if the project aims to provide social and economic benefit to a local community or Indigenous group, or a Public Involvement Program (PIP) for facilities that promote education, stewardship, and conservation through small-scale propagation of local salmon populations. In the scope of this study, we examine straying from 19 Chinook populations reared at 15 major production facilities in SBC, with a focus on those facilities with long time series of annual release and recovery records. Records from CIP hatcheries are provided when available, although annual sampling and reporting is more sporadic.

2. DEFINITION OF STRAYING IN HATCHERY CHINOOK

Quinn (1993) defined a salmon stray as a salmon spawning at a 'non-natal' site. Keefer and Caudill (2014) indicate that a natal or non-natal site can vary depending on the geographic range of spawning sites for a given population based on the shared genetic heritage of spawning individuals.

Scale is an important consideration in defining a non-natal site for a salmon stray. Most rivers reviewed in this assessment are distinct river basins emptying into the ocean; there is no mixing of freshwater prior to entering the ocean. The Fraser River (R) is an exception and is dealt with separately. For non-Fraser R basins a Chinook Salmon stray is an individual that spawned naturally or was taken as broodstock in a non-natal river basin, or simply an out-of-basin stray.

We do not define hatchery Chinook Salmon that did not return to the hatchery, instead spawning in the natal river basin, as strays. These hatchery-origin spawners pose a separate genetic risk to natural-origin salmon and are assessed separately, consistent with Withler et al. (2018).

In the Fraser R watershed, we propose following the definitions of home and strayed individuals based on the Columbia River, where Ford et al. (2015) and Pearsons and O'Connor (2020) define straying at the basin, sub-basin, and tributary scale. In the Fraser R, large reaches of the mainstem would be basins (e.g., the Lower Fraser R and Thompson R). The North and South Thompson would be classified as sub-basins, and the Coldwater R and Spius Creek (Cr) would be examples of tributaries.

In Canada, salmon populations are aggregated into CUs (Holtby and Ciruna 2007; DFO 2013, Appendix Table B1). We define a Chinook Salmon from one CU spawning in another as an out-of-CU stray.

Although a difference in scale exists between the terms, in this report the words 'population' and 'stock' are used synonymously, reflecting the variable nomenclature used in the literature.

In the literature, trends in straying are described from two distinct perspectives: from the population in which strays originate, and the populations that receive them, termed donor and recipient populations respectively.

> *Donor straying* is the loss of individuals from a source population or hatchery stock (Bett et al. 2017). The donor stray rate, referred to hereafter as the *stray rate* is defined for a given stock as the proportion of salmon returning to spawn at all non-natal sites out of the total number of spawners originating from that stock, both homed and strayed.
>
> *Recipient populations* are defined as any river or system that receives strays from a donor population. This includes both hatchery enhanced systems that may produce and receive strays, as well as unenhanced populations that only receive strays alongside natural-origin salmon. In this work, we describe the proportion of strays in a recipient population as the *contribution of strays to a river*.

Occasionally, hatchery facilities collect individuals from a given stock, and release their progeny into non-natal systems. These cases are termed *'transplants'*. While evidence for a genetic component to homing has been documented (Pascual and Quinn 1994; Candy and Beacham 2000), the majority of transplanted Chinook return to the location of release. Thus, a Chinook Salmon is considered to have homed correctly if it returns to spawn in the basin *of its release.* Under this definition, an individual that returns to the home-river system from which it was transplanted (i.e., the river of its parents), would be considered a stray. In this case, the genetic impact of straying would likely be less-so than if it occurred into a system with a more distant genetic history.

In this report, we estimate donor straying, recipient stray contribution, and the overall contribution of hatchery fish (both homed and strayed) to SBC rivers.

3. DATA AND METHODS

3.1. DATA SOURCES

Data used in this report were collected mostly as a result of monitoring efforts conducted under a framework for Chinook assessment in fisheries management. The core of this assessment framework was developed jointly with the US within the context of Chapter 3 of the Pacific Salmon Treaty and is described in various reports from the Pacific Salmon Commission (PSC) Joint Chinook Technical Committee (CTC).

This framework identifies key coded wire tag (CWT) indicator populations within Stock Management Units (SMUs) to provide stock-specific information on ocean distribution, exploitation and survival rates and to support annual forecasting. These CWT indicators were almost always systems that contained a hatchery, to enable consistent marking of Chinook. The adipose fin clip was used to identify the presence and facilitate the recovery of CWTs, but this was relaxed in the US to facilitate mass marking (adipose fin clipping) of all hatchery produced Chinook. Chinook escapement to river spawning grounds and hatchery swim-ins/broodstock were intensively monitored to sample and estimate the number of CWTs in each population. Annual assessments of the CWT indicators can be found in CTC Exploitation Rate.

In addition, escapement indicators were identified for each stock management unit to track trends in Chinook escapement over time against Treaty rebuilding objectives. Escapement monitoring was consistent over time and used methods such as Peak Live + Dead counts, Mark-Recapture, Area-Under-the-Curve, or Fixed Point Enumeration surveys (for example, using viewing towers, counting fences and weirs). Annual assessments of these escapement indicators can be found in CTC Catch and Escapement reports available from the Pacific Salmon Commission.

In Canada, DFO Science had the responsibility to monitor these first two levels of indicators, often working with First Nation partners. Additionally, DFO has applied CWTs to other non-indicator hatcheries and even some wild populations. Monitoring escapement in these rivers was conducted by DFO or in partnership with First Nations or community/stewardship groups. These were not part of the PSC Chinook assessment framework, but were important to managing fisheries or meeting domestic policy objectives such as Canada's Policy for the Conservation of Wild Pacific Salmon or SEP's biological guidelines. In these cases, sampling methods often did not have the same level of intensity and consistency as the PSC indicators identified above.

3.1.1. Spawner abundance data

Adult spawner abundance, or escapement, is defined as the number of fish arriving at a natal stream or river to spawn (having matured and "escaped" the fisheries). Where possible, jack returns are recorded separately. Escapement includes natural spawners as well as hatchery broodstock removals and hatchery swim-ins. In this analysis, we used Chinook escapement data from the New Salmon Escapement Database System (NuSEDS), managed by DFO. This database acts as a repository for salmon spawner enumeration data and supporting documentation. Only escapement data from NuSEDS since 1998 were used in this report.

Escapement estimates from NuSEDS were used in expanding samples to total abundance within river spawning populations. Calculations of hatchery- and natural-origin contribution of escapement as well as in expanding sample estimates, as is described below.

Escapement estimates in hatchery systems are collated by SEP and maintained in a separate database, called the Enhancement Planning and Assessment Database (EPAD). The primary focus of the EPAD database is to compile data related to enhancement activities, such as numbers of fish collected annually for broodstock, spawner data, and associated biological information. Data from EPAD was also used in this analysis.

The quality of DFO escapement surveys was reviewed by Brown et al. (2019), providing a qualitative assessment of sampling efforts in SBC. The enhancement level, start year, and data quality were assessed, and those data relevant to recipient populations investigated in the present study are described in Appendix C, Table C1, along with average decadal escapements derived from those estimates.

In total, 49 recipient rivers in SBC had both sampling and escapement estimates that could be used in this analysis. These data spanned four regions across SBC, including the west coast of Vancouver Island (WCVI), the east coast of Vancouver Island from Victoria to Campbell River (ECVI), the Lower Fraser, and to a much lesser extent the Middle Fraser. Samples from the WCVI, ECVI, and Lower Fraser likely represent >85% of total escapement in each of these regions.

The distribution of sampled rivers was sporadic, and many areas had few or no data available. These include parts of the WCVI such as Esperanza Inlet where six rivers with significant escapements were represented solely by the Zeballos R. On the ECVI, only two rivers north of Campbell R had sample data available. The mainland inlets of southern BC, from Howe Sound to Knight Inlet could not be included due to lack of sampling and escapement estimates. Similarly, samples in the Mid Fraser were limited to CWT indicator stocks.

Note that we do not expand estimates of stray rates to account for unsampled rivers; mean stray rates will be underestimated and represent lower limits.

3.1.2. Sample data

We assembled CWT and otolith thermal mark samples from two sources: the EPAD database for broodstock and hatchery samples and a dataset of biological sampling events (termed ‘Biodata’; maintained by the Stock Assessment Branch), for deadpitch and in-river samples. Samples that lacked an adipose fin were labelled with a Mark Recovery Program (MRP) head label and were dissected. Note that in Canada, in most cases, the absence of an adipose fin (mark) is indicative of the presence of an internal CWT (tag). This differs from US policy where all hatchery-origin Chinook are mass marked (i.e., the external mark is not indicative of an internal tag). CWTs were recovered and documented in the MRP database, and collated in the EPAD database. Samples that had an adipose fin were also dissected, and otoliths were removed and processed by the Uchucklesaht First Nation Otolith Lab and DFO. Mark status was recorded in the ‘Otomanager’ database. Otomanager records were joined to MRP and associated biological data in the ‘Biodata’ database along with relevant metadata for each sampling event.

Terminal fishery sampling and swim-in samples to the hatchery were also used in some areas to support or corroborate escapement samples, and were included in either the EPAD or Biodata repositories. Detailed descriptions of sampling methods for each recipient river are provided in Appendix C.

The types of samples collected in each river were variable, and covered a range of up to 24 years between 1998–2021, depending on the system. Appendix C, Table C2 describes the sample type(s) collected and number of years in which marked samples were obtained for each river.

In SBC, the majority of Chinook produced by hatcheries are reared at major SEP facilities. However, a small number of community hatchery facilities in SBC also have substantial release, marking, and sampling programs in place (e.g., Cowichan R and Nanaimo R); straying estimates were also calculated from samples collected by these facilities. Samples from populations that were not reared at facilities on their home river (i.e., are ‘satellite-reared’ at major facilities) were presented when available.

We analyzed stray rate for samples marked at 15 hatchery facilities, enhancing 20 stocks across SBC between 1998–2021. These included seven in the WCVI region (Conuma R, Burman R, Gold R, Robertson Cr, Nahmint R, Nitinat R, Sarita R), seven in the ECVI region (Cowichan R, Big Qualicum R, Nanaimo R – Fall, Nanaimo R – Summer, Puntledge R – Fall, Puntledge R – Summer, Campbell/Quinsam R), one in the Coastal Inlets region (Capilano R), and five in the Fraser region (Chilliwack R – Fall, Harrison R, Nicola R, Shuswap R Low, Shuswap R Middle). Straying from Nicola R was described separately as the only stream-type population examined in this analysis. For these stocks we calculated mean stray rate and magnitude, range and temporal trends over time.

A list of all hatcheries, donor stocks, available marks and years in which populations were marked is available in Appendix C, Table C3.

3.1.3. Hatchery mark data

There are currently three mark types broadly available for the assessment of straying in SBC Chinook Salmon: CWTs, otolith thermal marks, and parentage-based tags (PBT). Our assessment was based on CWT and otolith thermal mark recoveries. Marking methods and inclusion criteria for both mark types are provided in the following sections. While some PBT results were available, most marking programs only began in the last few years and had insufficient recovery data for this analysis. As PBT data are not the focus of this analysis, but will be used in the future analyses of stray rate, we discuss their use and utility in SBC in Appendix C.

3.1.4. Coded-wire tags

Coded-wire tags (CWT) were applied to SBC Chinook populations since the 1960s to estimate stock-specific harvest, migration, enhancement levels, and provide fisheries related data for hatchery systems (Jefferts et al. 1963; Nandor et al. 2010; Johnson 2004). Canada and the US have scientifically designed annual sampling programs to recover CWTs in all major fisheries and spawning escapements where tagged ‘CWT indicator’ stocks are expected to occur.

For each observed CWT tagcode, year and recovery location, we obtained information on the ‘observed’ number of tags from EPAD (the count of CWT recoveries). From these observations, we calculated the number of ‘estimated’ recoveries in the escapement as:

$$N_{est} = n \times MR \tag{1}$$

where N_{est} is the number of estimated Chinook Salmon in the sample represented by a single tag, n is the total number of tags observed in the sample, and MR is the mark rate observed in all sampling strata. We adjust N_{est} to account for cases in which marks were lost/shed or recovered CWTs could not be read using the following formula:

$$N_{est,adj} = N_{est} \times \left(1 + \frac{LP}{K_n} + \frac{\left(ND \times (K_n + LP)\right)}{K_n \times (K_n + LP + NP)}\right) \tag{2}$$

where $N_{est,adj}$ is the adjusted number of estimated recoveries, K_n is the total observed number of known tagcodes, LP is the total observed number of lost pin recoveries, ND is the total observed number of ‘no data’ recoveries, and NP is the total observed number of ‘no pin’ recoveries.

Finally, the ‘adjusted estimated’ recoveries are ‘expanded’ by the ratio of hatchery production to tagged releases to calculate the number of Chinook for each tagcode that are expected to be recovered in the entire catch:

$$N_{exp} = N_{est,adj} \times {}^{R}\!/_{M} \tag{3}$$

Where N_{exp} is the total number of expanded recoveries represented by each CWT recovery, R is the total number of juveniles released at the hatchery, and M is the number of juveniles marked with the given tagcode.

CWTs recovered in systems with no CWT program (i.e., non-enhanced rivers or rivers with hatcheries that do not use CWTs) were included in EPAD as ‘observed’ recoveries and were not expanded, due to the lack of a CWT-specific sampling rate. For these cases, unexpanded observations were still counted and used to calculate stray rate and hatchery contribution.

Throughout this analysis, expanded tags were used in all calculations and reported values of stray rate and contribution derived from CWTs.

We observed 26,767 CWT observations, representing approximately 2.5 million expanded hatchery Chinook between 1998–2021. CWT recovery records were joined to release records (also stored in EPAD) for all SBC hatchery Chinook stocks recovered from 1998–2021. Pertinent information from release records include release stage (fry, subyearling smolt, or yearling smolt), and whether or not the individual was reared in a seapen. Note that we report on CWT recoveries for Canadian populations only; while US records were available, they were outside the scope of this work.

3.1.5. Otolith thermal marks

DFO has used thermal marks to identify certain SBC Chinook hatchery releases since 1995 following work by Volk et al. (1994). This inexpensive mass marking method involves subjecting developing eggs or recently hatched alevins to changes in temperature to produce a specific banding pattern on the developing otoliths of the fish. A detailed summary of the objectives and methods of this technique are provided by O’Brien et al. (2012).

We obtained 86,757 Chinook recoveries from SBC rivers in recovery years 1998–2021 that were checked for thermal marks in the Otomanager database, of which 65,266 were marked. These samples were collected from rivers associated with SEP major production facilities and community hatcheries, as well as unenhanced systems.

‘Stock of Origin’ was assigned based on the otolith banding pattern observed, with each facility applying a unique mark. In instances where Chinook were checked for a thermal mark, but none was observed, the individual was assumed to have been a natural-origin Chinook that homed correctly. Thermal marks were associated with their age from scales where possible, and then joined with release information based on the thermal mark and brood year. If multiple rearing strategies could be assigned to a single sample, the designation of ‘mixed’ was assigned. These observations accounted for 20% of thermally mark recoveries (n = 13,337) and were *excluded from investigations into stray rate by rearing strategy*, but were included in our overall analysis of stray rate, straying magnitude, and stray contribution to recipient rivers.

We expanded thermal mark recoveries to estimate the total abundance of strays returning to recipient rivers. Our expansion methods were similar to those used to expand CWTs, except that we did not expand recoveries based on the ratio of hatchery production to marked releases (Equation 3), as thermally marked populations are typically marked at a rate of 100%. Individual recoveries were expanded using a modified catch-sample ratio:

$$N_{exp} = {}^{ESC_{tot}}\!\big/_{N_{samp}} \tag{4}$$

Where N_{exp} is the number of expanded Chinook represented by a single recovery, ESC_{tot} is the total estimated spawner abundance (escapement), and N_{samp} is the number of Chinook in a given year that were sampled for thermal marks. Note that for Robertson Cr and Conuma R populations, we also expanded values based on the total return to the terminal area (terminal fisheries catch + escapement). In these cases, ESC_{tot} represents the total terminal abundance, instead of the escapement. Unless otherwise stated, it can be assumed throughout this report that estimates of stray rate and contribution derived from thermal mark samples were calculated from total expanded values, N_{exp}.

3.1.6. Genetics

In three years (2013–15), this assessment included tissue sampling for the genetic analysis of WCVI Chinook sampled for otolith thermal marks and/or CWT. The methods, data, and results were reported and available on the Pacific Salmon Commission website[1]. We provide a brief summary of the results in this report. Each sampled Chinook Salmon was genotyped at 12 microsatellite loci, and the resulting data were examined in an admixture analyses using a Bayesian approach within the STRUCTURE program (developed by Pritchard et al. (2000)).

Note that in 2017, hatcheries in SBC initiated genetic sampling of all broodstock, which serves as the baseline for PBT analysis. We provide an outline of this tagging method in Appendix C of this report. Returns from genotyped broods were first observed in 2020; PBT was not used to assess hatchery straying in this report. In the future, PBT will resolve many of the sources of uncertainty discussed in Section 5, and will allow for the monitoring of stray rates at finer temporal and spatial scales (see Beacham et al. 2017, 2019, 2021b, 2022).

3.2. METHODS FOR ASSESSING STRAYING

In Canada, hatchery Chinook production operations are implemented as integrated programs, meaning that hatchery spawners return to both natural and hatchery environments and broodstock is taken from returns to both the hatchery and natural (river) environments. The extent of enhancement activities has varied significantly among regions, being more prevalent, and on a larger scale in some areas (e.g., the southern mainland area of BC) relative to others (e.g., most areas of the Fraser R above Hope).

Hatchery straying poses genetic and ecological risk to natural-origin populations. The impacts of hatchery fish on wild populations are well documented in the US; see Keefer and Caudill (2014) for a review of the literature.

Long-term estimates of stray contribution are necessary to assess the impacts of straying on a population. As we rely on CWT and thermally marked hatchery-origin Chinook Salmon for this analysis, we can only estimate the contribution of first generation hatchery strays to a population (i.e., we do not have information on the origin of the parents of a tagged fish). In order to assess the potential impacts of strays, we must examine long-term trends in return composition, or compare genetic samples of modern and historic spawners. In Canada's WSP, a focus on conserving stock- or CU-level genetics in wild-systems (e.g., the exclusion of strays), is evident from the requirement that 'wild' fish be at least one generation removed from a hatchery parent (i.e., both of its parents must be of natural-origin).

In BC, until recently (see Withler et al. (2018)) there has been limited effort to directly manage gene flow between the hatchery and natural environments to control the relative adaptive

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[1] Withler, R.E., Willis, D., Luedke, W, McHugh, D., Porszt, E., DiNovo, S., Lynch, C., and Wetklo, M. 2017. Interactions of Natural and Enhanced Chinook Salmon in WCVI River Systems. Report to the Southern Boundary Restoration and Enhancement Fund 2014-2016.

influence of each environment on the integrated population as a whole. The US Hatchery Scientific Review Group (HSRG 2009) developed the proportionate natural influence (*PNI*) as a metric to estimate the relative hatchery and natural influences on the selection experienced within a population. For integrated populations, such as those enhanced by SEP, the *PNI* metric can be calculated from two variables: the proportion of hatchery-origin spawners on the natural spawning grounds (*pHOS*) and the proportion of natural-origin spawners in the hatchery broodstock (*pNOB*).

Withler et al. (2018) utilized this metric to establish the guidance framework in Table 3.1 for Canadian salmon populations. The intent of this framework was to designate populations or spawning aggregations within CUs such that there is a clearly articulated target for the extent of the hatchery influence on each population. Designations can range from populations virtually free of hatchery influence, to those that are dominated by hatchery production.

Table 3.1. From Withler et al. (2018); designations for individual salmon populations that vary in the degree of influence from integrated hatchery programs. Note: PNI in Withler et al. (2018) was calculated using $pHOS_{eff}$, whereas we calculated PNI using $pHOS_{census}$ (described in section 3.1.7). pWILD column shows the expected proportions of WSP-defined wild fish in the spawning population.

Designation		$pHOS_{eff}$ $pHOS_{census}$	*pNOB*	*PNI*	*pWILD*	Comments
A	Wild	≤0.02 ≤0.03	n/a	n/a*	≥0.92	Designated wild populations that do not have hatchery programs (for at least two generations); strays from out-of-basin hatchery production are limited to <3% per year.
B	Wild-stray influenced	>0.02 >0.03	n/a	n/a*	*<0.92*	Population receives strays from an out-of-basin hatchery. A very large fraction of fish may be wild but gene flow modelling suggests a long-term decline in *PNI* as *pHOS* increases.
C	Integrated wild	≤0.19 ≤0.23	≥0.77	≥0.80	≥0.50	Hatchery production is managed to keep wild fish ≥50% of the spawning population.
D	Integrated-transition	≤0.47 ≤0.53	≥0.47- <0.77	≥0.50- <0.80	≥0.13- <0.50	*PNI* ≥ 0.5 ensures natural-origin influence predominates but wild fish are in the minority.
E	Integrated-hatchery	>0.47 >0.53	<0.47	<0.50	<0.13	Net gene flow from hatchery environment; most fish are hatchery origin. Few fish are wild.

* When pNOB=0, *PNI* is computed from simulations based on Equation 33 of HRSG (2009, App. C); results depend on assumed values for h2 and ω2 and are not reported here.

3.2.1. Calculation of donor stray rates and magnitude

To estimate the degree to which donor straying is occurring in SBC, we used Chinook Salmon obtained as broodstock or natural spawners returning to SBC rivers between 1998–2021. If multiple sample types were available for a given stock or year, observations were pooled and analyzed together. The methods for assessing strays in Quinn (1993), Labelle (1992), and Candy and Beacham (2000) were used in this analysis. Similarly, the calculation of *PNI* and associated metrics developed by the US Hatchery Scientific Review Group (HSRG 2009) and used by Withler et al. (2018) were used in this analysis.

We designated individuals as either ‘homed’ and ‘strayed’ based on the definition laid out in section 2: hatchery marked fish were assigned a ‘homed’ designation if their hatchery mark indicated a location of release that matched their recovery location. In this case the recovery location could include the hatchery of origin, the river below the hatchery, or spawning grounds within the same river (Quinn 1993; Candy and Beacham 2000). A ‘strayed’ designation was assigned if the location of release differed from the location of recovery.

Given that the total number of expanded strays across all sampled rivers is denoted by S_{TOT} and the total number of Chinook sampled in a hatchery stock (including those returning to the natal stream, or to a non-natal system as strays) is H_{TOT}, the relevant calculations for stray rate (SR) is:

$$SR = {}^{S_{TOT}}/_{H_{TOT}} \tag{5}$$

Stray Rate (*SR*) was further broken down geographically into the rate observed inside and outside the Conservation Unit (CU) of origin (SR_{ICU}, SR_{OCU}, respectively) as:

$$SR_{ICU} = {}^{S_{ICU}}/_{H_{TOT}} \tag{6}$$

$$SR_{OCU} = {}^{S_{OCU}}/_{H_{TOT}} \tag{7}$$

The reliability of *SR* estimates depends on two factors:

1. the scope and extent of recipient river sampling; and
2. the precision of donor river abundance estimates.

To address the latter, we used an annual sample size cutoff of ≥ 3 CWT recoveries or ≥ 20 thermal mark recoveries in the donor river to be included in average estimates of *SR*. This removed outlying years in which imprecise donor river estimates biased estimates towards high SRs. We calculated mean *SR* and SR_{OCU} by donor river from all years that met this cutoff.

Hatcheries in SBC vary widely in the level of production across facilities, and years in some cases, so we contextualize stray rates by discussing the magnitude of strays observed originating from each donor river. We present the average magnitude of Chinook Salmon strays observed (S_{TOT}) by donor river alongside descriptions of stray rate.

3.2.2. Calculation of hatchery stray contribution to natural spawning in recipient rivers

To determine the contribution of hatchery strays in recipient populations in SBC, we first determined the proportion of Chinook in each system that were of hatchery origin (local or strayed):

$$pHOS_{local} = \frac{N_{H,local}}{(N_{H,local} + N_{H,stray} + N_N)} \tag{8}$$

$$pHOS_{stray} = \frac{N_{H,stray}}{(N_{H,local} + N_{H,stray} + N_N)} \tag{9}$$

Where $N_{H,local}$ and $N_{H,stray}$ are the number of hatchery-origin Chinook Salmon from local or strayed (out-of-basin) populations, respectively, and N_N is the number of natural-origin Chinook in a sample. We then calculated a total *pHOS* to estimate the cumulative hatchery influence in the recipient river:

$$pHOS = pHOS_{local} + pHOS_{stray} = \frac{(N_{H,local} + N_{H,stray})}{(N_{H,local} + N_{H,stray} + N_N)} \tag{10}$$

We report estimates of $pHOS_{local}$, $pHOS_{stray}$ for all rivers and years where data were available, following the same sample size requirement used in reporting mean stray rates (≥ 3 CWT recoveries or ≥ 20 thermal mark recoveries). If possible, samples of natural spawners were used in these calculations (deadpitch or carcass recovery) as hatchery samples may be biased towards hatchery-origin fish depending on the method of broodstock collection used. If natural spawner samples were unavailable, *pHOS* metrics were calculated from broodstock samples. We estimated these metrics using thermal mark and CWT data separately, and compared values in rivers where both hatchery marks were applied.

All *pHOS* calculations in this report reflect the census counts of hatchery-origin fish within natural-origin or hatchery broodstock samples. As such, *pHOS* values reported here are equivalent to $pHOS_{census}$ as described in Withler et al. (2018). These authors also considered the related metric of the “effective” proportion of hatchery Chinook Salmon on the natural spawning grounds ($pHOS_{eff}$). Hatchery-origin spawners typically see reduced reproductive success on the spawning grounds relative to their natural-origin counterparts (Araki et al. 2008; HSRG 2009, 2014; Withler et al. 2018), and the HSRG introduced $pHOS_{eff}$ to more accurately reflect the relative genetic contribution of hatchery-origin spawners (HSRG 2009). The relative reproductive success (RRS) of hatchery-origin salmon is often approximated as 0.8 which allows calculation of $pHOS_{eff}$ from $pHOS_{census}$ as:

$$pHOS_{eff} = \frac{0.8}{\left(0.8 + \frac{(1 - pHOS_{census})}{pHOS_{census}}\right)} \tag{11}$$

We chose to use census counts to estimate *pHOS*, because the estimated RRS of 0.8 is an assumed value for enhanced populations in Canada, and with respect to assessing the genetic influence of hatchery fish, $pHOS_{census}$ is conservative relative to $pHOS_{eff}$. In other words, accounting for a RRS ≤ 1 lowers the estimated genetic influence of hatchery-origin fish in the integrated system. Additionally, it is important to note that the PNI thresholds for biological designations in Table 3.1 were calculated using $pHOS_{eff}$, and thus the use of $pHOS_{census}$ indirectly results in targeting thresholds that produce slightly higher proportions of wild or natural-origin fish than described in Withler et al. (2018); again, this provides a conservative estimate of *pHOS* in the context of preserving natural influences within an integrated population.

Where broodstock was taken, the proportion of natural-origin broodstock (*pNOB*) was calculated as:

$$pNOB = \frac{N_N}{(N_{H,local} + N_{H,stray} + N_N)} \tag{12}$$

We then used estimates of *pHOS* and *pNOB* (Equations 10 and 12, respectively) to assess the genetic impacts of hatchery influence in each population by calculating PNI (HSRG 2009; Withler et al. 2018) as:

$$PNI = \frac{pNOB}{(pNOB + pHOS)} \tag{13}$$

In these calculations, *pHOS* is the sum of $pHOS_{\text{local}}$ and $pHOS_{\text{stray}}$, which assumes equivalent genetic effects associated with local and stray hatchery fish. This assumption is unlikely to be accurate, as fish from an out-of-basin hatchery are produced from broodstock that do not include natural-origin fish from the local habitat of the population under consideration. This limitation is, in part, why straying was evaluated with an alternative *PNI* equation in Withler et al. (2018). Despite this, we utilize Equation 13 here, since the difference between local and stray hatchery contributions may be small when the two populations are genetically similar or located within the same CU. Furthermore, regardless of this potential difference, our *PNI* calculations are still relevant to the biological designations in Table 3.1, because the thresholds for the designations are based on the expected proportions of wild or natural-origin spawners they will produce, which are independent of the source of hatchery-origin fish in the system (i.e., they are only dependent on the natural-origin fish). However, we emphasize that methods to accurately account for the effects of stray hatchery fish on the *PNI* of a population that is also integrated with local enhancement should be a priority for future analyses to safeguard the long-term maintenance of fitness in those populations.

Finally, we performed an additional *PNI* calculation in which stray hatchery-origin spawners were ignored. We term this value PNI_{local}:

$$PNI_{local} = \frac{pNOB}{(pNOB + pHOS_{local})} \tag{14}$$

PNI_{local} does not reflect the current genetic dynamics of an integrated population. Instead, PNI_{local} provides a purely theoretical value for management use, in comparison to *PNI* as calculated in Equation 13. PNI_{local} illustrates the possible *PNI* that could be attained were stray hatchery-origin fish completely removed from the population (i.e., if $pHOS_{\text{stray}} = 0$).

3.2.3. A benchmark for hatchery stray contribution to recipient rivers

As displayed in Table 3.1, Withler et al. (2018) also used the *PNI* metric to assess the impact of out-of-basin hatchery strays on a wild population. For those populations, *PNI* could not be calculated from *pHOS* and *pNOB* alone, because there were no natural-origin spawners from the wild population in the hatchery broodstock that are the source of the strays (see Equation 6 in Withler et al. (2018)).

The influence of out-of-basin hatchery strays on the *PNI* of a wild population depends on both the *heritability* of the hatchery influence and *selection against* the hatchery influence in the wild habitat. Withler et al. (2018) assessed the impacts of out-of-basin strays on wild populations across a range of plausible heritabilities and selection pressures, and recommended a benchmark of $\text{pHOS} \leq 0.03$ for out-of-basin hatchery strays per year to safeguard *PNI* and the long-term fitness of the wild population.

However, this recommendation was specific to wild populations experiencing out-of-basin hatchery strays *without local hatchery enhancement* (i.e., without additional hatchery influence). It is likely that the 0.03 benchmark for out-of-basin strays may be insufficient to preserve natural adaptive influences when local hatchery spawners are also present on the spawning grounds. In this paper we acknowledge this possibility as relevant for many Chinook Salmon populations in SBC; however, we still employ the 0.03 stray benchmark for comparison, as an equivalent benchmark accounting for local hatchery contribution is not currently established. In addition, where relevant we present pHOS broken down into component parts of $pHOS_{\mathrm{local}}$ and $pHOS_{\mathrm{stray}}$, and report $pHOS_{\mathrm{stray,OCU}}$ to specifically consider and highlight the proportion of stray hatchery spawners from outside the basin or outside the CU of the assessed population.

4. RESULTS

4.1. DONOR STRAY RATE AND MAGNITUDE IN SOUTHERN BC

Below we provide an overview of samples analyzed in this work, taken from 1998 through 2021 from 49 rivers in southern BC including 27 from the west coast of Vancouver Island (WCVI), 10 from the east coast of Vancouver Island (ECVI)/Georgia Basin, 12 from the Fraser River, and 5 from rivers in coastal inlets off of the west coast of mainland BC.

4.1.1. Donor stray rates to non-natal rivers

Summary results of straying between river basins are provided in the following Tables 4.1 and 4.2, as well as in Appendix D for both CWT and thermal marks.

Based on CWT sampling between 1998–2021 from 17 donor stocks and 49 sampled recipient rivers in SBC, a mean annual donor stray rate for ocean-type hatchery Chinook was estimated to be 2.0% (range 0–7.6%) at the basin scale (that is, straying between river systems).

We found considerable variation in mean stray rate between hatcheries and years. Based on CWT recoveries, the following donor rivers saw the highest stray rates: Capilano R (7.6%), Cowichan R (7.2%), and Nahmint R (4.2%). Interannual variation within each basin is presented in Section 7.

Based on otolith samples collected between 1998–2021, from 12 thermally marked donor stocks and 49 sampled recipient rivers in SBC, a mean annual donor stray rate for ocean-type hatchery Chinook of 4.2% (range 0–17%) was estimated at the basin scale.

Considerable variation between hatcheries and across years was also observed in thermal mark data. The following donor rivers, all on the WCVI, had the highest mean stray rates based on thermal marks: Nahmint R (17.7%; range 0–50%), Gold R (13%; range 0–37.8%), Burman R (4.3%; range 0–26.3%), and Conuma R (3.7%; range 0–3.8%). The remaining nine hatcheries that used thermal marking each had a mean stray rate <1%. Interannual variation for each population and contributing factors are described in the following sections.

4.1.2. Magnitude of donor straying

A low stray rate from a large production hatchery facility can still results in a high number of strays, which can overwhelm a small population of natural spawners. The magnitude of strays from each donor hatchery are summarized across years in Table 4.3 (total strays) and 4.4 (strays outside the CU of origin) and are reported by year in Appendix D.

Note that the magnitude of strays spawning in each non-natal river basin will be reviewed separately in the recipient rivers section of this report.

Between 1998–2021, the average magnitude of stray Chinook recovered in SBC, estimated from 12 donor hatcheries that used thermal marking and sampling in 49 recipient rivers, was approximately 2000 (Table 4.3). More than 50% of this average magnitude originated from Robertson Cr Hatchery and strayed into the Gold R (see Candy and Beacham 2000 and the

Section 7 discussion of Gold R). The average magnitude of strays estimated from 17 donor stocks that used CWT marking was 810 individuals. Hatcheries with the highest average number of strays annually were Robertson Cr Hatchery and Conuma R Hatchery.

The extent of donor river straying into recipient rivers is shown in the following chord diagram (Figure 4.1) and in Appendix D.

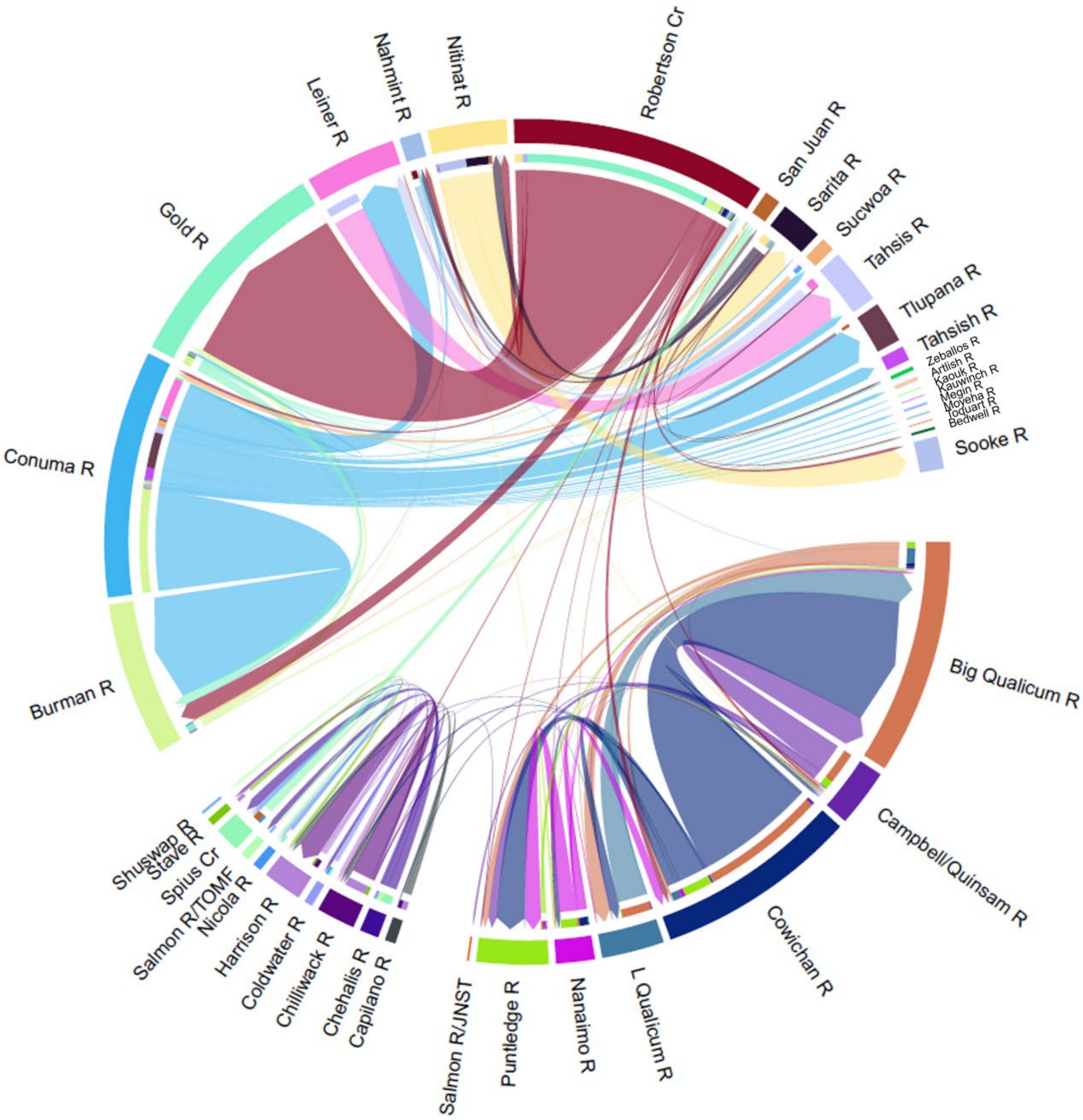

Figure 4.1. Chord diagram of total expanded stray recoveries observed in SBC (using both thermal and CWT data) between 1998–2021 for recipient systems. The outer most band displays donor rivers in SBC; the interior band is colour matched to the recipient system, and arrows direction and thickness indicate the direction and magnitude of straying from donor systems respectively. Donor rivers are partitioned into WCVI rivers on the upper half, ECVI rivers on the bottom right, and Fraser watershed/coastal inlet tributaries on the bottom left.

For the WCVI, note the extent of Robertson Cr Hatchery straying into the Gold River (a system over 200 km away), and the extent of Conuma strays into the Burman R, Leiner R, and Tlupana R. For the ECVI note the straying of Cowichan into the Big Qualicum R and

Puntledge R. A description of each donor-recipient trend observed, and potential causal factors are explored in Section 7.

The distance between donor population and recipient river was assessed for strays on the WCVI, from river mouth to river mouth (Figure 4.2). Stray rate generally declined with distance; with the exception of Robertson Cr Hatchery straying into the Gold R, likely due to a similar olfactory signal created by similar pulp mills on both systems. On the WCVI, a stray distance < 75 km usually denoted straying within a sound. Within-sound straying was dominated by Conuma R Hatchery strays within Nootka Sound. Stray distances between 75 km and 150 km usually indicated straying into an adjacent Sound. In this range, Nitinat R Hatchery stands out in straying to Sooke R (a transplanted population from Nitinat R, where straying could be the result of an error in the transfer of a marked group, or after 25 years of transplanting, a relationship in homing between Sooke R and Nitinat R may exist). All major hatcheries on the WCVI 'satellite-rear' populations that occur in nearby rivers within 50–75 km of the hatchery. This practice may create a higher risk of straying, which may be a contributing factor in observed trends of straying at that distance.

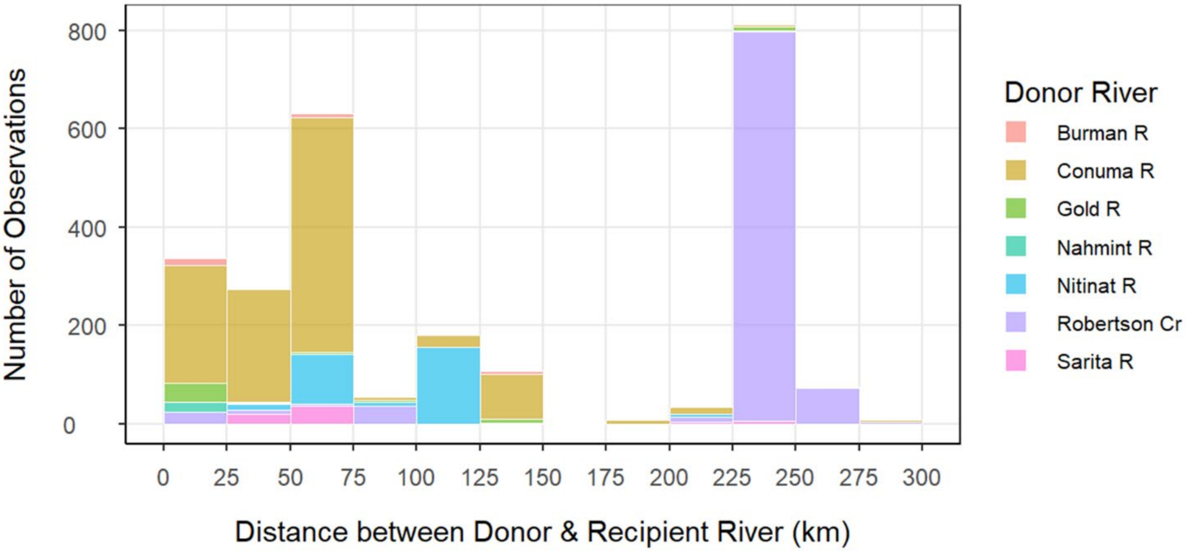

Figure 4.2. Distance strayed from donor rivers estimated using thermally marked recoveries (not expanded) in systems on the West Coast Vancouver Island from 1998–2021.

4.1.3. Donor stray rates to other Conservation Units

Canada's Wild Salmon Policy defines CUs as a group of genetically distinct and isolated wild salmon and seeks to maintain diversity within these units. Straying from rivers outside the CU can affect this genetic distinctiveness. To assess this, we reviewed donor straying to river basins outside the CU of origin.

Both CWT and thermal mark stray rates from donor hatcheries to river basins outside the CU of origin are presented in Table 4.4.

Based on CWT recoveries from 1998–2021, in 17 donor stocks and 49 sampled rivers in SBC, a mean annual stray rate from outside the CU-of-origin (SR_{OCU}) was estimated to be 1.5% (range 0–7.6%) for ocean-type, hatchery Chinook Salmon. There was considerable variation in SR_{OCU} between hatcheries and years. For CWT recoveries, the following donor rivers had the highest stray rates; Capilano R (7.6%), Cowichan R (7.2%), and Nanaimo R – Fall (4.0%). The remaining nine donor systems had a mean SR_{OCU} <1%.

Based on thermal mark recoveries between 1998–2021, from 12 donor stocks and 49 sampled rivers in SBC, mean annual SR_{OCU} was estimated to be 1.4% (range 0–8.9%) for ocean-type, hatchery Chinook Salmon. If straying from Gold R to Robertson Cr was excluded from this average, SR_{OCU} drops to <1%. For thermal mark recoveries, there was also considerable variation between hatcheries and years. The following donor rivers had the highest average stray rates: Gold R at 8.9% (range 0–27%), Nanaimo R – Summer at 2.7% (range 0–10.4%), Robertson Cr at 1.8% (range 0–12%), and Cowichan R at 1.5% (range 0–10.5%). The remaining eight donor rivers that used thermal marking had a mean stray rate <0.2%.

4.1.4. Donor stray rates to other Stock Management Units

DFO has aggregated Conservation Units into Stock Management Units (SMUs), reflecting similar genetic, ocean distribution, and life history characteristics to support management at a broader scale. In SBC, Chinook SMUs are delineated into geographic regions (WCVI, Georgia Basin/ECVI, and Fraser) and run timing groups. We observed negligible straying between SMUs (Figure 4.3). Most strays were observed within the WCVI, accounting for more than 50% of all hatchery strays estimated for SBC Chinook in this report.

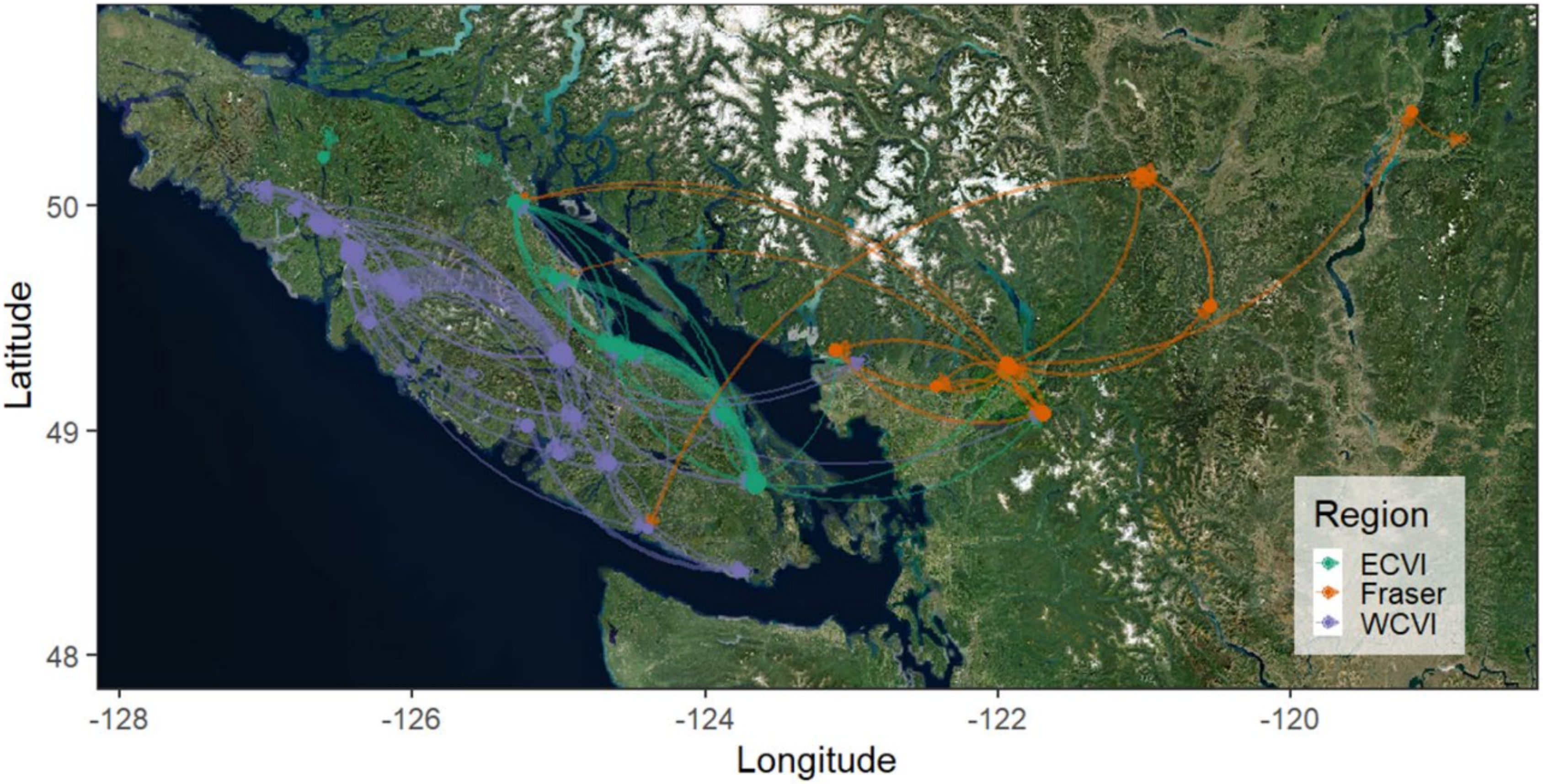

Figure 4.3. Map of stray recoveries across SBC to systems with escapements greater than 500 individuals between 1998–2021. Circles at each hatchery are scaled to the magnitude of donor strays observed from that facility and arrow thickness is scaled to the number of hatchery strays straying from donor to recipient populations.

*Table 4.2. Mean annual donor stray rates (SR) from hatchery-origin, ocean-type Chinook Salmon returning to SBC rivers, estimated from expanded CWT or thermal mark recoveries. The number and range of years used in calculations (n) and standard deviation of estimates are provided (SD). *Estimates in brackets for Conuma R and Robertson Cr represent mean stray rates for the population calculated using terminal abundance to expand hatchery recoveries instead of escapement alone.*

Donor River	**CU**	**STRAY RATE (SR)**							
		CWT				**THERMAL MARK**			
		Mean	**Range**	**(n) Years and Range**	**SD**	**Mean**	**Range**	**(n) Years and Range**	**SD**
Conuma R	CK-032	0.0%	0.0 - 0.1%	(10) 1998–2007	0.0%	3.7% (2.0%)*	0.0–3.8%	(23) 1998–2021	3.2%
Burman R	CK-032	–	–	–	–	4.3%	0.0–26.3%	(16) 2006–2021	6.9%
Gold R	CK-032	–	–	–	–	13.0%	0.0–37.8%	(5) 2012–2020	26.2%
Robertson Cr	CK-031	0.5%	0.0–4.8%	(24) 1998–2021	1.2%	2.0% (0.9%)*	0.0–12.1%	(24) 1998–2021	2.7%
Nahmint R	CK-031	4.2%	0.0–13.5%	(7) 2002–2021	5.5%	17.7%	0.0–50.3%	(10) 2002–2019	19.9%
Nitinat R	CK-031	0.1%	0.0–0.5%	(9) 1998–2019	0.2%	0.9%	0.0–2.3%	(23) 1999–2021	0.6%
Sarita R	CK-031	2.3%	0.0–13.4%	(11) 1998–2021	4.2%	3.1%	0.0–15.6%	(21) 2000–2021	3.9%
Cowichan R	CK-022	7.2%	0.6–29.2%	(24) 1998–2021	6.8%	1.5%	0.0–10.5%	(12) 2009–2021	3.1%
Big Qualicum R	CK-027	1.6%	0.0–5.1%	(13) 1999–2021	1.5%	–	–	–	–
Nanaimo R - Fall	CK-025	4.0%	1.0–13.4%	(11) 1998–2008	3.8%	0.7%	0.0–4.1%	(12) 2007–2018	1.2%
Nanaimo R - Sum	CK-083	2.9%	0.0–5.3%	(7) 1998–2004	2.7%	2.7%	0.0–10.4%	(9) 2008–2021	4.4%
Puntledge R - Fall	CK-027	1.2%	0.0–9.3%	(21) 1998–2021	2.4%	–	–	–	–
Puntledge R - Sum	CK-083	0.3%	0.0–3.7%	(24) 1998–2021	0.8%	–	–	–	–
Campbell/Quinsam R	CK-029	1.2%	0.0–4.7%	(24) 1998–2021	1.3%	0.3%	0.0–2.4%	(21) 2000–2021	0.6%
Capilano R	CK-9007	7.6%	0.0–32.9%	(14) 1998–2021	9.8%	–	–	–	–
Chilliwack R	CK-9008	0.7%	0.0–5.0%	(24) 1998–2021	1.1%	0.0%	0.0–0.1%	(14) 1998–2011	0.0%
Harrison R	CK-003	0.4%	0.0–1.7%	(19) 1998–2019	0.5%	–	–	–	–
Shuswap R Low	CK-015	0.1%	0.0–1.3%	(24) 1998–2021	0.3%	–	–	–	–
Shuswap R Middle	CK-015	0.0%	0.0–0.0%	(19) 1998–2021	0.0%	–	–	–	–
Overall mean (ocean type):		**2.0%**				**4.2%**			

*Table 4.3. Mean annual donor stray rates outside the CU (SR_{OCU}) from hatchery-origin, ocean-type Chinook Salmon returning to SBC rivers, estimated from expanded CWT or thermal mark recoveries. The number and range of years used in calculations (n) and standard deviation of estimates are provided (SD). *Estimates in brackets for Conuma R and Robertson Cr represent mean stray rates for the population calculated using terminal abundance to expand hatchery recoveries instead of escapement alone.*

Donor River	CU	STRAY RATE OUTSIDE THE CU (SR_{OCU})							
		CWT				THERMAL MARK			
		Mean	Range	(n) Years and Range	SD	Mean	Range	(n) Years and Range	SD
Conuma R	CK-032	0.0%	0.0–0.1%	(10) 1998 - 2007	0.0%	0.2% (0.1%)	0.0–0.6%	(23) 1998–2021	0.2%
Burman R	CK-032	–	–	–	–	0.1%	0.0–1.9%	(16) 2006–2021	0.5%
Gold R	CK-032	–	–	–	–	8.9%	0.0–27.0%	(5) 2012–2020	11.8%
Robertson Cr	CK-031	0.4%	0.0–4.8%	(24) 1998–2021	1.2%	1.8% (0.8%)	0.0–12.0%	(24) 1998–2021	2.7%
Nahmint R	CK-031	0.5%	0.0–13.4%	(9) 1998–2019	4.2%	0.2%	0.0–2.4%	(10) 2002–2019	0.7%
Nitinat R	CK-031	0.0%	0.0–0.4%	(10) 2002–2021	0.1%	0.1%	0.0–0.9%	(23) 1999–2021	0.2%
Sarita R	CK-031	0.0%	0.0–0.0%	(11) 1998–2021	0.0%	0.4%	0.0–4.4%	(21) 2000–2021	1.0%
Cowichan R	CK-022	7.2%	0.6–29.2%	(24) 1998–2021	6.8%	1.5%	0.0–10.5%	(12) 2009–2021	3.1%
Big Qualicum R	CK-027	0.7%	0.0–3.4%	(24) 1998–2021	0.9%	–	–	–	–
Nanaimo R – Fall	CK-025	4.0%	1.0–13.4%	(11) 1998–2008	3.8%	0.7%	0.0–4.1%	(12) 2007–2018	1.2%
Nanaimo R - Sum	CK-083	1.1%	0.0–5.0%	(7) 1998–2004	2.0%	2.7%	0.0–10.4%	(9) 2008–2021	4.4%
Puntledge R – Fall	CK-027	1.2%	0.0–9.3%	(21) 1998–2021	2.3%	–	–	–	–
Puntledge R – Sum	CK-083	0.3%	0.0–3.7%	(24) 1998–2021	0.8%	–	–	–	–
Campbell/Quinsam R	CK-029	1.2%	0.0–4.7%	(24) 1998–2021	1.3%	0.0%	0.0–0.0%	(21) 2000–2021	0.0%
Capilano R	CK-9007	7.6%	0.0–32.9%	(14) 1998–2021	9.8%	–	–	–	–
Chilliwack R	CK-9008	0.7%	0.0–5.0%	(24) 1998–2021	1.1%	0.0%	0.0–0.1%	(14) 1998–2011	0.0%
Harrison R	CK-003	0.4%	0.0–1.7%	(24) 1998–2021	0.5%	–	–	–	–
Shuswap R Low	CK-015	0.1%	0.0–1.3%	(19) 1998–2021	0.3%	–	–	–	–
Shuswap R Middle	CK-015	0.0%	0.0–0.0%	(24) 1998–2021	0.0%	–	–	–	–
Overall mean (ocean type):		**1.5%**				**1.4%**			

Table 4.4. Magnitude of donor straying (S_{TOT}) from hatchery-origin, ocean-type Chinook Salmon into 49 recipient rivers across SBC, estimated from expanded CWT and thermal mark recoveries. The mean, range, standard deviation (SD), number (n) and range of years used in calculations are provided.

Donor River Stock	**CU**	**MAGNITUDE OF HATCHERY STRAYS TO NON-NATAL RIVERS (S_{TOT})**							
		CWT				**THERMAL MARK**			
		Mean	**Range**	**(n) Years and Period**	**SD**	**Mean**	**Range**	**(n) Years and Period**	**SD**
Conuma R	CK-032	2	0–15	(10) 1998–2007	5	848	0–3790	(23) 1998–2021	980
Burman R	CK-032	–	–	–	–	99	0–712	(16) 2006–2021	185
Gold R	CK-032	–	–	–	–	114	0–425	(5) 2012–2020	175
Robertson Cr	CK-031	152	0–1388	(24) 1998–2021	363	644	0–4246	(24) 1998–2021	948
Nitinat R	CK-031	17	0–80	(9) 1998–2019	32	158	0–599	(23) 1998–2021	164
Nahmint R	CK-031	18	0–67	(10) 2002–2021	21	32	0–140	(13) 2001–2019	42
Sarita R	CK-031	5	0–22	(11) 1998–2021	8	71	0–338	(21) 2000–2021	100
Cowichan R	CK-022	118	8–497	(24) 1998–2021	117	12	0–49	(12) 2009–2021	19
Big Qualicum R	CK-027	76	0–322	(24) 1998–2021	80	–	–	–	–
Nanaimo R - Fall	CK-025	32	4–116	(11) 1998–2008	34	15	0–51	(12) 2007–2018	21
Nanaimo R - Summer	CK-083	9	0–24	(7) 1998–2004	9	13	0–51	(9) 2008–2021	20
Puntledge R – Fall	CK-027	48	0–316	(21) 1998–2021	93	–	–	–	–
Puntledge R – Summer	CK-083	3	0–47	(24) 1998–2021	10	–	–	–	–
Campbell/Quinsam R	CK-029	43	0–128	(24) 1998–2021	36	60	0–119	(21) 2000–2021	32
Capilano R	CK-9007	52	0–119	(14) 1998–2021	52	–	–	–	–
Chilliwack R	CK-9008	213	0–1061	(24) 1998–2021	292	5	0–21	(14) 1998–2011	6
Harrison R	CK-003	19	0–94	(24) 1998–2021	27	–	–	–	–
Shuswap R Low	CK-015	3	0–61	(24) 1998–2021	12	–	–	–	–
Shuswap R Middle	CK-015	0	–	(21) 1998–2021	–	–	–	–	–
Total	–	810	–	–	–	2071	–	–	–

Table 4.5. Magnitude of donor straying into rivers outside the CU (S_{OCU}) from hatchery-origin, ocean-type Chinook Salmon into 49 recipient rivers across SBC, estimated from expanded CWT and thermal mark recoveries. The mean, range, standard deviation (SD), number (n) and range of years used in calculations are provided.

Donor River Stock	**CU**	**MAGNITUDE OF HATCHERY STRAYS OBSERVED OUTSIDE THE CU (S_{OCU})**							
		CWT				**THERMAL MARK**			
		Mean	**Range**	**N of Years and Period**	**SD**	**Mean**	**Range**	**N of Years and Period**	**SD**
Conuma R	CK-032	2	0–15	(10) 1998–2007	5	31	0–145	(23) 1998–2021	45
Burman R	CK-032	–	–	–	–	4	0–56	(16) 2006–2021	14
Gold R	CK-032	–	–	–	–	70	0–303	(5) 2012–2020	130
Robertson Cr	CK-031	134	0–1377	(24) 1998–2021	362	263	0–4202	(24) 1998–2021	915
Nitinat R	CK-031	6	0–57	(9) 1998–2019	18	8	0–59	(23) 1998–2021	18
Nahmint R	CK-031	1	0–13	(10) 2002–2021	4	1	0–7	(13) 2001–2019	2
Sarita R	CK-031	0	–	(11) 1998–2021	–	6	0–61	(21) 2000–2021	14
Cowichan R	CK-022	118	8–497	(24) 1998–2021	117	12	0–49	(12) 2009–2021	19
Big Qualicum R	CK-027	28	0–117	(24) 1998–2021	24	–	–	–	–
Nanaimo R - Fall	CK-025	32	4–116	(11) 1998–2008	34	15	0–51	(12) 2007–2018	21
Nanaimo R - Sum	CK-083	4	0–24	(7) 1998–2004	9	13	0–51	(9) 2008–2021	20
Puntledge R - Fall	CK-027	44	0–316	(21) 1998–2021	90	–	–	–	–
Puntledge R - Sum	CK-083	3	0–47	(24) 1998–2021	10	–	–	–	–
Campbell/Quinsam R	CK-029	43	0–128	(24) 1998–2021	36	49	0–77	(21) 2000–2021	17
Capilano R	CK-9007	52	0–119	(14) 1998–2021	52	–	–	–	–
Chilliwack R	CK-9008	213	0–1061	(24) 1998–2021	292	5	0–21	(14) 1998–2011	6
Harrison R	CK-003	19	0–94	(24) 1998–2021	27	–	–	–	–
Shuswap R Low	CK-015	3	0–61	(24) 1998–2021	12	–	–	–	–
Shuswap R Middle	CK-015	0	–	(21) 1998–2021	–	–	–	–	–
Total	–	702	–	–	–	477	–	–	–

4.2. RECIPIENT RIVERS: HATCHERY STRAY CONTRIBUTION TO SPAWNERS IN SOUTHERN BC

Natural straying can benefit a species or population through colonization and increased diversity (Milner and Bailey 1989). However, as HSRG (2009, 2014) and Withler et al. (2018) describe, consistent straying from large-scale hatchery releases can have negative consequences, such as the loss of genetic diversity, a decreased ability to adapt to habitat conditions, and changes in population structure, which can reduce the viability of natural spawners. McElhaney et al. (2000) define viability in terms of productivity, abundance, diversity, and spatial structure. In this analysis we focus on the contribution of hatchery-origin spawners to escapement as estimated by *pHOS*, *pNOB* and *PNI*. We also delineate *pHOS* into out-of-basin strays ($pHOS_{\text{stray}}$) and local hatchery Chinook Salmon spawning naturally ($pHOS_{\text{local}}$). These results are summarized in Figure 4.4 and Table 4.5. The annual contribution of local and strayed hatchery fish to each recipient river are provided in Section 7 of this report and in Appendix E.

49 rivers were sampled routinely from 1998–2021 for adipose clips (CWT) and/or otolith thermal marks. The distribution of recipient river sampling programs across southern BC was patchy; mostly occurring on the WCVI and ECVI within the Georgia Basin. Within these areas, we estimate >85% of the natural spawning was included in this analysis. Most areas had some level of enhancement, and almost all had some type of marking and sampling.

Significant areas across SBC were not sampled. These include: Esperanza Inlet on the WCVI where only Zeballos R was sampled; the mainland inlets from Howe Sound to Knight Inlet; and much of the Fraser River. Most unsampled regions saw little to no enhancement between 1998–2021. Only six rivers with available data had no direct enhancement, all on the WCVI: Kauwinch R, Tashish R, Artlish R, and Kaouk R in Kyuquot Sound and Megin R and Moyeha R in Clayoquot Sound.

4.2.1. $pHOS_{\text{stray}}$

Withler et al. (2018) recommended benchmarks for $pHOS_{\text{stray}}$ (Table 3.1) in populations with no hatchery enhancement. For recipient rivers with no direct enhancement, the benchmark for out-of-basin stray contribution was $pHOS_{\text{stray}} \leq 0.03$ to maintain a ‘wild’ designation or $pHOS_{\text{stray}} > 0.03$ to have a designation of ‘wild – stray influenced’. For the latter designation, the authors used gene flow modelling to describe a long-term decline in fitness as $pHOS_{\text{stray}}$ increases. Here, we consider this benchmark in the context of populations that also experience local enhancement, as a similar benchmark for populations with both local and stray hatchery-origin spawners has not been established. However, it is possible that $pHOS_{\text{stray}} \leq 0.03$ is not sufficiently conservative to maintain long-term fitness within a locally enhanced population.

On the WCVI, of the six river populations which had no local hatchery enhancement, all had an average $pHOS_{\text{stray}} > 0.18$, which far exceeded the benchmark set out by Withler et al. (2018) for wild-stray influenced populations ($pHOS_{\text{stray}} > 0.03$). There was little to no information for unenhanced systems in the inside waters of Vancouver Island (ECVI and mainland inlets) or the Fraser R.

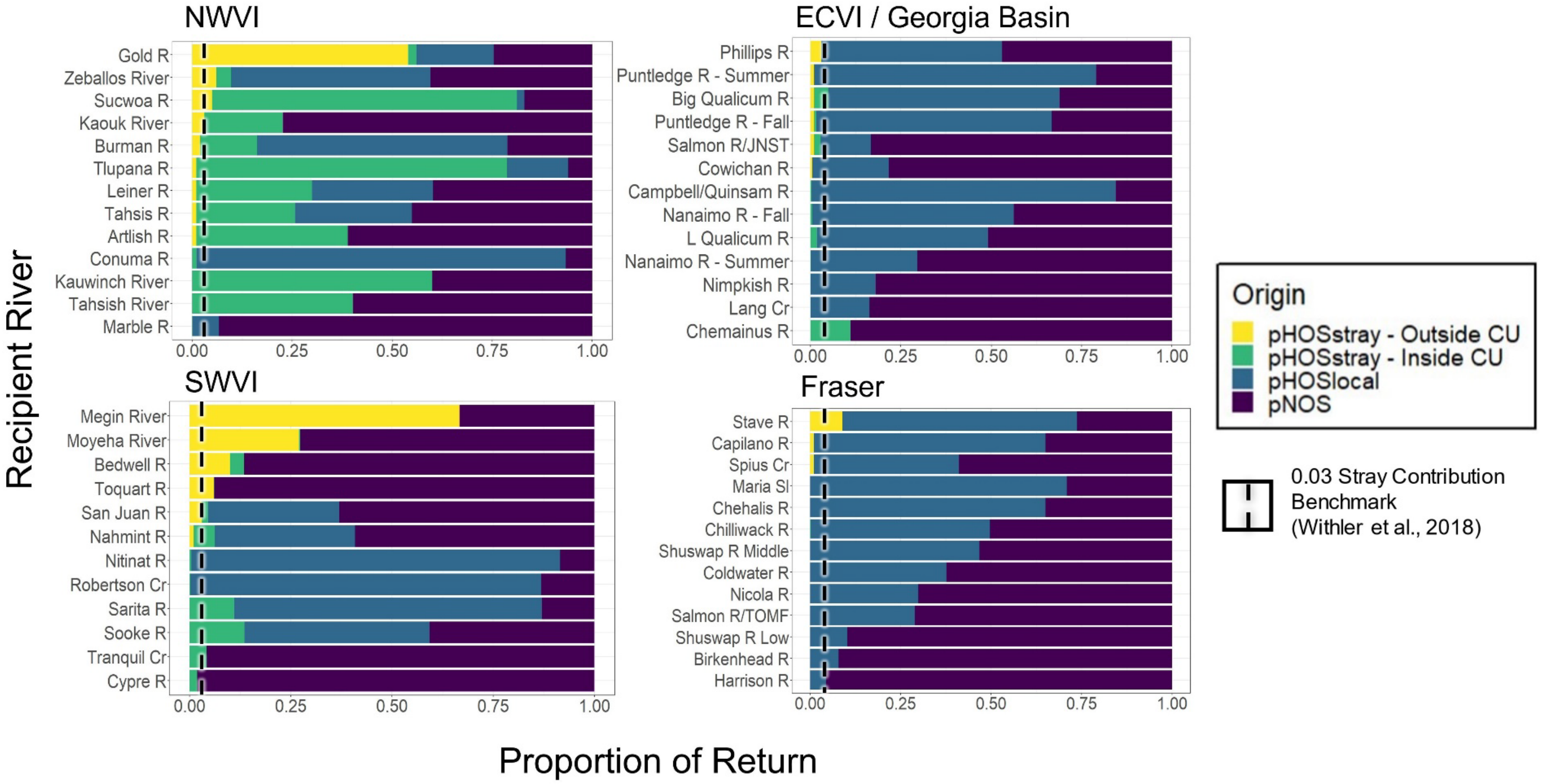

Figure 4.4. Mean (1998–2021) proportion of spawners returning to 49 recipient river populations from four regions of southern BC. Different coloured bars correspond to the respective origin of spawners observed; hatchery-origin strays (Yellow = pHOSstray,OCU, Green = pHOSstray), local hatchery-origin returns that homed to the natal rivers (Teal = pHOSlocal) or natural-origin spawners based on no adipose clip, CWT, or otolith thermal mark (Dark Blue = pNOS).

It is important to note that some rivers with enhancement were excluded, including Thornton Cr, Henderson R/Clemens R, and the Kennedy watershed. These systems have no CWT or thermal marking and thus were not present in the data compiled here. Some rivers such as Marble R and Tranquil R were intermittently enhanced and marked over our period of analysis, thus average *pHOS* values were likely underestimated in these systems.

The Bedwell R, in Clayoquot Sound, is under special management due to its previous categorization as a 'wild' escapement indicator in Clayoquot Sound. In 2011, after six consecutive years of returns less than 100 adult Chinook Salmon, it was decided to initiate enhancement. The production target was set at 25,000 eggs (approximately 6–8 females), and all local hatchery releases were adipose fin clipped. Since 2013, the return has averaged about 500 Chinook per year.

Hatchery contribution was calculated for this stock based on observed adipose fin clips. $pHOS_{\text{local}}$ reached as high as 0.42 in the first cycle of returns, but in the most recent five years (2017–2021) $pHOS_{\text{local}}$ fell to an average of 0.18. Thermal mark sampling results in the Bedwell R indicated 18% of the return was comprised of unclipped hatchery strays ($pHOS_{\text{stray}}$ = 0.18). Combining the two produces *pHOS* = 0.36. The selection of unclipped Chinook in the broodstock would result in a *pNOB* = 0.82 and *PNI* = 0.70 indicating an 'Integrated-Transition" designation for Bedwell R Chinook. Note *PNI* = 0.70 assumes that stray hatchery fish do not have a disproportionately negative effect on natural adaptive influence in the population, which as discussed above is unlikely. Thus, *PNI* = 0.70 is likely an overestimate for the Bedwell R. However, in any case, hatchery straying at a rate above the Withler et al. (2018) benchmark (i.e., $pHOS_{\text{stray}} > 0.03$) suggests that the overall fitness of the Bedwell Chinook population will decline over time.

One key observation from Figure 4.4 and Table 4.5 is that the influence of hatchery strays can be substantial even in populations that are integrated with local hatchery enhancement. For instance, in 13 WCVI rivers where hatchery-origin Chinook are released as sub-yearling smolts (excluding the three major facilities of Nitinat R, Robertson Cr, Conuma R, as well as Gold R), $pHOS_{\text{stray}}$ accounts for an average of 0.32 of the total *pHOS*. This is particularly true in the Nootka-Kyuquot CU (CK-32), due to the contribution to $pHOS_{\text{stray}}$ from Conuma R Hatchery Chinook. Consequently, removing or reducing the extent of hatchery strays would result in a marked decrease in *pHOS* in many systems.

Of the remaining rivers with directed enhancement and marking we review $pHOS_{\text{stray}}$ from Table 4.5 by region.

In the NWVI, Quatsino Sound (CK-33) had an average $pHOS_{\text{stray}}$ of 0.00 across the time series, compared to the Nootka-Kyuquot region (CK-32), which averaged 0.37. Of the 12 river populations sampled there, only Conuma R fell below the 0.03 benchmark for $pHOS_{\text{stray}}$ (reflecting the fact that Conuma R Hatchery was the *source* of most strays in this region).

$pHOS_{\text{stray}}$ for the South West Vancouver Island averaged 0.04. This includes Barkley Sound and rivers down to Sooke which is a portion of Conservation Unit CK-31. We excluded Sooke R in this calculation as it received transplants from the Nitinat R stock for over 25 years and there appears to be an outlying stray relationship between the two systems. We also note that rivers in Clayoquot Sound were not included here as they were covered earlier in this section. Across the five rivers sampled for thermal marks in Clayoquot Sound, an average $pHOS_{\text{stray}}$ of 0.20 was observed. This value is likely an underestimate due to lack of marking at Tofino, Thornton Cr, and Kennedy R hatcheries which did not have the capacity to mark releases. Strays from these facilities will be covered in a subsequent section on genetic results. Thornton Creek Hatchery represents a special case of a system with a high donor stray rate into Clayoquot Sound that was only detectable with the use of genetic tools. We elaborate on this point further in Section 5 (Sources of Bias and Uncertainty).

On the ECVI, within the Georgia Basin, average *pHOS*$_{stray}$ was 0.03. This includes 12 populations from Victoria to North of Campbell River in four CUs for fall run Chinook (CK-22, CK-25, CK-27, and CK-29) and one for summer run Chinook (CK-83). As average *pHOS*$_{stray}$ was ≤ 0.3, most populations in this region fell within the Withler et al. (2018) guidance benchmark. Only the Chemainus R regularly exceeded this benchmark, likely due to transplanting populations into the system. Calculations of *pHOS*$_{stray}$ on the ECVI were based on CWT data except in Chemainus R and Nanaimo R where otolith samples were taken (both CWT and thermal marks were available). Thermal mark samples from Campbell/Quinsam R were not used to calculate average *pHOS*$_{stray}$ values, but are presented in Section 7. However, thermal marks from Quinsam R Hatchery were recovered in the Salmon R just north of the Quinsam R Hatchery.

Southern fjords from Howe Sound to Loughborough Inlet had an average *pHOS*$_{stray}$ of 0.01. Only three rivers with samples were used in this analysis including Capilano R and Lang Cr in CK-9007 and Phillips R in CK-28. This analysis was based on CWT only.

Lower Fraser R estimates of *pHOS*$_{stray}$ included five CUs: CK-003, CK-004, CK-007, CK-9006, and CK-9008. Average *pHOS*$_{stray}$ was 0.02 but only exceeded the 0.03 benchmark in the Stave R where average *pHOS*$_{stray}$ was 0.09. This regional analysis was based on CWT only.

Analysis in the Thompson River drainage included CUs CK-14, CK-15, and CK-17. Strays were only observed in one of six systems, and only in one year (Spius Cr, 2000). There was no other evidence of straying based on CWT samples from each of six systems.

The WCVI saw the greatest risk due to *pHOS*$_{stray}$. The Conuma Hatchery stands out as the main contributor of strays to WCVI rivers. In all other areas, strays from donor hatcheries appear to approach or fall below the benchmark for a ‘wild’ designation (with regard to stray contribution). It should be noted that most of these rivers had significant local enhancement (*pHOS*$_{local}$). If we adjust these spawner estimates to exclude local enhancement, *pHOS*$_{stray}$ would be significantly greater and above the 3% benchmark in Withler et al. (2018).

4.2.2. *pHOS*$_{stray}$ to rivers outside the CU of origin

Hatchery straying into rivers and spawning populations outside the CU of origin has the potential to adversely affect recipient populations. Of the 49 recipient rivers reviewed in this report, ten had a mean *pHOS*$_{stray,OCU}$ that exceeded the 0.03 benchmark for *pHOS*$_{stray}$ (Table 4.5). These include:

- Gold R, CK-032. *pHOS*$_{stray,OCU}$ = 0.59. As indicated previously this is a special case of mass straying from Robertson Creek Hatchery, likely due to olfactory similarities with the Somass R.
- Sucwoa R, CK-032. *pHOS*$_{stray,OCU}$ = 0.04. There was a Robertson Cr Hatchery stray in 1 out of the 5 years sampled. Sucwoa R is near Conuma R and saw very high straying from Conuma R. Sucwoa R, Canton R, and Conuma R are now managed as a single stock.
- Zeballos R, CK-032. *pHOS*$_{stray,OCU}$ = 0.06. There were Robertson Cr Hatchery strays in 2 out of the 7 years sampled; Nitinat R strays were observed in 1 out of 7 years; and Sarita R strays were observed in 4 out of 7 years sampled. Zeballos R sees a high magnitude of strays from Conuma R.

- Bedwell R, CK-031. $pHOS_{\text{stray,OCU}}$ = 0.09. Thermal marks indicated strays from Gold R (reared at Conuma R Hatchery) in 4 out of 8 years sampled, recoveries from Conuma R and Leiner R were also observed in 1 out of 8 years sampled.
- Megin R, CK-031. $pHOS_{\text{stray,OCU}}$ = 0.58. Strays only from Conuma R; observed in 1 of 5 years sampled.
- Moyeha R, CK-031. $pHOS_{\text{stray,OCU}}$ = 0.18. Strays from Conuma R observed in 1 of 2 years sampled.
- Toquart R, CK-031. $pHOS_{\text{stray,OCU}}$ = 0.06. Strays only from Conuma R, observed in both years sampled.
- San Juan R, CK-031. $pHOS_{\text{stray,OCU}}$ = 0.03. Strays mostly from Nitinat R were observed in 8 out of 10 years sampled. Strays from Conuma R, Robertson Cr, and Tlupana R were each observed in 2 out of 10 years sampled. Strays from Spius Cr were allegedly observed in 2019, but may be the result of data entry error.
- Phillips R, CK-028. $pHOS_{\text{stray,OCU}}$ = 0.03. Strays outside-the-CU originated from Puntledge R, Campbell/Quinsam R, and US hatcheries. Straying did not occur in most years, but in two years exceed 10% of total spawners.
- Stave R, CK-9006. $pHOS_{\text{stray,OCU}}$ = 0.09. Sampling only occurred from 1998–2003 during our time series. Out-of-CU strays were primarily from Chilliwack R, recovered in 3 of 6 years sampled; Harrison R strays were observed in smaller numbers, in 5 of 6 years sampled, and 1 Cowichan R stray was observed in 1999.

4.2.3. PNI

Average *PNI* values are presented for each recipient river in Table 4.5. A heat map of annual estimates, where calculable, is provided in Figure 4.5, and the designation of each system based on Withler et al. (2018), is described in Section 7. In this section, we describe differences in hatchery influence (*PNI*) among regions by comparing the number of populations that fall into the designations of integrated-hatchery (*PNI* < 0.5), integrated-transition (*PNI* between 0.5 and 0.8), and integrated-wild (*PNI* > 0.8) populations, in the last five years of available sampling.

In the NWVI region, most rivers had low *PNI* values indicative of integrated-hatchery populations (*PNI* < 0.5). Here, eight of the nine systems for which *PNI* could be calculated had an average *PNI* < 0.5 in the last five years. Most of these populations were located in Nootka Sound and were enhanced by Conuma R Hatchery between 1998–2021. One population in the northern CU (CK-33), Marble R, fell within the integrated-wild designation.

On the SWVI, four of nine systems were designated as integrated-hatchery, three as integrated-transition, and two as integrated-wild. The two integrated-wild designated populations, Toquart R and Tranquil Cr, were estimated from only a single year, and should not be taken as indicative of trends for the region. However, in comparison to the NWVI, southern rivers generally had higher PNIs; the exception being those systems with large-scale hatchery production (Robertson Cr, Nitinat R, and Sarita R) and the transplanted Sooke R population.

On the ECVI, five populations were designated integrated-hatchery populations; all systems that support large-scale hatchery production (Quinsam R, Punteldge R (both fall and summer runs), Big Qualicum R, and Nanaimo R (fall run)). Two populations were designated integrated-transition, the Nanaimo summer run population (a conservation stock) and the Salmon R/JNST population. Three populations were designated as integrated-wild in the ECVI (Nimpkish R, Cowichan R, and Little Qualicum R). When compared to the WCVI (both North and South), *PNI* values were generally higher, including those calculated in integrated-hatchery systems.

In the Fraser R, the only three integrated-hatchery populations observed were transplanted and supported by a major hatchery facility (Chilliwack R, Chehalis R, and Stave R). Beyond these populations, six stocks were designated as integrated-transition populations (Maria Slough, Coldwater R, Spius Cr, Nicola R, Salmon R/TOMF, Shuswap R Middle), and two as integrated-wild populations (Harrison R and Shuswap R Low). These two integrated-wild populations were the most consistently high *PNI* values observed over the time-series.

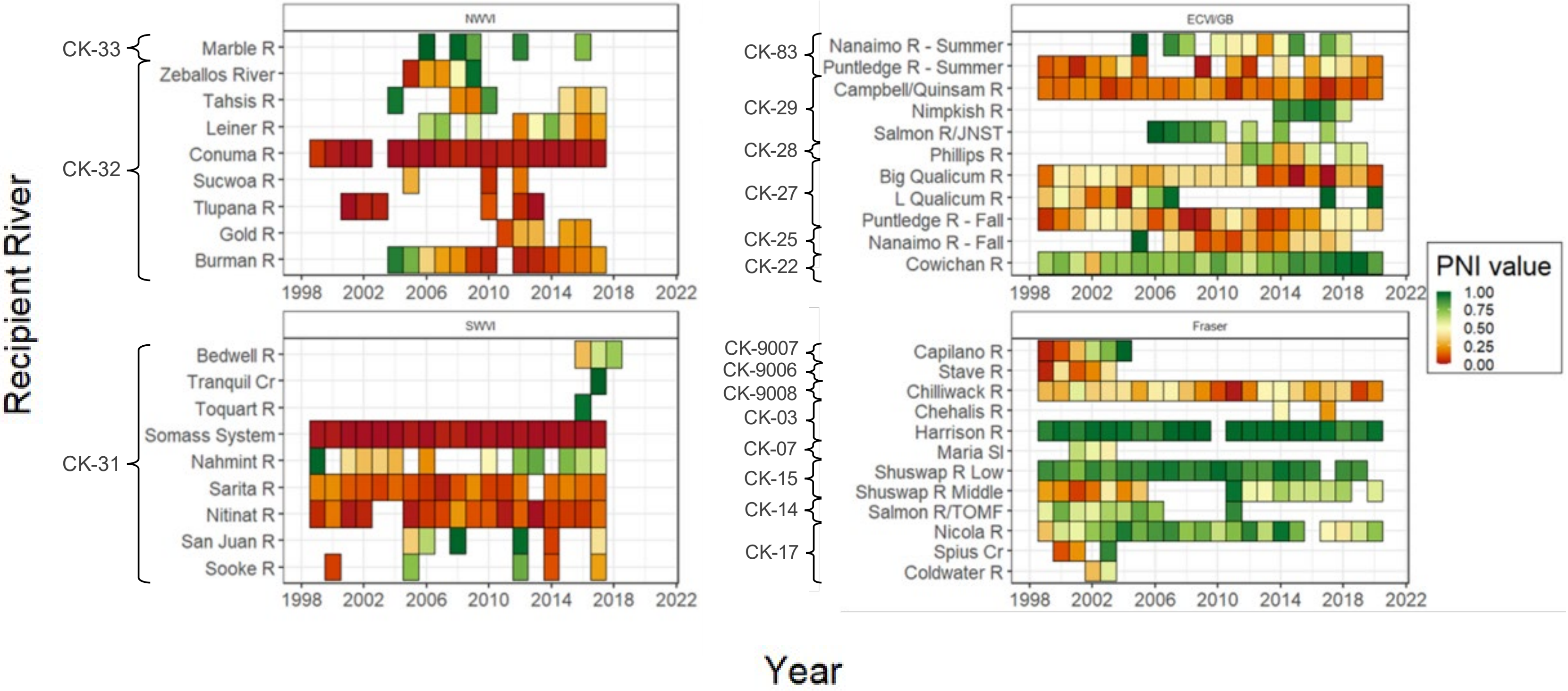

Figure 4.5. Heat map of proportionate natural influence (PNI) estimates calculated annually for rivers in SBC, presented by Conservation Unit (CU) and geographic region for 41 spawning populations. NWVI = Northwestern Vancouver Island; SWVI = Southwesertern Vancouver Island; ECVI/GB = East Coast Vancouver Island/Georgia Basin; Fraser = Fraser River Drainage.

Table 4a. Mean escapement, hatchery contribution and proportionate natural influence (PNI) for recipient rivers in the WCVI region between 1998–2021. Mean proportions of local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners ($pHOS_{stray}$), strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray,OCU}$), proportionate natural influence (PNI), and PNI from local-only spawners (PNI_{local}) are described for each river. Mean PNI values are colour-coded based on benchmarks from Withler et al. (2018): Integrated Wild (IW) = Green; Integrated-Transition (IT) = Orange; Integrated-Hatchery (IH) = Red. Data are presented by Conservation Unit (CU), and the data type used in the estimate is indicated (CWT = coded-wire tag, TM = thermal mark). Rivers in grey and marked with an asterisk indicate systems that did not have >20 samples taken in any year of the analysis.

CU	Recipient River	Region	Data	ESCAPEMENT	$pHOS_{local}$	$pHOS_{stray}$	$pHOS_{stray,OCU}$	$pHOS$	PNI_{local}	PNI	Designation
CK-033	Marble R	Quatsino Sound	TM	3028	0.06	0.00	0.00	0.06	0.91	0.91	IW
CK-032	Artlish R	Kyuquot Sound	TM	333	0.00	0.39	0.01	0.39	--	--	–
	Kaouk River*		TM	429	0.00	0.04	0.00	0.24	--	--	–
	Kauwinch River*		TM	104	0.00	0.60	0.00	0.60	--	--	–
	Tahsish River		TM	648	0.00	0.52	0.00	0.52	--	--	–
	Conuma R	Nootka Sound	TM	21916	0.96	0.01	0.00	0.97	0.03	0.03	IH
	Burman R		TM	2630	0.63	0.16	0.02	0.79	0.29	0.25	IH
	Gold R		TM	2397	0.17	0.61	0.59	0.78	0.62	0.26	IH
	Leiner R		TM	691	0.30	0.30	0.01	0.60	0.69	0.47	IH
	Sucwoa R		TM	96	0.01	0.86	0.04	0.87	0.83	0.17	IH
	Tahsis R		TM	739	0.29	0.26	0.01	0.55	0.76	0.58	IT
	Tlupana R		TM	379	0.15	0.79	0.01	0.94	0.45	0.07	IH
	Zeballos River		TM	248	0.50	0.10	0.06	0.60	--	--	–
CK-031	Bedwell R	Clayoquot Sound	TM	222	0.00	0.15	0.09	0.15	1.00	0.85	IW
	Cypre R		TM	780	0.00	0.03	0.03	0.03	--	--	–
	Megin River*		TM	74	0.00	0.58	0.58	0.58	--	--	–
	Moyeha River*		TM	124	0.00	0.18	0.18	0.18	--	--	–
	Tranquil Cr		TM	543	0.00	0.04	0.00	0.04	1.00	1.00	IW
	Robertson Cr	Barkley Sound	TM	41965	0.91	0.00	0.00	0.91	0.01	0.01	IH
	Nahmint R		TM	519	0.28	0.11	0.01	0.40	0.61	0.57	IT
	Sarita R		TM	2022	0.76	0.11	0.00	0.87	0.15	0.14	IH
	Toquart R		TM	290	0.00	0.06	0.06	0.06	1.00	0.95	IW
	Nitinat R	Nitinat - Sooke	TM	21151	0.89	0.00	0.00	0.89	0.09	0.09	IH
	San Juan R		TM	1831	0.32	0.05	0.03	0.37	0.59	0.58	IT
	Sooke R		TM	770	0.48	0.05	0.00	0.53	0.48	0.48	–

Table 4b. Mean escapement, hatchery contribution and proportionate natural influence (PNI) for recipient rivers in the ECVI, Coastal Inlet and Fraser regions between 1998–2021. Mean proportions of local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners ($pHOS_{stray}$), strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray,OCU}$), proportionate natural influence (PNI), and PNI from local-only spawners (PNI_{local}) are described for each river. Mean PNI values are colour-coded based on benchmarks from Withler et al. (2018): Integrated Wild (IW) = Green; Integrated-Transition (IT) = Orange; Integrated-Hatchery (IH) = Red. Data are presented by Conservation Unit (CU), and the data type used in the estimate is indicated (CWT = coded-wire tag, TM = thermal mark). Rivers in grey and marked with an asterisk indicate systems that did not have >20 samples taken in any year of the analysis.

CU	Recipient River	Region	Data	ESCAPEMENT	$pHOS_{local}$	$pHOS_{stray}$	$pHOS_{stray,OCU}$	$pHOS$	PNI_{local}	PNI	Designation
CK-083	Nanaimo R - Sum	ECVI	TM	657	0.31	0.00	0.00	0.32	0.65	0.65	IT
	Puntledge R - Sum		CWT	1083	0.77	0.01	0.01	0.78	0.20	0.20	IH
CK-029	Campbell/Quinsam R		CWT	7522	0.67	0.01	0.01	0.68	0.16	0.16	IH
	Nimpkish R		TM	1118	0.18	0.00	0.00	0.18	0.84	0.84	IW
	Salmon R/JNST		TM	787	0.14	0.03	0.01	0.17	0.84	0.81	IW
CK-028	Phillips R		CWT	59	0.48	0.03	0.03	0.52	0.51	0.51	IT
CK-027	Big Qualicum R		CWT	8002	0.63	0.04	0.01	0.67	0.30	0.28	IH
	L Qualicum R^		CWT	5178	0.49	0.02	0.00	0.51	0.50	0.50	IT
	Puntledge R - Fall		CWT	8156	0.66	0.01	0.01	0.67	0.31	0.31	IH
CK-025	Chemainus R*		TM	238	0.00	0.16	0.00	0.16	--	--	–
	Nanaimo R - Fall		TM	3758	0.56	0.01	0.01	0.57	0.33	0.33	IH
CK-022	Cowichan R		CWT	9658	0.23	0.01	0.01	0.24	0.75	0.75	IT
CK-9007	Capilano R	Coastal Inlets	CWT	1130	0.66	0.01	0.01	0.66	0.44	0.32	IH
	Lang Cr^		CWT	1269	0.16	0.00	0.00	0.16	0.84	0.84	IW
CK-9006	Chehalis R	Lower Fraser	TM	323	0.65	0.00	0.00	0.65	0.35	0.35	IH
	Stave R		CWT	588	0.56	0.08	0.08	0.64	0.27	0.26	IH
CK-9008	Chilliwack R		CWT	45690	0.51	0.00	0.00	0.51	0.32	0.32	IH
CK-003	Harrison R		CWT	83766	0.04	0.01	0.01	0.04	0.95	0.95	IW
CK-004	Birkenhead R*		CWT	581	0.08	0.00	0.00	0.08	--	--	–
CK-007	Maria Sl		CWT	489	0.31	0.00	0.00	0.31	0.44	0.44	IH
CK-015	Shuswap R Low	South Thompson	CWT	30052	0.10	0.00	0.00	0.10	0.89	0.89	IW
	Shuswap R Middle		CWT	2784	0.47	0.00	0.00	0.47	0.56	0.56	IT
CK-014	Salmon R/TOMF		CWT	788	0.29	0.00	0.00	0.29	0.71	0.71	IT
CK-017	Coldwater R	Lower Thompson	CWT	494	0.40	0.00	0.00	0.40	0.62	0.62	IT
	Nicola R		CWT	5315	0.30	0.00	0.00	0.30	0.69	0.69	IT
	Spius Cr^		CWT	497	0.29	0.01	0.01	0.30	0.56	0.56	IT

^ population was not tagged with a CWT or thermal mark in some years included in this analysis; *PNI* values are likely overestimated.

4.3. GENETIC ASSESSMENT OF CHINOOK STRAYING ALONG THE WCVI

In 2013, 2014, and 2015 funding was provided to increase sampling for this assessment of Chinook straying along the WCVI and to conduct genetic analyses as reported to Southern Endowment Fund in 2017 (see Section 3.1.6).

Genetic analysis of microsatellite loci was used to (1) provide a parallel assessment of hatchery straying, and (2) to estimate the cumulative genetic introgression associated with stray fish from enhanced populations. The analysis was conducted on the same samples as those subjected to thermal otolith analysis, and on historical samples from WCVI hatchery-enhanced and unenhanced watersheds. This enabled an examination of the degree and stability of population structure in WCVI Chinook Salmon and a elucidation of the effects of hatchery-wild interactions since the inception of enhancement efforts in the late 1970s.

Genetic variation among populations across the WCVI is summarized in Figure 4.6. There was strong genetic differentiation between the Robertson Cr, Conuma R and Nitinat R large-scale hatchery stocks with genetic variation within each stock that has been maintained relatively consistently since the initiation of enhancement in the 1970s. Comparisons with the variation observed in other WCVI populations suggests that genetic variation from the major hatcheries (Robertson Cr, Conuma R and Nitinat R) has been introduced into the majority of populations within the same CU as the hatchery, resulting in a ‘genetic homogenization’ across populations. This pattern is consistent with the impacts of straying from enhanced systems on the genetics of recipient systems presented here. Furthermore, homogenization has potentially been exacerbated by at least one transplant of a stock from a major hatchery (Robertson) to a smaller facility near Ucluelet (Thornton Creek Hatchery) followed by subsequent straying along the coast.

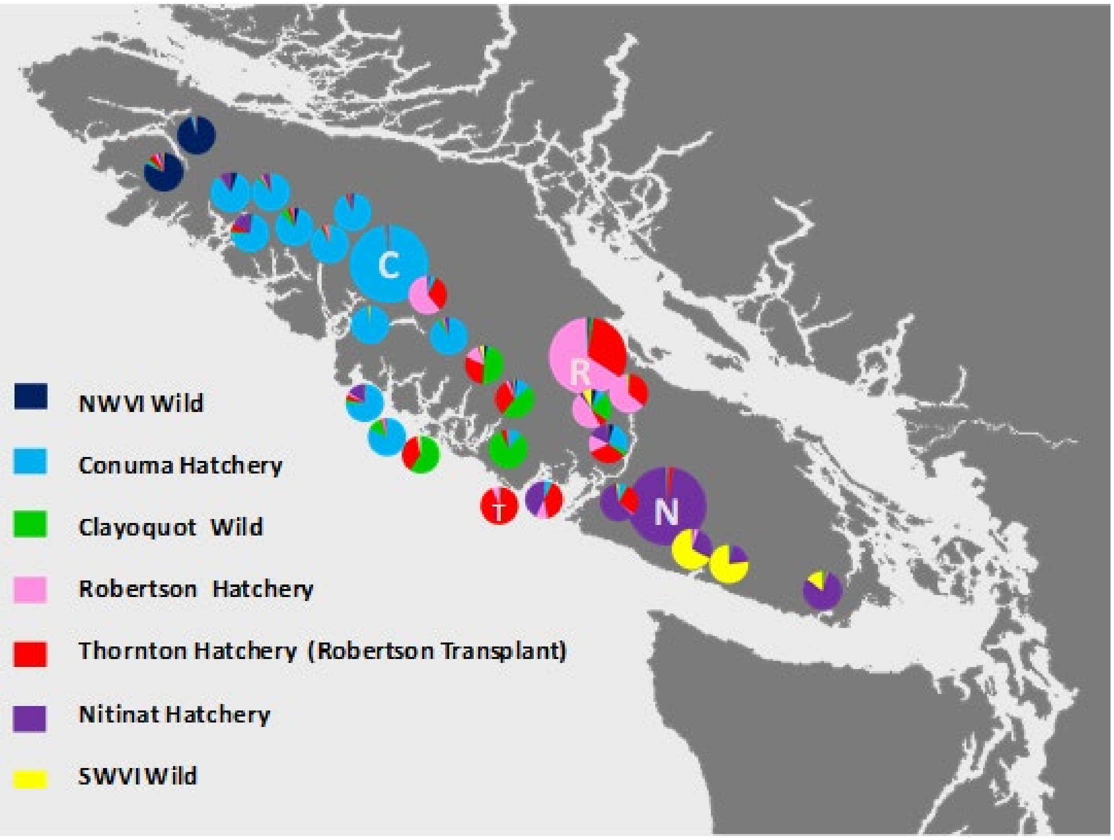

Figure 4.6. Genetic ancestries of Chinook populations sampled between 2013–2015 along the West Coast of Vancouver Island. The size of the pie slice indicates the average proportion of the sample identified by STRUCTURE analysis to be of a given genetic ancestry corresponding to the colour in the legend.

Despite the degree of genetic homogenization observed across the WCVI, there are still a number of distinct ‘wild’ genetic signals in Chinook Salmon from several locations. Populations in Clayoquot Sound and Quatsino Sound, as well as the populations in the San Juan R and Gordon R, remain relatively distinct from the major hatchery stocks (green, navy and yellow in Figure 4.6, respectively). To a lesser extent this is also true of Chinook found in the Sarita R. Nahmint R Chinook are another relatively distinctive population, but note that the Nahmint R hatchery brood has been genetically screened to remove strays and fish of mixed ancestry for several years.

In the companion assessment to this work described in Section 3.1.6, several of these populations were assessed over time, using both a neighbour-joining dendrogram of population samples and a STRUCTURE admixture analysis showing the genetic ancestries present within different samples. Two of these analyses are highlighted below: the Burman R compared to the Conuma R (Figure 4.7), and Tranquil Cr and the Cypre R compared to Thornton Cr (Figure 4.8). Analogous comparisons and results observed in the Toquart R, Nahmint R and San Juan R can be found in the assessment’s report to the Southern Endowment Fund (see Section 3.1.6).

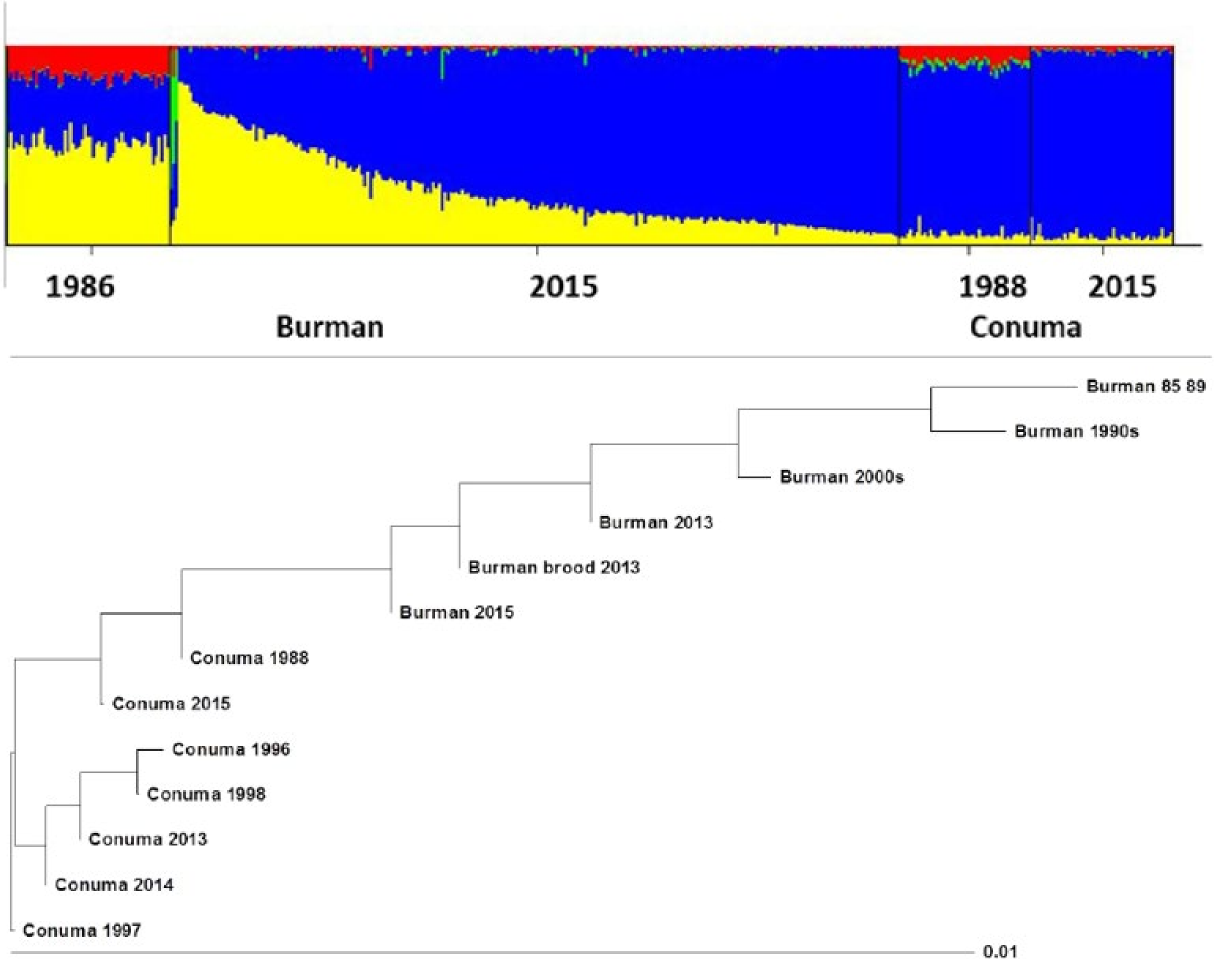

Figure 4.7. The top figure shows the output of the STRUCTURE analysis of Burman R compared to Conuma R Chinook spawners in 1986/88 and 2015. Each vertical line represents the genetic variants within an individual spawner, with the different colours representing different genetic ancestries (blue = dominant Conuma R ancestry; yellow = dominant Burman R ancestry). Below is a neighbour-joining dendrogram of Chinook samples collected from the Burman and Conuma rivers over the same time period.

Both the STRUCTURE and dendrogram analyses indicate that the genetic differentiation between Conuma R and Burman R Chinook Salmon has dramatically decreased from the 1980s to 2015 (Figure 4.7). This decrease is not a direct result of strays from the Conuma R Hatchery spawning in

Burman R, because thermal marks have confirmed high Conuma R ancestry in both Chinook carrying a Burman R Hatchery thermal mark or lacking a thermal mark entirely. Therefore, the increasing genetically similarity between Chinook in the Burman and Conuma rivers is a consequence of straying *and introgression* of Conuma R genetic variation into the Burman River population over this time period. Since Conuma River Hatchery strays were likely present in many of the Burman R brood collections over this 30-yr period, hatchery enhancement of the Burman R population almost certainly contributed to the observed introgression.

Similar to the example of the Burman R and Conuma R, both the STRUCTURE and dendrogram analyses of samples from Tranquil Cr, the Cypre R and Thornton Cr indicated that the genetic variation in the two former populations was largely independent of the latter population in the 1990s and the early 2000s (Figure 4.8). In contrast, Tranquil Cr/Cypre R samples in 2014 and 2015 display clear evidence of Thornton Cr ancestry. Again, this pattern is consistent with increased straying from Thornton Cr, likely dominated by hatchery-origin fish, resulting in introgression of Thornton Cr genetic variation into the Tranquil Cr and Cypre R populations.

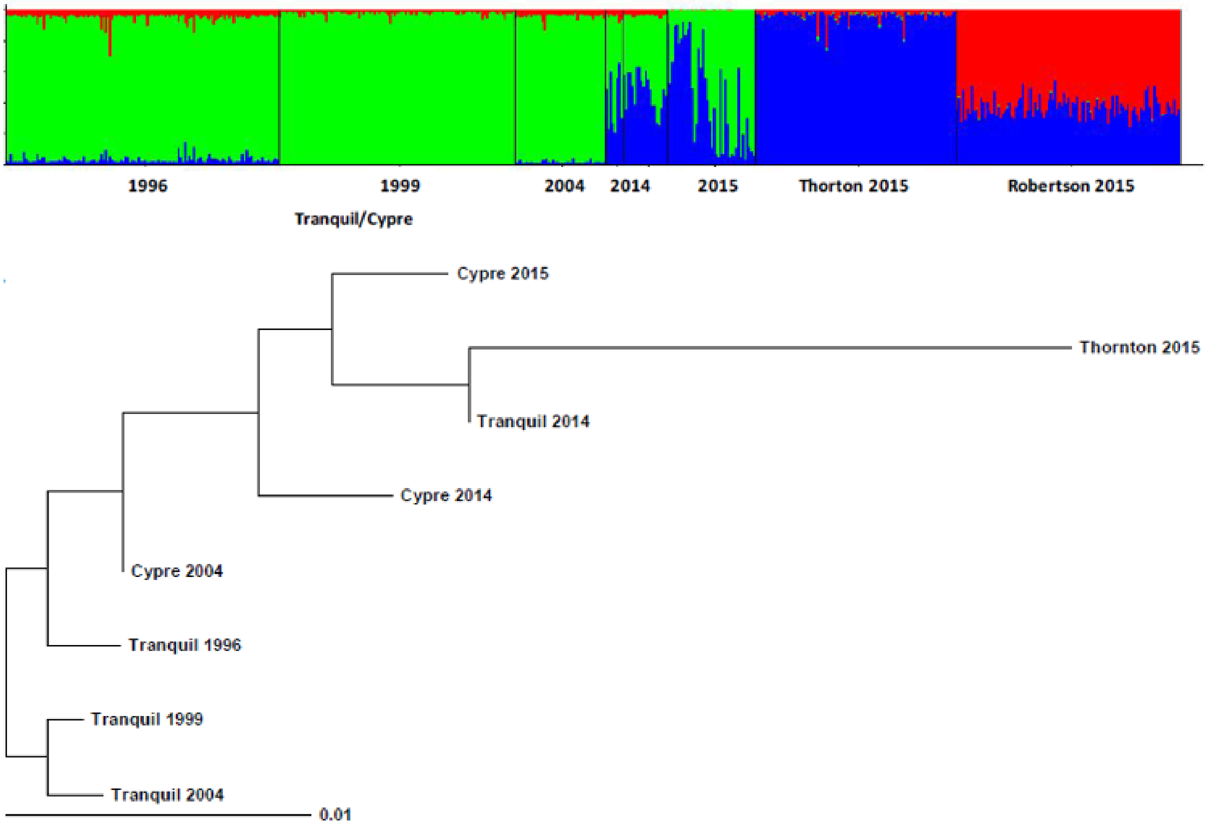

Figure 4.8. The top figure is a STRUCTURE analysis of Tranquil Cr, Cypre R, Thornton Cr and Robertson Cr Chinook spawners from 1996 to 2015. Each vertical line represents the genetic variants within an individual spawner with the different colours representing different genetic ancestries (green – dominant Tranquil/Cypre ancestry; blue – dominant Thornton ancestry; red – dominant Robertson ancestry). Note the original Thornton Cr broodstock was a Robertson Cr transplant likely accounting for the shared blue ancestry between those stocks. Below is a neighbour-joining dendrogram of Chinook samples collected from Tranquil Cr, Cypre R and Thornton Cr over the same time period.

4.4. FACTORS AFFECTING DONOR STRAY RATE

Straying is a component of the life history in each salmon species (Waples et al. 2008), which has been the basis for colonization of Pacific salmon. However, the stray rate is also typically low enough to allow for adaptation and genetic similarities to develop within groups of stocks (e.g., Wild Salmon Policy CUs) and diversity between the groups (Holtby and Ciruna 2007).

External environmental factors can affect stray rate. In the ocean environment, salmon navigation may be affected by ocean temperatures, light, and geomagnetic fields, senescence, toxic chemical exposure. (Dat et al. 1995; Putman et al. 2013).

Once they return to coastal marine and/or freshwater environments, straying may be affected by olfactory detection of chemical odors imprinted on juveniles during early rearing in freshwater and parr-smolt transformation, or a change in the natal river's chemical signature over time (Zimmer-Faust et al. 1995; Quinn 2005). While a shared river drainage or water source would certainly produce a similarity in water odours, it could be hypothesized that even distant rivers can share similar attributes. On the WCVI, Robertson Cr Hatchery Chinook from the Somass R regularly stray in large numbers to the Gold R 250 km away; both rivers contained similar pulp mills that may have created similar olfactory signals affecting homing (Candy et al. 2009).

In adult salmon, Keefer and Caudill (2014) describe several freshwater factors, including water temperature, river discharge, dissolved oxygen, chemical signatures, and more which have the potential to affect homing/straying.

In years of extreme temperatures and/or low flows (e.g., Figure 4.9, Figure 4.10), suitable river area for spawning may be inaccessible, so returning Chinook may seek more accessible spawning habitat nearby. Natural water flow buffers, such as lakes and glaciers, can provide more stable flows throughout the year; and so are more likely have lower stray rates. Anthropogenic water flow buffers (e.g., dams and weirs), which are typically found in hatchery-enhanced systems, can also help maintain flows at sufficient levels for Chinook upriver migration, resulting in lower stray rates compared to systems with no flow buffer.

Figure 4.9. Tahsis R in mid-September 2014. Nearly 100% of the Chinook homing to the Tahsis R would have been in the terminal area waiting to go up the river. Low flows in 2013 and 2014 likely influenced straying throughout Nootka Sound. These were 2 of the 3 years where we conducted genetic analysis to assess population structure.

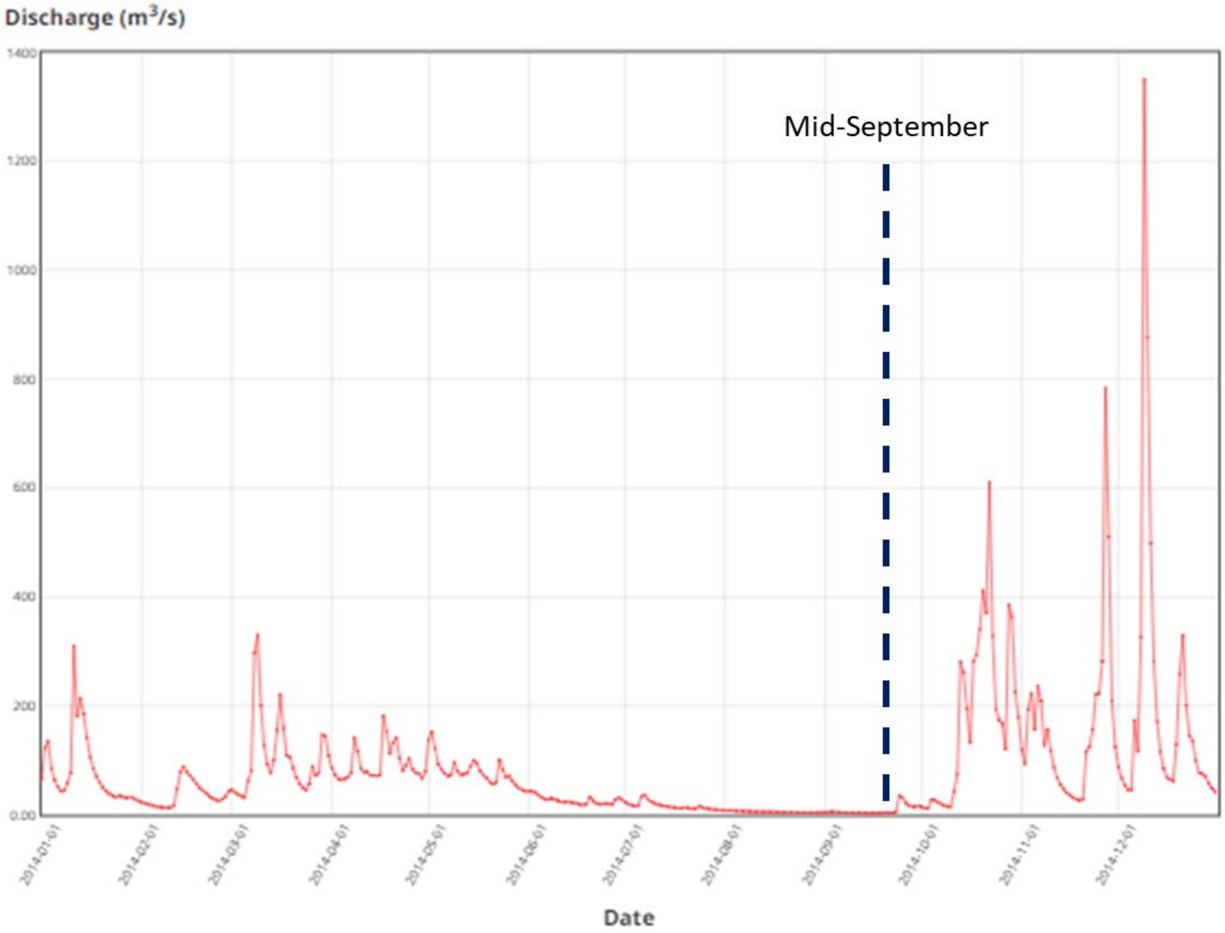

Figure 4.10. Daily discharge graph for the Gold R in 2014, which is the Water Survey Canada station nearest to the Tahsis R. The Gold R is lake fed and so is buffered from low and high flows unlike the Tahsis R and other rivers in Nootka Sound.

Age has been found in some studies to be a significant predictor of straying probability but the direction and magnitude of impacts reported has been mixed, perhaps because of interaction effects. Some studies show a positive correlation between propensity to stray and age in Chinook (Quinn and Fresh 1984; Quinn et al. 1991), while others have found a negative correlation (primarily driven by an abundance of young males; Hard and Heard 1999). Increased competition for spawning sites during years of high abundance may cause salmon to seek out alternative spawning sites in nearby streams (Mortensen et al. 2002), which could confound correlations between straying and age. Pollock et al. (2020) showed that length was a primary factor in propensity to stray; bigger fish strayed less and bigger females strayed less than bigger males.

During juvenile outmigration, low hormone levels during smolting phase may cause incomplete imprinting of the natal site (Le Luyer 2017) . It is during this phase that exposure to some chemical agents may also impair successful imprinting of the natal site (Moore et al. 2007; Arkoosh et al. 2011).

Hatchery produced Chinook stray more than those Chinook originating from natural spawners. In a survey of all studies into ocean-type hatchery-Chinook stray rates, Keefer and Caudill (2014) found a mean stray rate of approximately 35% for hatchery origin Chinook. However, many studies of straying in ocean-type Chinook include hatchery populations subjected to experimental releases, transplants, and various rearing treatments that make comparisons across hatchery studies difficult. In addition, straying from the release location to other reaches or tributaries of the same river have often been included in these calculations of stray rate. In this report, a donor stray is defined as spawning in a non-natal river basin. Candy and Beacham (2000) reported stray rates averaging 1.2% for hatchery Chinook reared entirely within their natal spawning system, and reported stray rates two to five times higher for Chinook transplanted during early rearing. As with most studies reporting straying rates, these observations are based on salmon tagged at hatcheries and are likely greater than expected for naturally spawning populations (Keefer and Caudill 2014).

Some hatchery specific factors may lead to increased straying. Dittman and Quinn (1996) and McCormick et al. (2003) documented hatchery released salmon producing lower hormone levels compared to their wild counterparts during rearing; potentially contributing to incomplete imprinting and increased straying.

Labelle et al. (1992), Healey (1991), Keefer and Caudill (2014), and others reported that hatchery-specific rearing strategies (e.g., size, timing, fry/smolt/sub-yearling/yearling) influenced stray rates. Almost all (95%) of the releases reviewed in this report were sub-yearling (Smolt 0+) releases consistent with the ocean-type life-history attributes of the populations being enhanced. Westley et al. (2013) observed patterns of increased straying when ocean-type Chinook populations were released as yearlings rather than sub-yearlings.

Displacement rearing is an additional factor that may increase straying in populations that are satellite-reared at major facilities or reared in out-of-basin small facilities. Juveniles are commonly transported from the rearing facility to their location of release. This is typically done so that individuals from multiple river systems can be supplemented using a single facility. This practice assumes that imprinting from the final few days in freshwater is sufficient for homing to be successful; however Chapman et al. (1997) and Keefer et al. (2008) report that this may interrupt imprinting and increase the propensity to stray.

The use of ground water rather than river water during hatchery rearing has also been hypothesized to affect imprinting (Labelle 1992). This is thought to be a key reason for high stray rates exhibited by production from the Conuma R Hatchery, where the balance between fish health (increased use of ground water) and effective imprinting has been weighted to the former.

Within SBC, and among recoveries that could be assigned a valid rearing strategy, we observed a significant decrease in stray rate with rearing time spent at the hatchery (Fisher exact binomial test, N = 31,028, $p < 0.001$). Later releases strayed less.

We also found that life stage at release influenced straying. Fry strayed at a rate of 9% (n = 1,416), Smolt 0+ individuals strayed at a rate of 6% (n = 29,392), and Smolt 1+ individuals strayed at a rate of 0% (n = 220). Unfortunately, many thermally marked recoveries were not included in this analysis as their release stage was defined as ‘mixed’, meaning that more than one rearing strategy was used for a single thermal mark. This problem was most acute in the WCVI where 76% of the thermal mark recoveries were categorized as having a ‘mixed’ rearing strategy.

CWT-marked recoveries showed significant differences in stray rate with release stage that contrasted with our thermal mark results (Fisher exact binomial test, N = 26,499, $p < 0.001$). Fry releases strayed at a rate of 7% (n = 540), Smolt 0+ releases strayed at a rate of 10% (n = 24,635), and Smolt 1+ releases strayed at a rate of 7% (n = 1,323). Again, sample sizes were biased strongly toward Smolt 0+ recoveries, with 92% of samples being of this release type.

Seapen use during rearing has been correlated with an increased stray rate in SBC Chinook (Candy and Beacham 2000). Thermal mark recoveries did not show a significant difference in stray rates among seapen and non-seapen reared groups, with mean stray rates for both groups averaging 6% (Fisher exact binomial test, N = 31,325, $p = 0.7$). Similarly, CWT data showed no significant difference between seapen and non-seapen releases, with mean stray rates of 11% (n = 2,875) and 10% (n = 23,623), respectively (Fisher exact binomial test, N = 26,498, $p = 0.12$).

Note that the above analysis represents a cursory review of the effect of hatchery rearing strategies on stray rate, and our investigation did not include confounding environmental factors described above. There are few data easily accessible regarding environmental conditions in local rivers to assess straying. Further, uncertainty in the data, including the non-random exclusion of records that had a ‘mixed’ designation for rearing strategy meant that the number of defensible conclusions that could be drawn from the available data were limited. An experimental study design and a detailed investigation of confounding factors precludes our ability to draw conclusions about the effect of rearing strategy on stray rate. A more comprehensive review may be possible, but will be a significant task that was not within the scope of this report.

5. SOURCES OF UNCERTAINTY AND BIAS

While we made every attempt in this analysis to screen data in order to provide accurate estimates of stray rate and contribution to rivers in SBC, several sources of potential bias and uncertainty still exist. These are outlined below.

Low precision and/or bias in data:

Obtaining samples of spawners can be difficult. Many of the rivers used in this analysis are remote. Fall rains bring river flows up quickly, washing out carcasses. Predators can also remove spawners and carcasses. The data used in this analysis, were not collected specifically to assess straying. Most sampling in SBC has been opportunistic. These factors and others often result in low sample sizes. In our analysis, we reviewed samples to eliminate biases where we could and pooled sample types to increase sample sizes. In addition, each sample type (broodstock collection, in-river deadpitch sampling, fence count estimates, and hatchery swim-ins) can have their own potential sources of bias. Sample data in this analysis were screened for obvious or suspected sources of bias based on interviews of hatchery managers, or limited meta-data. Judgment in this process could potentially lead to an inclusion of biased samples. Some potential sources of sampling bias include:

- During broodstock sampling Chinook may be sorted prior to sampling to achieve specific sex ratios, or to manage *PNI* by sorting based on adipose clips. Broodstock can be taken at the hatchery (higher proportion hatchery), in the river (higher proportion natural), or a combination of both. Broodstock sampling could occur at different locations in the river, including near the river mouth where Chinook from other systems could be ‘nosing’ in for a period of time but not migrating up to the spawning grounds.
- Some live sampling was included through angling, catch and release, which could have biases based on angling method or fish behaviour.
- Deadpitch samples in the river can be biased towards females and larger fish. Differences in flow regime can bias river samples.
- Because biological sampling is undertaken to meet numerous objectives at DFO, and these objectives may change over time, some of the trends reported may be caused by methodological, as opposed to hatchery or biological effects.
- Because run-timing of donor populations may differ from the recipient populations they are straying into, sample design tailored to the recipient population may miss returning strays.

Low precision in the underlying spawner data used to expand observed recoveries:

Brown et al. (2019) reviewed spawner escapement data for SBC Chinook and assessed the reliability of the data based on the methods used. These were adapted for the data available in rivers reviewed in this report (see Appendix C). Varying precision and accuracy in these escapement estimates will create uncertainty in catch/sample ratios used to expand the sample of observed recoveries of marks (CWT, otolith, genetic) to the full population.

Incomplete sampling and assessment of rivers in southern BC:

One of the most substantial sources of uncertainty in our estimates of stray rate in SBC, is the magnitude of strays returning to unenhanced, systems across the region. Sampling efforts in SBC are typically based on ecological/fishery importance of the system, accessibility, capacity within DFO or local First Nations or local community groups, location/distance relative to that capacity. For example, along the WCVI Chinook returns have been observed and enumerated in over 60 rivers since 1953. Only ~20 were assessed on a consistent basis within the period used in this report (1998–2021) and consistent annual sampling has been conducted at only about 50% of these, with periodic or opportunistic sampling at the other 50%. This leaves 40 rivers with little, to no assessment or sampling. Based on observations since 1953, and using a p_{average} approach (English et al. 2007) we calculated that the 20 consistently assessed rivers comprised about 90% of the spawning biomass of Chinook along the WCVI. Many of these rivers are a significant distance from hatchery facilities. So it is likely that stray rates reported here are underestimated, likely by less than 10%.

In addition, not all hatcheries have marks used to assess straying. A good example is Thornton Cr Hatchery, near Ucluelet on the WCVI. This hatchery is located on a small creek. Robertson Cr Hatchery Chinook were used as broodstock to found this population, with the objective to support fisheries in this area. The hatchery was successful, with a relatively high survival rate. Early success here resulted in increased production. Over time, the production from this hatchery became somewhat distinct genetically from the Robertson Cr population. Genetic analyses summarized in this report showed that Thornton Cr Hatchery production was a significant component of natural spawners in several rivers around Thornton Cr. A key determinant of these straying events was thought to be a mismatch in production size and available spawning habitat in the creek. Since there was no otolith or CWT marking associated with this hatchery, estimates of stray rate and magnitude were not included. We think this situation is relatively unique, but it does constitute a potential source of bias in local *pHOS* values observed from the production of small, unmarked hatchery production.

Lack of environmental data at appropriate temporal and spatial scales related to hatchery rearing strategies:

Hasler (1971), Dittman and Quinn (1996), Keefer and Caudill (2014) and several other authors since have investigated factors affecting homing and straying. These factors range from global oceanic to local river conditions. Olfactory discrimination of natal water is generally accepted as the primary determinant of homing in the interface between open ocean and river, and this factor has been related to the duration of in-river rearing. Additionally, adult migration can be affected by local river conditions such water temperature, dissolved oxygen levels, flow levels, physical barriers, etc. Additionally, rearing strategies likely affect stray rates. We had limited ability to assess hatchery stray rates in relation to all these factors. Environmental data at the appropriate spatial and temporal scale was generally not available.

Thermal Mark error:

Otolith thermal marks are an internal mark which has proven to be a useful tool for broad assessment of hatchery production and interaction with natural origin Chinook. Thermal marks are applied to the whole of hatchery production or multiple stocks within a hatchery if plumbing infrastructure allows. Potential sources of error in thermal mark data were described by O’Brien et al. (2012). Hatchery specific marks are assigned to a hatchery by the North Pacific Anadromous Fish Commission (NPAFC) using an internationally accepted format. Application of the assigned mark has potential variation due to human error such as opening and closing of valves at specific times, mechanical errors such as problems with chillers changing temperatures by the required amount, or environmental variation if the temperature change is based on two natural water sources. The quality of the thermal banding pattern can result in reading error when adult otoliths are analyzed. These variations are less likely in major hatcheries and more likely in a small community hatchery due to infrastructure costs, maintenance and expertise. There is also potential human error in reading, but this was estimate at less than 1% based on a comparison of thermal mark and CWT results for the same fish. Few hatcheries had multiple thermal marks, which precluded the differentiation of rearing strategies, or assignment of ages from the mark.

CWT error:

Limitations and sources of uncertainty in CWT were outlined in PSC (2008). Both thermal marks and CWTs have uncertainty related to the expansion of samples to the total population. CWTs have an added uncertainty in expansion from the marked component to the total estimated and associated hatchery release (Equations 1–3). CWT mark rates vary based on PSC requirements and production level in the hatchery. At Robertson Cr Hatchery, 600,000 CWT marks represent less than 10% of the total production while at Cowichan R Hatchery the same number of marks represent over 80% of the total production. This equalization of marks between different sizes of hatcheries is beneficial to assessing exploitation rates in fisheries, but creates increased uncertainty (or variability in uncertainty by hatchery) in the use of CWTs when stray rates are low (i.e., rare CWT recoveries) as identified in Keefer and Caudill (2014) and Bett et al. (2017) among others. The comparison of CWT and thermal mark data within the same samples suggest a potential bias (underestimate) using CWT. This will be explored in the next section.

An Investigation into CWT - Thermal Mark Bias:

The analyses in this report facilitated a comparison between thermal mark and CWT estimates of hatchery contribution within specific samples such as natural spawning populations as well as fisheries. Our results suggested that CWT based estimates of hatchery contribution may be biased low. This observation was first observed in the mid-2010s and was reported to the Northern Fund Committee in 2018 (see Appendix F for original note and associated data).

In the Robertson Cr spawner deadpitch sample data, *pHOS* values, estimated from CWT recoveries, were consistently lower compared to the thermal mark data, by an average of near 30% between 1998–2021. Assuming otolith thermal marks, which cover 100% of the releases, represent the true total production from the hatchery, the difference represents an average underestimate (or low bias) by CWT-based estimates.

We can eliminate sampling as a source for this bias. Separate samples (hatchery swim-ins and river spawner sampling via deadpitch) with relatively high sample rates, were collected by DFO crews in the same manner over the period reviewed. Almost all hatchery swim-ins were examined for adipose clips (indicative of a CWT) and 400 were randomly sampled from the same group for thermal marks. In the river, deadpitch sample rates averaged 16% (range 5–33%). These two sampling groups consistently produced the same result; the CWT based estimates of hatchery contribution were less than the thermal mark estimates. In addition, terminal fisheries in Alberni Inlet were sampled, producing similar results: thermal marks consistently produced higher estimates of hatchery contribution when compared to CWT.

Few hatchery facilities have used both CWT and thermal marking, for a significantly long period of time to allow for this type of analysis, along with equal sampling priority for both. These other locations include Chilliwack R Hatchery in the Lower Fraser R and Quinsam Hatchery on the ECVI. In both cases estimates of hatchery contribution to spawning (*pHOS*) derived from CWT recoveries were lower than thermal mark estimates, albeit the magnitude of this difference between hatcheries was not consistent.

The implication of this result is that CWT-based estimates of straying are underestimating stray rate and contribution to the river (*pHOS*). It is not clear at this time what the cause or origin of these differences between otolith based and CWT based estimates is. Some potential sources of bias include:

- Adult sampling, biases in design or implementation: The likelihood of this is low given paired results from independent samples in Robertson Cr Hatchery swim-in and deadpitch samples in the adjacent reaches of the Stamp R.
- Visual detection of external marks (adipose fin clip) as the basis for CWT vs. random sampling for an internal otolith mark: Masuda and Celewycz (2019) found electronic detection increased CWT recovery rates 20–24% over visual detection methods. Sampling of swim-ins at hatcheries switched to electronic detection of CWT about mid-way through the 1998–2021 period used in this analysis;

our results do not show a significant change in the difference between CWT and thermal mark results over this time.

- Increased straying or mortality of Chinook with CWT application, placement of the CWT, or adipose fin clipping: There is limited evidence that CWT application affects straying. One example is Habicht et al. (1998), who found inconsistent annual correlations between CWT location in the snout tissue and straying in Pink Salmon in Alaska.
- Uncertainty in the estimation of releases in both CWT and unmarked Chinook propagated through to catch/sample expansions.
- Significant production not associated with CWT, being included in regular CWT expansions.
- Shedding of the CWT.

While we do not currently know what the cause of this observed bias may be, we may be able to address it with the implementation of parentage-based tags (PBT). PBT provides a third, independent sample type to compare to CWT and thermal mark results providing a significant opportunity to examine this bias further in the broader context of SBC hatcheries.

6. SUMMARY AND DISCUSSION

Straying of salmon into non-natal river basins is a natural occurrence, where the rate and magnitude of straying have been important drivers of genetic diversity and stock structure in Chinook Salmon along the west coast of North America. The natural stray rate of a donor salmon population is likely variable and dependent on numerous environmental factors, while the magnitude of strays depends on the abundance of the donor population. The purpose of this report was to assess the rate and magnitude of straying from hatchery-origin Chinook into non-natal river basins in Southern British Columbia, as well as their effect on natural spawning in recipient rivers.

Hatchery-origin salmon are generally more abundant than natural populations due to a reduction in freshwater mortality associated with spawning, incubation, and rearing in the river environment. This has provided significant fishery benefits and has increased the overall returns to rivers. But, as summarized in HSRG (2017, 2020), hatchery produced salmon are less well adapted to the natural environment, which lowers their reproductive fitness. In SBC, Brown et al. (2019) provided specific examples such as declining age-at-maturity and size-at-age in returning hatchery-origin salmon.

An improved understanding of straying in hatchery-origin salmon to non-natal spawning populations has been well documented in the Pacific Northwest: Ricker (1972), Quinn (1984), Dittman and Quinn (1996), Keefer et al. (2005), Westley et al. (2013), Keefer and Caudill (2014), Ford et al. (2015), Pearsons and O'Connor (2020), Pearsons and Miller (2023). In BC, there have been fewer studies, including Labelle (1992) on Coho Salmon and Candy and Beacham (2000) on Chinook Salmon.

In this study, we use samples collected over a period of 24 years between 1998–2021 from 49 recipient rivers in SBC. Many of these samples were associated with broodstock collection efforts, while others were associated with monitoring/sampling programs in rivers where government, First Nations, or local stewardship groups were within a few hours travel from hatchery facilities, staff offices, or population centers. As a result, remote locations were poorly represented in the samples; potentially resulting in an underestimation of donor stray rates. We suggest this potential bias was minor (< 10%) since most rivers with significant Chinook escapements were sampled.

The majority of samples were of ocean-type Chinook, which generally migrate to the ocean within a few weeks to months after hatching. Westley et al. (2013) used CWT recoveries to show that ocean-type Chinook consistently stray more than stream-type Chinook, reflecting the amount of time spent in freshwater and the resultant imprinting.

Our assessment of hatchery-origin Chinook straying into non-natal rivers was based on otolith thermal mark samples and/or CWT recoveries to delineate the origin of spawners as either first generation hatchery or naturally produced. The implementation of otolith thermal marking and subsequent sampling was most extensive along the WCVI, less so on the ECVI and in the Lower Fraser, and did not occur in the Upper Fraser. The available CWT data originated mainly from Pacific Salmon Commission CWT indicator stocks, with periodic CWT application in other systems. There was no mass marked (adipose fin clip) production from BC hatcheries during the period of this study. It should be noted that the CWT-based estimates of hatchery contributions in this study were consistently lower compared to estimates based on thermal marks; on the WCVI, CWT estimates of hatchery contribution averaged 30% lower over the period. We could not find conclusive evidence implicating a source of this bias and recommend that this topic be further investigated using emerging results from PBT application in SBC hatcheries.

We first compiled strays from 'donor' hatchery stocks recovered in non-natal river basins. Based on otolith samples collected from 12 thermally marked donor hatchery stocks and 49 sampled rivers in SBC, we estimated a mean annual stray rate of 4.2% (range 0–17%). This estimate was lower, 2%, based on CWT recoveries. Donor stray rate was highest on the WCVI, with an average annual donor stray rate of 6.4% based on otolith thermal marks. Note that these are conservative estimates based only on escapement estimates rather than the total return to the river. Donor stray rates are expected to be lower if terminal fishery catch is used in calculations. This difference would be most pronounced in the case of Robertson Cr Hatchery which has terminal area fishery two to three times larger than the escapement.

The donor stray rate on the ECVI was 2.6% based on CWT data and < 1% in the Fraser River. Note that strays were most often recovered in non-natal systems close in proximity to the donor river.

The mean annual donor stray rate to non-natal CUs was estimated at approximately 1.5% across the sampled populations, including 3 outliers with greater than 7% straying to other CUs. These outliers include the exchange between Stamp R (Robertson Cr Hatchery) and Gold R (approximately 134 km away), which has been theorized as an artifact of similar pulp mills affecting olfactory signals in each system. On the ECVI, CWT data suggests a high stray rate for Cowichan R, hatchery-origin Chinook; theorized to be due to high copper levels in the hatchery's well water. The third system with a high outside-CU stray rate was Capilano R hatchery-origin Chinook; which are a transplant from Chilliwack R/Harrison R stock. Excluding these 3 outliers, the majority of donor hatchery stocks exhibited mean annual stray rates to non-natal CUs of < 1%.

Donor hatchery stray rates between major SMUs and geographic units such as WCVI, ECVI, and Fraser River were negligible.

There was also considerable variation in donor stray rates between hatcheries and within a hatchery between years. We could not statistically delineate any influence of hatchery practices, on stray rate from potential environmental factors. Local knowledge often provided logical reasons for understanding specific observations of straying, such as low dissolved oxygen levels in upper portions of inlets close to natal rivers, in-river migration barriers such as low flows or high water temperatures, high fish density in hatchery systems, and poor imprinting due to hatchery reliance on well water, among others. A photo of Tahsis R in Nootka Sound from September 2014 (Figure 4.9) exhibiting no flow to the system was one of the more obvious explanations for increased straying to Nootka Sound in that year.

Conuma R Hatchery in Nootka Sound had the highest donor stray rate among major hatchery facilities. Upon receipt of this information, Conuma R hatchery practices were reviewed, which identified potential causal factors, including lack of river water during incubation, hatchery rearing and then trucking the smolts to net pens located far outside the influence of the Conuma River; both likely resulting in poor imprinting. Action was taken by hatchery staff, including moving the net pens to an area with greater freshwater influence and some use of river water during later stages of hatchery rearing. In addition, Conuma R Hatchery became the first in BC to begin mass marking Chinook releases for the subsequent management of both broodstock and natural spawners. This is an example of monitoring for risk, and a hatchery rapidly adapting practices to improve and manage genetic outcomes related to straying.

Even low stray rates can result in a significant magnitude of fish interbreeding with non-natal ‘recipient’ populations which can lead to decreased fitness and increased homogenization of spawning populations. As Pearsons and O’Connor (2020) indicate, this is particularly true when

1. the donor populations are large,
2. donor straying is frequent, and
3. the recipient population is small.

Withler et al. (2018), extending works by Ford (2002) and others, showed that one-way gene flow, even at low levels of immigration can result in significant changes in genetic composition and potential impacts on fitness. Their modelling showed that low levels of out-of-basin hatchery straying into wild populations can have strong effects on *PNI*, and that to maintain a *PNI* > 0.50, $pHOS_{\text{census}}$ had to be less than 0.02–0.03. They categorized these populations as ‘wild-stray influenced’. We used this benchmark for categorizing both wild and hatchery enhanced populations, recognizing that this likely underestimated the influence of out-of-basin hatchery strays on *PNI* in populations where local hatchery spawners were also present. To report the level of hatchery origin Chinook strays spawning naturally in ‘recipient’ populations we delineated $pHOS_{\text{census}}$ (HSRG 2009, 2014, 2017) into $pHOS_{\text{local}}$ plus $pHOS_{\text{stray}}$ (i.e., the proportion non-natal hatchery origin strays in a recipient population of natural spawners). In this work, $pHOS_{\text{stray}}$ was used as the key metric to estimate the effects of out-of-basin strays on recipient populations.

The highest $pHOS_{\text{stray}}$ levels were found in rivers on the WCVI, consistent with the frequent high donor stray rates in this region, combined with significant hatchery production. This was especially evident in the area from Kyuquot Sound down through Nootka Sound into Clayoquot Sound. In Kyuquot Sound, which is managed as a ‘wild’ refugia with no active hatchery enhancement, 4/4 river systems sampled had an average $pHOS_{\text{stray}}$ > 0.18. In Nootka Sound, an area managed to harvest surplus production to the Conuma R Hatchery, $pHOS_{\text{stray}}$ was 0.37. In Clayoquot Sound, also managed as a ‘wild’ refugia, the average $pHOS_{\text{stray}}$ was 0.20 across five rivers sampled for thermal marks. In all these areas, most strays originated from Conuma R Hatchery, suggesting a significant influence of strays within about 60 km. $pHOS_{\text{stray}}$ in Clayoquot was certainly underestimated as Thornton Creek Hatchery strays were not represented by otolith thermal marking yet were identified as a significant component in the genetics of these populations.

In other sampled areas of SBC, $pHOS_{\text{stray}}$ was considerably lower. In natural spawning populations from Barkley Sd to San Juan R, the average $pHOS_{\text{stray}}$ was 0.03, declining to an average $pHOS_{\text{stray}}$ of 0.02 in the Georgia Basin (ECVI), and even lower in the Fraser R.

In 2013 to 2015 genetic samples were taken from river spawners along the WCVI to assess the genetic make-up of these populations and how it changed over time. This analysis indicated that the genetic variation within each of the three major WCVI hatchery populations had remained relatively consistent since the late 1980s to 2015 (last year of analysis). The same could not be said for most other populations on the WCVI. The three major hatchery populations contributed to the majority of genetic introgression into surrounding populations on the WCVI. For example, Conuma R and Burman R Chinook became much more genetically similar over the period 1986–2015 (7–8 generations). In another key example, straying of Thornton Cr Hatchery production, which was originally transplanted from Robertson Cr Hatchery, distributed those genetics throughout Barkley and Southern Clayoquot Sounds. This analysis showed that a significant magnitude of out-of-basin hatchery straying into surrounding natural spawning populations reduced genetic variation among WCVI populations of ocean type Chinook; resulting in increased homogenization. However, the analysis also revealed that local population genetics are still visible in many rivers.

Similar genetic change due to out-of-basin hatchery introgression was also identified in stream-type Chinook populations in the Columbia River system. Hess and Matala (2014) showed significant change within 5–6 generations in the John Day River sub-basin. Ford et al. (2015) showed reduced among-population regional diversity within the Wenatchee River sub-basin.

In the same way that within-population genetic variation is a key determinant of population resilience, among-population genetic variation is a key determinant of species resilience. This is known as the portfolio effect (Schindler et al. 2010) in which diverse populations contribute to species-level resilience as sensitivities to novel stressors are likely to vary among populations (i.e., not all populations will be susceptible to new conditions). It is challenging to predict the ultimate risk of hatchery straying maintaining or increasing genetic homogenization; the level of risk likely varies according to hatchery practices, species life history and trends, natural diversity, and environmental stressors (Anderson et al. 2020). It is important that agencies monitor and understand these risk factors and hatcheries adapt accordingly. Moreover, as described in the HSRG (2017, 2020) white papers, adaptation requires documentation, review, and lessons learned from case studies. These scientists, along with Withler et al. (2018) all espouse the need for setting clear genetic (*PNI*) objectives for each population in combination with abundance objectives for rebuilding/recovery, harvest, and food security.

Following on this advice, we include in Section 7 a river by river review of available knowledge, meant to be a starting point for monitoring, reporting, learning, adapting, and planning. This applies to major hatchery facilities as well as smaller production hatcheries. An example is the production at Thornton Cr Hatchery near Ucluelet on the WCVI. Thornton Cr Hatchery did not have the capability or funding to mark its production. When returns exceeded available habitat capacity, this small scale hatchery became an unknowing and significant source of introgression into nearby spawning populations in southern Clayoquot Sound and northern Barkley Sound.

Another case study of this can be found in the Huu-ay-aht First Nation management of Chinook Salmon in the Sarita R, which includes mass marking of local hatchery production and mark selective removal of visibly marked hatchery returns. The mark selective fishery has been successful in reducing $pHOS_{\text{local}}$ in the system, with the unintended result that unmarked hatchery strays from other WCVI hatcheries will have increased genetic influence.

The work by Withler et al. (2018), HSRG (2017, 2020), and Anderson et al. (2020) provide principles and a framework with which we can improve the genetic diversity within and among salmon populations. This report focuses on a small component of their advice, namely the degree to which hatchery straying can impact the principles and objectives they espouse. In this light, we reiterate the framework originally laid out in Withler et al. (2018), and provide the following advice as it pertains to each of their described principles:

1. Develop clear biological goals for hatchery-influenced populations through an integrated planning process which is transparent in trade-offs.
   - Reiterate the need to define and actively manage toward genetic goals (*PNI*, $pHOS$, $pNOB$) and to consider hatchery straying at the river basin/population/conservation unit and stock management unit level.
   - Promote healthy habitats and self-sustaining naturally-spawning populations to mitigate the risks that hatchery straying poses to the fitness of wild Chinook Salmon.
2. Design and operate hatchery programs in a scientifically defensible manner.
   - Use $pHOS_{stray}$ and *PNI* in tandem as metrics for enhanced contribution management in instances where $pHOS_{local}$ and $pHOS_{stray}$ are both >0.
   - Increase emphasis on known hatchery rearing practices that reduce stray rate (e.g., imprinting with natal water sources).
   - Quantitatively assess hatchery management practices and environmental factors to inform best practices and management decisions to reduce straying, ideally with the use of controlled experiments.
3. Monitor, evaluate and adaptively manage hatchery programs.
   - Include monitoring of $pHOS_{stray}$ into hatchery management and stock assessment programs.

- Initiate additional, strategically planned, in-river stray monitoring programs and extend the evaluation of hatchery straying beyond southern BC to Chinook populations across the Pacific Region.
- Use visual marking to monitor and actively manage $pNOB$ and $pHOS$ (including both local and stray Chinook).
- Use an internal tag (e.g., otolith thermal mark, PBT, or CWT) to refine estimates of $pHOS_{stray}$, $pHOS_{local}$ and donor stray rates. Southern BC Chinook hatchery broodstocks are widely genotyped and thus PBT is recommended as the preferred tagging method.
- Improve data quality, integration, and accessibility; including a targeted effort towards integrating environmental data when evaluating hatchery straying.

7. HATCHERY AND STOCK-SPECIFIC TRENDS BY GEOGRAPHIC REGION

We found trends in hatchery straying across SBC to be variable, with regional trends evident across spatial and temporal scales. Relationships between individual donor and recipient rivers were observed that warrant further investigation. However, prior to this work, a detailed summary of stray rate and the contribution of strays to rivers across SBC did not exist. Here, we aim to summarize observations made in individual rivers, and across regions, to allow groups to assess the potential impacts of straying on a local scale. We hope that by describing past trends, we can provide context to ongoing monitoring and assessment efforts for hatchery straying across SBC, and identify gaps to be addressed with future work.

Estimates of straying provided in this document are determined from sampling programs with known biases and uncertainties. Further, limited sampling in remote areas means that our ability to determine impacts of hatchery introgression for all regions is limited. We understand that our estimates represent a snapshot of the overall picture. We anticipate that our estimates will be used in conjunction with local knowledge to identify appropriate management actions required to reduce the genetic impacts associated with straying.

In the following section, we present a summary of stray rate and magnitude from donor rivers based on CWT and thermal mark recoveries. We then describe the contribution of both local and strayed hatchery Chinook to recipient rivers, when available. We report averages based on years in which systematic sampling of the home river was performed (based on sample size requirements outlined in Section 3). Rivers in which sporadic sampling was performed, and strays were observed, are described as stray events, but were not included in calculated averages of stray rate, contribution or natural influence ($pHOS$, $pHOS_{stray}$, PNI, and PNI_{local}). Presently, this section includes only those rivers where CWT and thermal mark recoveries were observed. It does not include WCVI hatcheries that do not mark releases (e.g., Thornton Cr).

We hope that this section will serve as a living profile of these systems and will be expanded going forward as monitoring of hatchery straying continues in these systems.

7.1. STOCK MANAGEMENT UNIT: WCVI CHINOOK SALMON

7.1.1. Conservation Unit: CK-33 – West Vancouver Island-North

In CK-33 (West Vancouver Island-North), Chinook Salmon occur mostly within Quatsino Sound, with the largest returns to Marble R, and minor runs occurring in Colonial R, and Cayeghle Cr, among others (Figure 7.1). No large-scale hatchery enhancement occurs in this CU, and escapement sampling is limited. In CK-33, 17 rivers have had at least one observation of Chinook since 1953, and three were sampled between 1998–2021, representing an estimated 78% of total average escapement to the CU, based on NuSEDS records. Only Marble R was consistently sampled during this time. $pHOS_{stray}$ and $pHOS_{stray.OCU}$ for this river averaged < 0.01, based on thermal mark recoveries. PNI values for this population, when available, were > 0.80, indicative of an integrated-wild population.

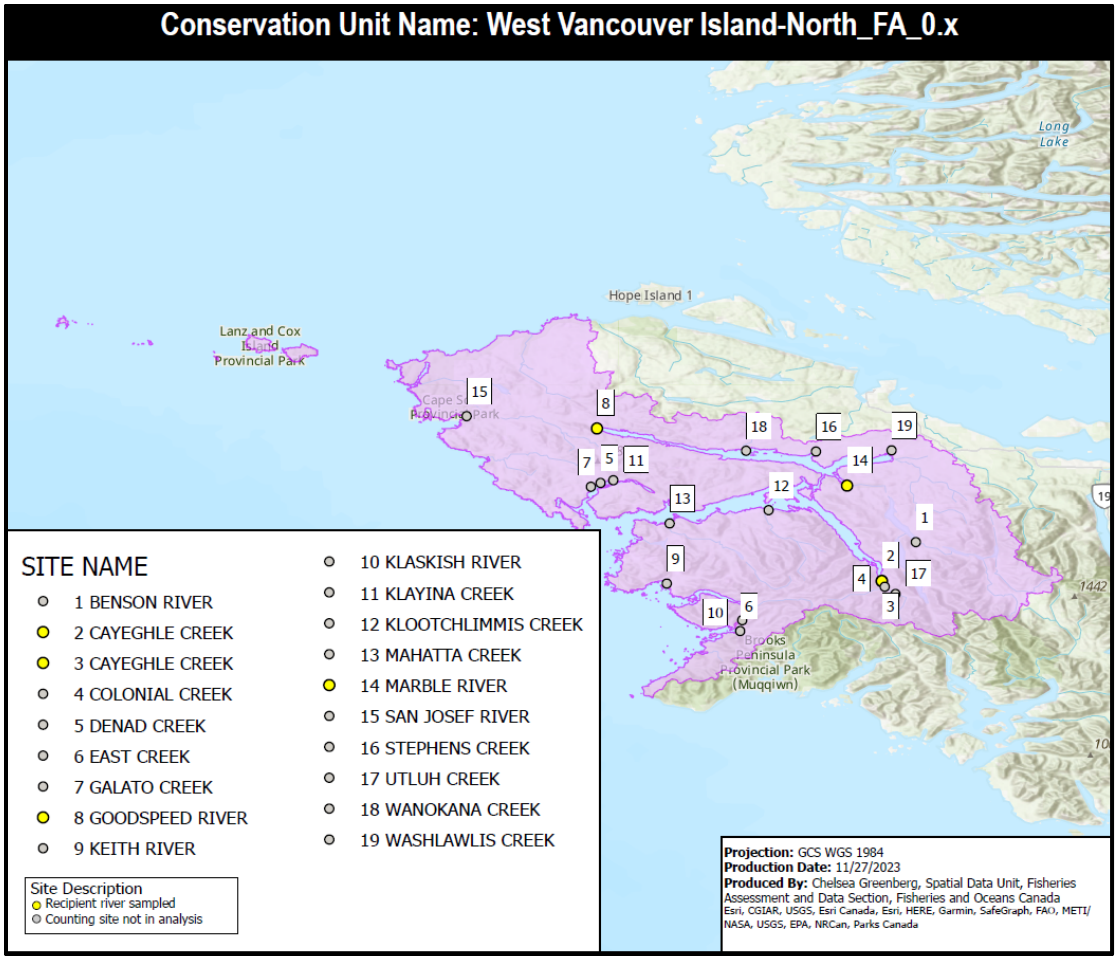

Figure 7.11. Boundary map of the CK-33 Conservation Unit (West Vancouver Island-North) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

Marble R – Recipient River

The Marble R has been supplemented by the Quatse (Marble River) community hatchery since 1983, primarily enhancing Coho, Chum, and Pink Salmon. Chinook were regularly sampled in the Marble R, between 2005 and 2019, and in all years except 2015, were estimated from broodstock removals. Only two strayed Chinook were observed in thermal mark samples, both in 2016, originating from Conuma R and Robertson Cr hatchery stocks respectively, ($pHOS_{stray} < 0.01$; Table E1). While CWT marking occurred at Marble R hatchery up until 2008, only nine CWT recoveries are recorded in the EPAD database since 1998, all as homed, Marble R hatchery Chinook.

pHOS values averaged 0.07 for this system and were consistently low, as the majority of returning Chinook each year were of natural-origin (Figure 7.2). Out-of-system strays were negligible and *PNI* values were greater than 0.80 in all years, indicating an integrated-wild hatchery system.

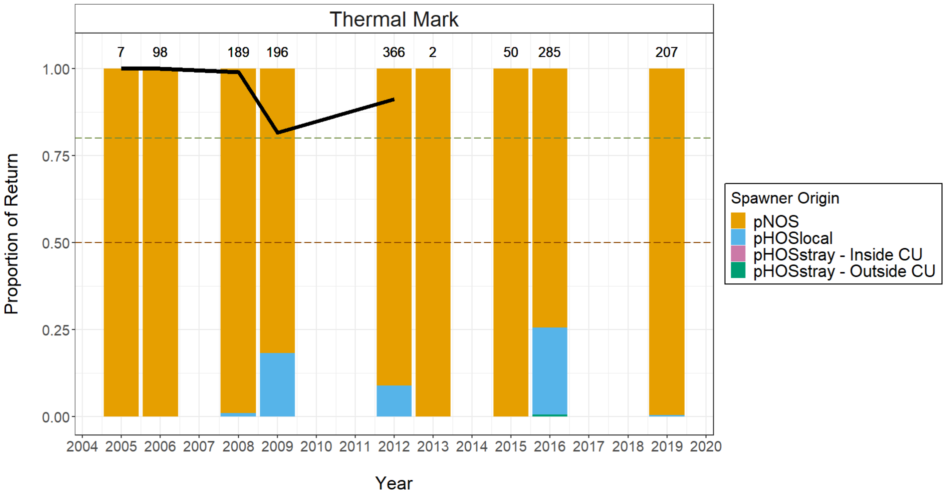

Figure 7.12. Origin of spawners returning to Marble R between 2004 and 2020 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Cayeghle System, Colonial Creek and Goodspeed R – Recipient Rivers

Sporadic recoveries in Quatsino Sd from the Cayeghle System and Colonial Cr revealed one hatchery stray in 2016 from Conuma R. Goodspeed R was sampled in 2004 for thermal marks, and no stray recoveries were observed. Although sampling is limited in Quatsino Sd, these recoveries do not indicate that hatchery strays are placing significant pressure on the genetic integrity of these stocks.

7.1.2. Conservation Unit: CK-32 – West Vancouver Island-Nootka & Kyuquot

In CK-32 (West Vancouver Island-Nootka and Kyuquot), Chinook occur in two distinct Sounds: Kyuquot Sound and Nootka Sound (Figure 7.3). The CU contains one large production facility, Conuma River Hatchery, that releases approximately 2.7 million Chinook annually. Of 36 river basins where Chinook were regularly observed since 1953, 12 were sampled between 1998–2021, accounting for an estimated 88% of total escapement to the CU. All enhanced stocks were identified with thermal marks and Conuma R was marked with CWTs until the 2002 brood year. Average $pHOS_{stray}$ for all rivers in CK-32 was 0.40, and average $pHOS_{stray,OCU}$ was 0.07 based on thermal mark recoveries. Average *PNI* values were calculable for eight stocks in this CU, all of which indicated integrated-hatchery populations (*PNI* < 0.5).

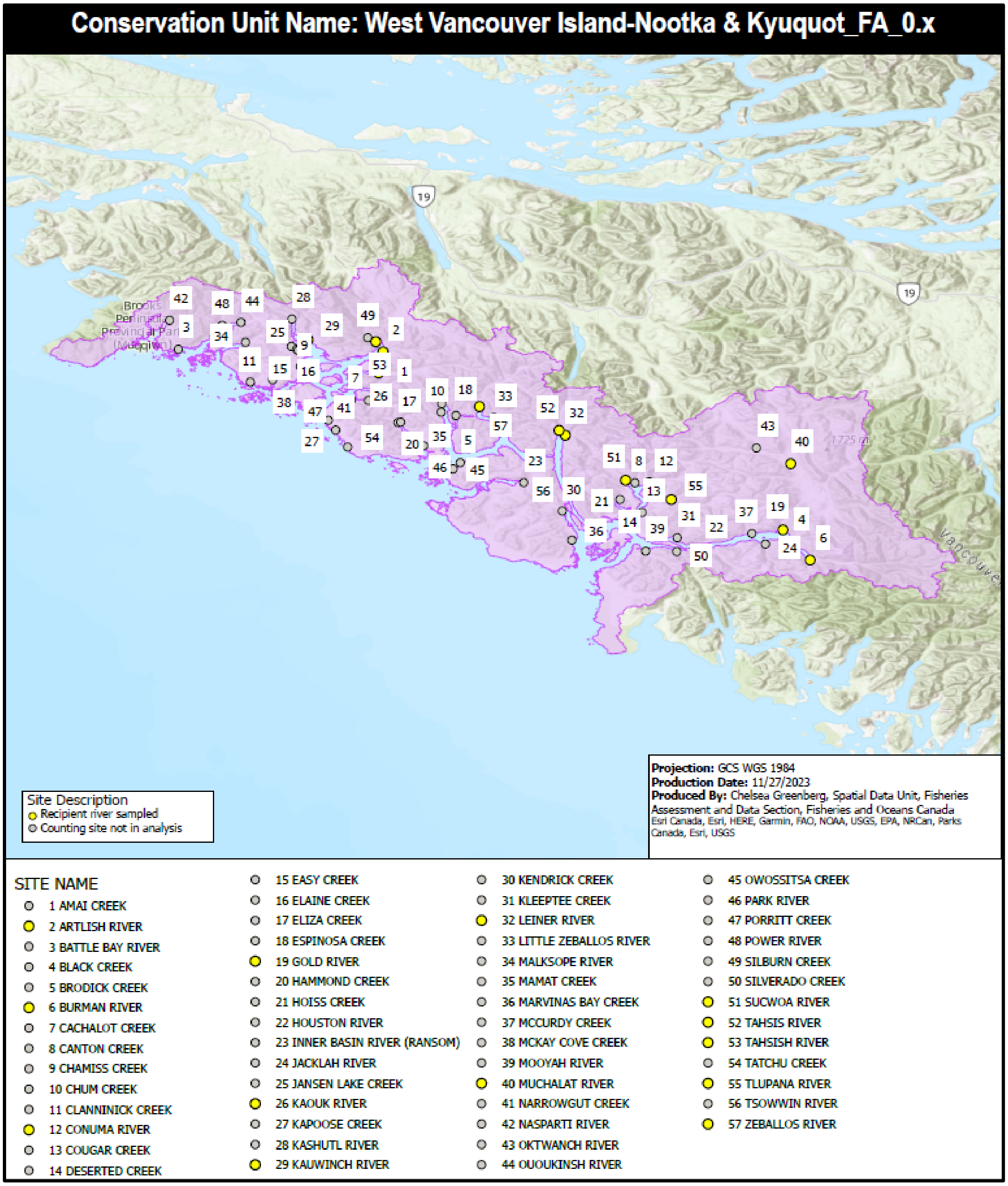

Figure 7.13. Boundary map of the CK-32 Conservation Unit (West Vancouver Island-Nootka & Kyuquot) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

7.1.2.1. Kyuquot Sound

Kyuquot Sound, located in the Northern end of the CU, is comprised of four river basins that contribute the majority of Chinook returns: Tahsish R, Kaouk R, Artlish R, and Kauwinch R. As there are currently no enhancement projects or hatcheries in the area, *pHOS* and $pHOS_{\text{stray}}$ values were equivalent, and

PNI was not estimated. Sampling was largely sporadic, but has increased in frequency since 2014. Currently, the level of uncertainty in our estimates is high for this region.

Most strays to Kyuquot Sd originated from the Conuma R hatchery stock. Strays from this system were observed in most years since 2014. Genetic results presented above, support the trend of Conuma R introgression into these systems. However, a lack of consistent sampling in these remote systems means the potential impact of these strays across the region is not yet fully understood. Regular, systematic sampling of Kyuquot Sd rivers is recommended to more precisely quantify the magnitude of straying here.

Tahsish R – Recipient River

Tahsish R had the most abundant returns to the Sound, with an average escapement of 648 individuals since 1998. Average *pHOS*/*pHOS*$_{\text{stray}}$ values were 0.40 and ranged from 0.00 in 2014 (where only eight samples were taken) to 0.71 in 2017 (Figure 7.4). Systematic sampling occurred in the Tahsish R between 2015 and 2017. The majority of stray recoveries in this period originated from Conuma R. Occasional strays from other populations within Nootka Sd, reared at Conuma R Hatchery – Burman R and Leiner R – were observed from 2015–2017, but represented a small proportion of total escapement (Table E2).

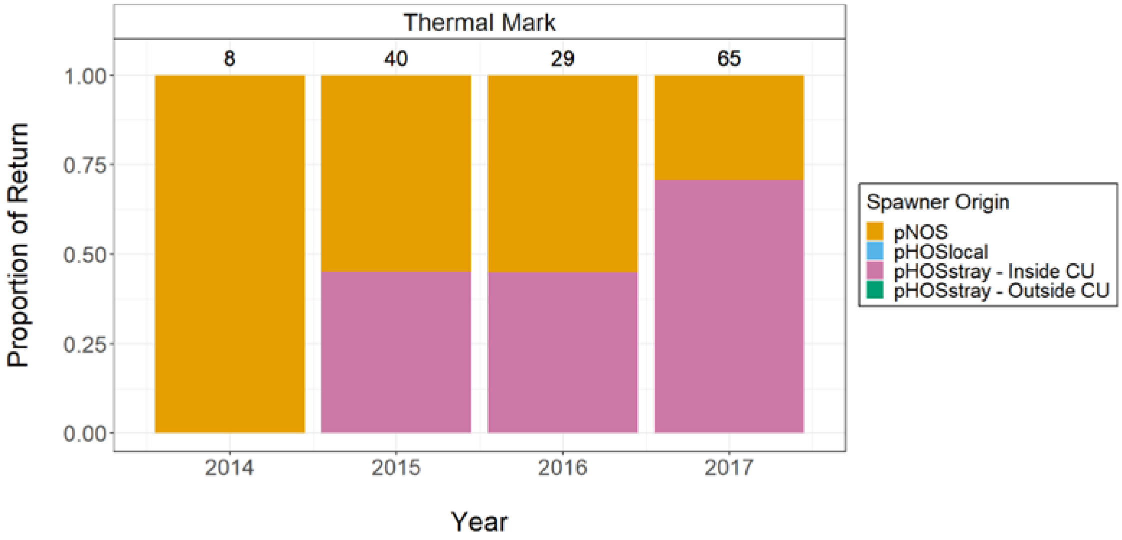

Figure 7.14. Origin of spawners returning to Tahsish R between 2014 and 2017 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners (pHOS$_{local}$), strayed hatchery-origin spawners originating from inside the CU (pHOS$_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU (pHOS$_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. As this stock is not enhanced, no PNI estimates were calculated.

Kaouk R – Recipient River

Kaouk R was sporadically sampled between 2009 and 2017, however, a sufficient sample size for analysis was only obtained in 2015, when 28 fish were sampled (Figure 7.5). In this year, one Burman fish was observed. Sporadic recoveries in Kaouk R suggest that strays from Conuma R, Robertson Cr and Sarita R have also contributed to the escapement in this system historically (Table E3), but without sufficient and consistent sampling in the river, it is difficult to determine stock-specific trends in straying.

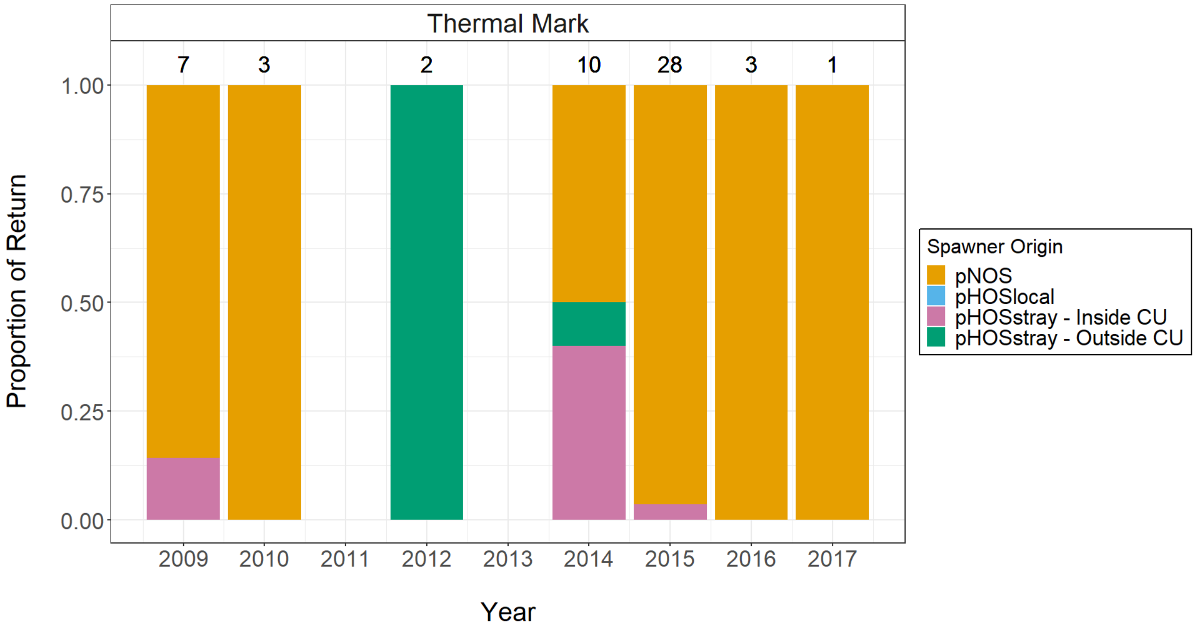

Figure 7.15. Origin of spawners returning to Kauok R between 2009 and 2017 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. As this stock is not enhanced, no PNI estimates were calculated.

Artlish R – Recipient River

In 2015, 36 Chinook were sampled in the Artlish R, the only year in which a sufficient sample size was only obtained. In this year, 47% of recoveries had correctly homed, 50% were of Conuma R-origin, and 3% were of Robertson C-origin (Figure 7.6; Table E4). Sporadic sampling in 2016 suggested that Conuma R strays contributed to the escapement in this year as well.

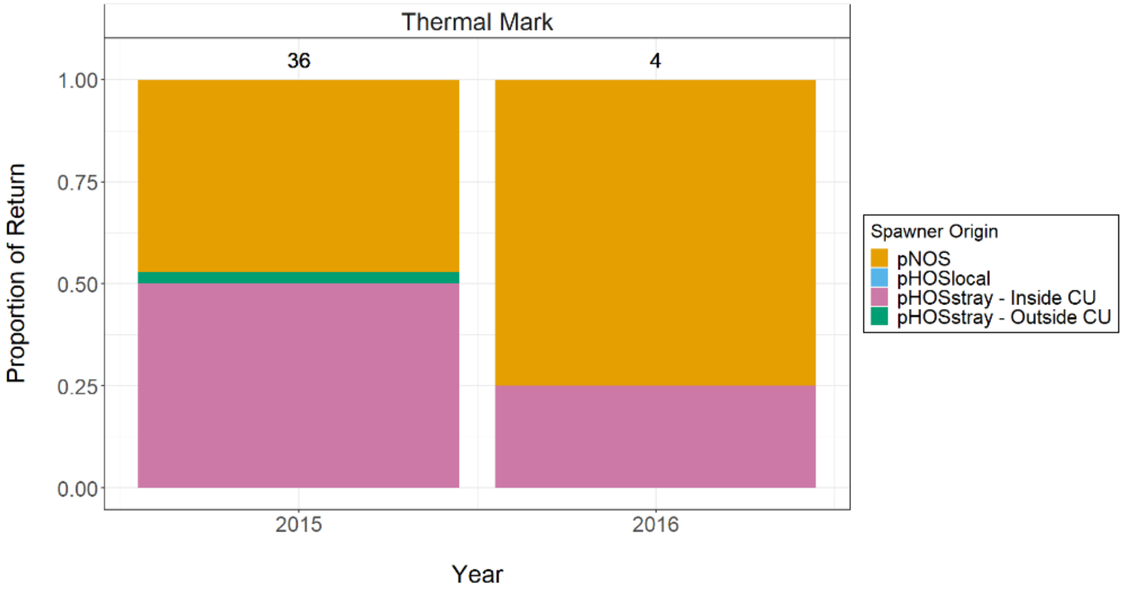

Figure 7.16. Origin of spawners returning to Artlish R between 2015 and 2016 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. As this stock is not enhanced, no PNI estimates were calculated.

Kauwinch R – Recipient River

Kauwinch R was sporadically sampled in 2015, with three of five samples analyzed of Conuma R origin (Table E5). These sporadic observations support the hypothesis of widespread straying from Conuma R into Kyuquot Sd in recent years.

7.1.2.2. Nootka Sound

In Nootka Sound, Chinook escapement is largely dominated by hatchery production from Conuma R. Escapement to Nootka Sd since 1953, excluding the hatchery component, has averaged an estimated 5,164 individuals per year. Escapement including Conuma R hatchery Chinook has averaged 30,565 fish since 1990 when significant returns of hatchery-reared Chinook were first observed. There are eight rivers in Nootka Sound monitored regularly for escapement, and all have, at some point, historically been enhanced by Conuma R hatchery: Conuma R, Burman R, Gold R, Leiner R, Tahsis R, Sucwoa R, Tlupana R, and Zeballos R.

Conuma R Hatchery – Conuma R donor stock

Conuma River Hatchery is midway up the WCVI, in Nootka Sound (Figure 7.3). It is one of SEP's 12 'major OPS facilities' with production of ocean-type Chinook and Chum Salmon, currently enhancing Chinook in the Conuma, Burman, and Gold rivers.

CWTs were applied to a portion of Conuma R hatchery releases from the early 1980s to 2002, with recoveries observed until 2007 in systems around SBC (Table D1). Stray CWT recoveries for Conuma R Chinook between 1998–2007 were only observed in two years: in 1999, when an expanded 15 recoveries were observed straying into the Puntledge R, and in 2004, when an expanded three recoveries were observed straying into Sarita R. Stray rates were nearly 0% in all years sampled between 1998–2007 (Table D1).

Thermal marking was conducted at Conuma River hatchery since 1996. Over the period 1998–2021 the average donor stray rate from Conuma R Hatchery was approximately 3.7% (Table D2). Mean stray rate was generally low between 1998–2014 at 2.4%, however since 2014, stray rates have been considerably higher, with an average of 6.4% between 2014–2021, and a high of 13.8% in 2018 (Figure 7.7). Donor strays were most often observed in rivers within the same CU (i.e., Nootka and Kyuquot sounds).

The average stray rate from Conuma R for Chinook recovered outside of the CU was < 1%.

Recent high stray rates are presumed to be related to:

1. the use of well water during rearing which may reduce imprinting;
2. transfer of hatchery smolts directly into seapens 2 km outside the river mouth to improve overall survival;
3. changing the course of the river mouth, reducing freshwater influence at the site of the seapens; and
4. increased frequency of drought conditions and high water temperatures during return migration in recent years resulting in fish 'nosing in' or straying into surrounding rivers.

The magnitude of strays originating from Conuma R Hatchery, estimated using thermal marks, was also the highest among SBC facilities, averaging 839 individuals per year between 1998 and 2021 (Table D2). Stray rates and magnitude for Conuma River Chinook have increased considerably since 2013 (Figure 7.7), with a high of 3,790 estimated strays into non-natal river basins in 2015. During this time, the distance of straying has also increased with significant numbers (relative to recipient stock) straying into rivers in Kyuquot Sd (located within the same CU; Figure 7.3) and Clayoquot Sd (different CU). The genetic composition of Chinook populations along the WCVI presented in Section 4, indicated that the Conuma River stock had a significant influence on many central WCVI rivers from Kyuquot to Clayoquot Sound.

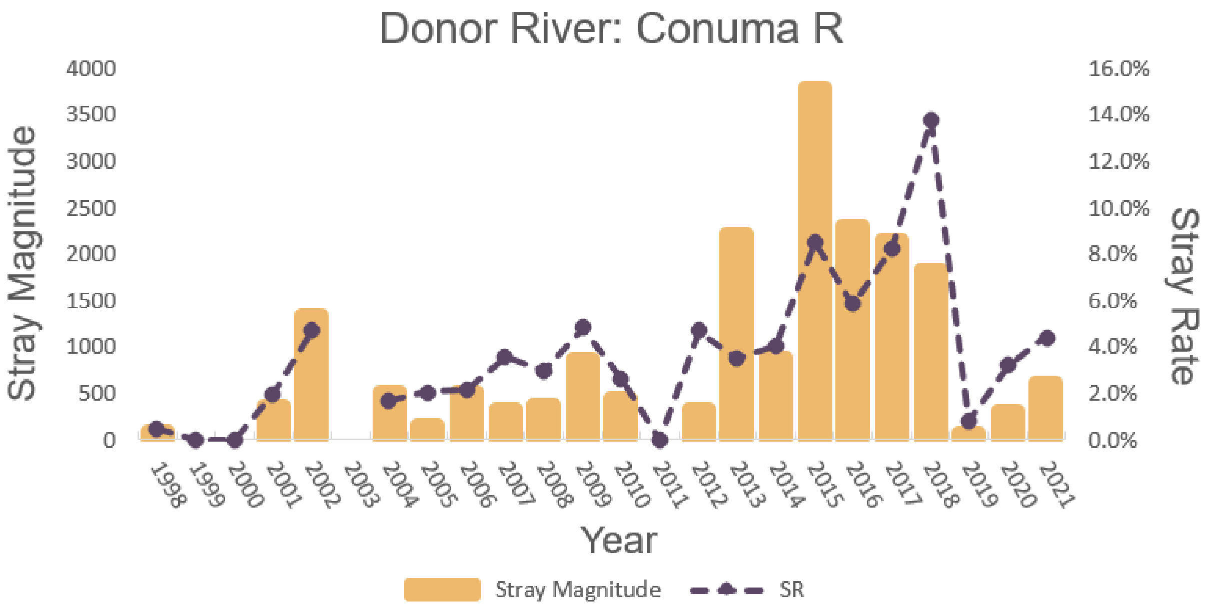

Figure 7.17. Temporal trends in stray rate and magnitude from Conuma R Hatchery Chinook calculated from thermal mark recoveries in systems sampled across SBC.

Conuma R – Recipient River

The largest number of Chinook returning to Nootka Sd originate from and return to Conuma R hatchery. As a large production facility, it is assumed that the majority of returns will be of hatchery origin. *pNOS* values in this system consistently approached or 0.00 between 1998–2021 (Table E6). Much like other river systems in Nootka Sd, Conuma R received strays from other stocks that originated in the Sound, and were reared at Conuma R Hatchery. However *$pHOS_{stray}$* in this system averaged only 0.01

(Table E6). Sporadic recoveries from Burman R, Gold R, Sucwoa R, and Tlupana R were all observed between 1998–2021. $pHOS_{\text{stray,OCU}}$ was > 1% of total escapement and was comprised mainly of Robertson Cr strays. *PNI* was predictably low in all years, with an average of 0.02 since 1998.

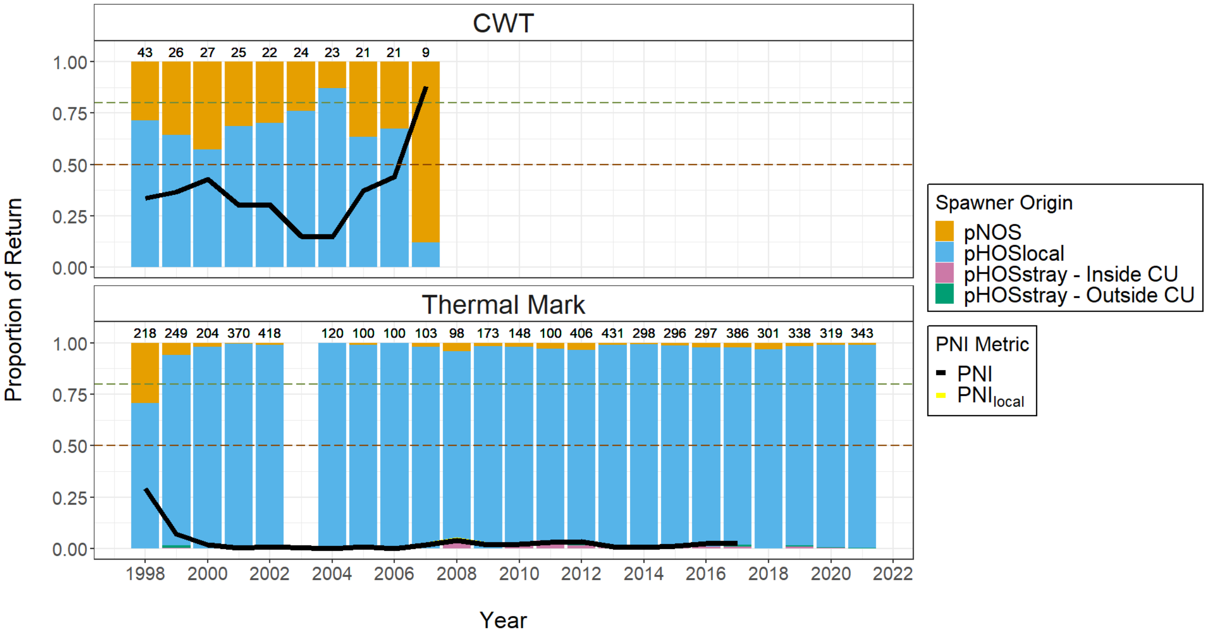

Figure 7.18. Origin of spawners returning to Conuma R between 1998 and 2021 estimated from CWT and thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs or otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Conuma R Hatchery – Burman R donor stock

Burman R Chinook have been enhanced since the 1980s, first by a community run (CIP) hatchery on the Gold River until 2005, and presently through the Conuma River hatchery. The Burman River stock was only thermally marked during this time.

Thermal mark recoveries of Burman R Chinook revealed an average donor stray rate of 4.3% between 2006–2021. Burman strays were regularly observed in samples taken from non-natal rivers in Nootka Sd and to a lesser extent Kyuquot Sd (i.e., straying within the Conservation Unit of origin).

There were two observations of Burman River Chinook straying outside their CU of origin; in 2009 a single stray was observed in the Cowichan R, and in 2015 a stray was observed in the Stamp River, adjacent to the Robertson Creek Hatchery.

Stray rates from the Burman R stock oscillated between high and low values annually (Figure 7.9). The largest observed magnitude of straying was in 2011 when an expanded 698 Chinook (26% of Burman R observations that year) strayed into the Conuma River, the hatchery system in which they were incubated and initially reared. However, in the Conuma River this represented a small proportion of total spawners ($pHOS_{stray}$= 0.03).

While this would be problematic in a small, unenhanced system, straying of this magnitude into a large production facility to reproduce among other individuals close in genetic signature to Burman R stock poses much less of a threat to the local population.

Straying magnitude from Burman R was relatively low, with an annual average of 99 individuals observed in non-natal rivers (Table D3). However, this average was biased high from a few outlying years where a small number of Burman R recoveries returning to Conuma R were expanded from a small sample to represent a large number of fish. While few fish tend to stray from the Burman R stock, it should be noted that since 2015, when regular, annual sampling of Kyuquot Sound began, Burman R Chinook were regularly observed.

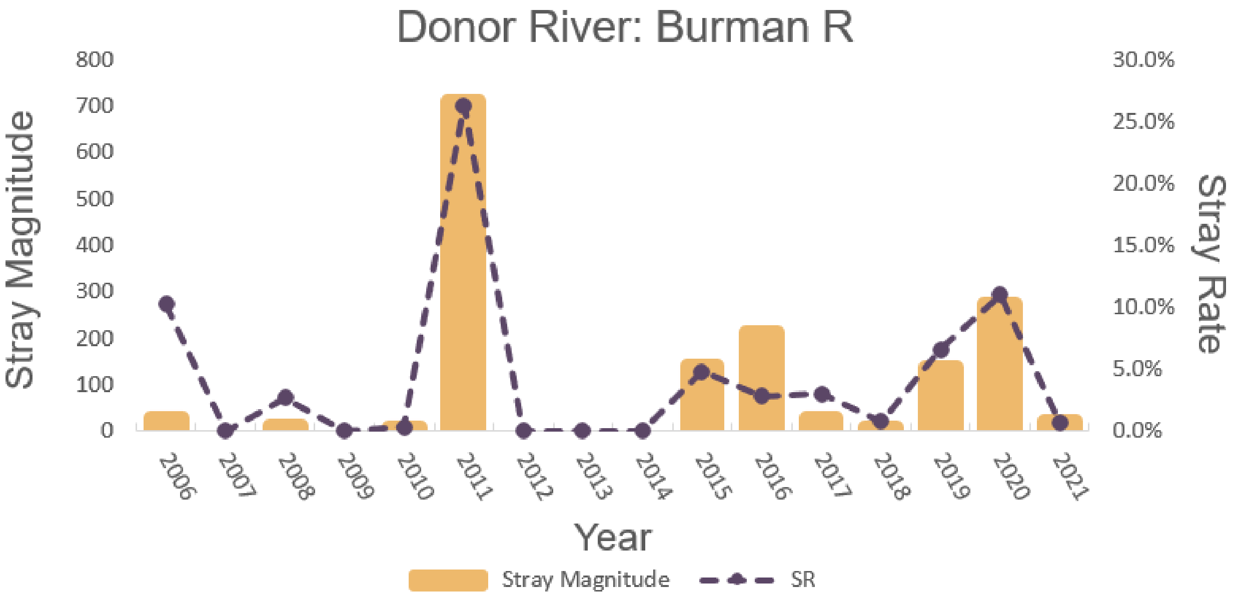

Figure 7.19. Temporal trends in stray rate and magnitude from Burman R Hatchery Chinook (reared at Conuma R Hatchery) calculated from thermal mark recoveries in systems sampled across SBC.

Burman R – Recipient River

Burman R escapement was sampled for thermal marks since 2004. In all years, except for 2008, 2011, and 2019, Conuma R fish were observed in Burman R escapement with an average $pHOS_{\mathrm{stray}}$ of 0.13 (Table E8). From within the Sound, Gold R, Leiner R and Sucwoa R origin fish were also observed, but in smaller proportions. The only outside-CU recoveries returning to the Burman R originated from Robertson Cr hatchery, (average $pHOS_{\mathrm{stray,OCU}}$ = 0.02). $pHOS_{\mathrm{local}}$ in the Burman R was high during our period of analysis (Figure 7.10), averaging 0.63 across years. As a result, *PNI* was generally low. Differences between average PNI_{local} and *PNI* were small (0.32 vs. 0.26), and indicated that $pHOS_{\mathrm{local}}$ was driving trends in enhanced contribution, more so than strayed fish, In this case, removing local Burman R hatchery Chinook would be of far greater impact to increasing the natural-origin contribution to escapement than would an attempt to reduce the influence of out-of-system strays.

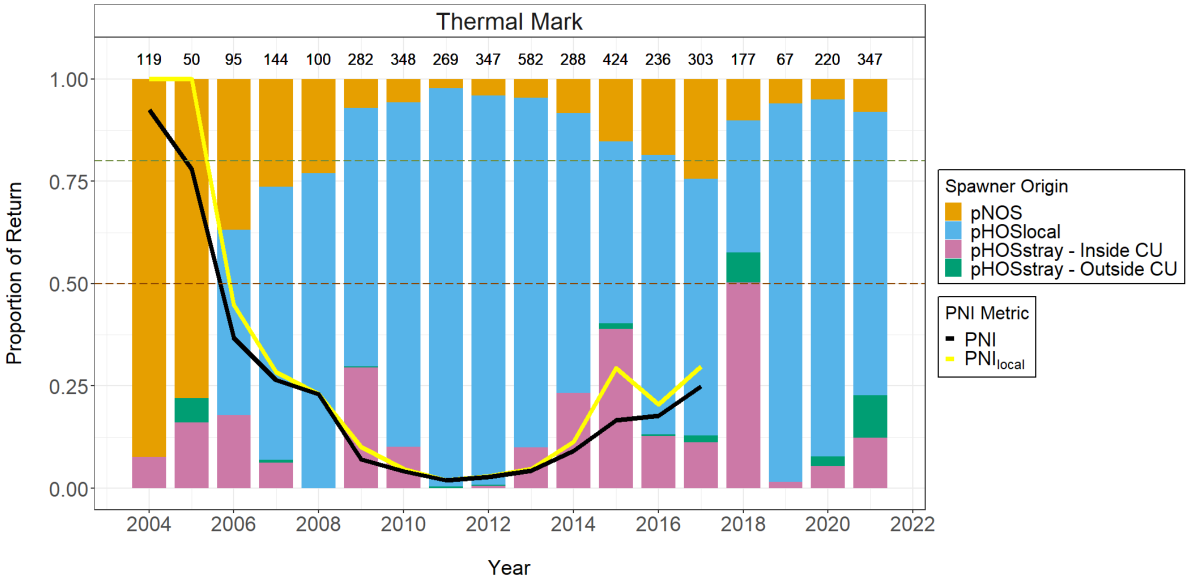

Figure 7.20. Origin of spawners returning to Burman R between 2004 and 2021 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Conuma R Hatchery – Gold R donor stock

Gold R Chinook are currently enhanced at Conuma R Hatchery. This population was historically reared at the Gold R CIP facility until the 2005 brood year. Thermal mark recoveries show that Gold R had a high average stray rate of 13.0%. Unfortunately, escapement estimates for Gold R were only available for a small subset of years and expansions of Gold R Chinook could not be calculated. Thus, estimates of mean stray rate were calculated from only five years when both donor and recipient systems were sampled (Table D4). However in three of five of these years, stray rates were high, ranging from 10.5–37.8% (Figure 7.11).

Outside-CU straying for Gold R fish was also high, averaging 8.9% across years. Strays were observed in 2012, 2015, 2016, 2017, and 2019 straying into streams in Clayoquot Sd and Barkley Sd. This continued observation of strays outside of Nootka Sd suggests a recent increasing trend of outside-CU straying from the Gold R stock. Straying magnitude averaged 114 individuals per year; a relatively large number compared to the average estimated escapement to the river, which averaged over 1,600 individuals per year since 1980.

Several factors may be responsible for this trend. First, Gold R is a satellite reared population, meaning broodstock is taken from the natal system, and reared in a large production, before being released back into the home river. A portion of this population is also reared in seapens, a process along with satellite rearing, the use of non-natal water during rearing and estuary/marine broodstock sampling have been associated with impaired imprinting and heightened stray rates (Candy and Beacham 2000; Labelle 1992).

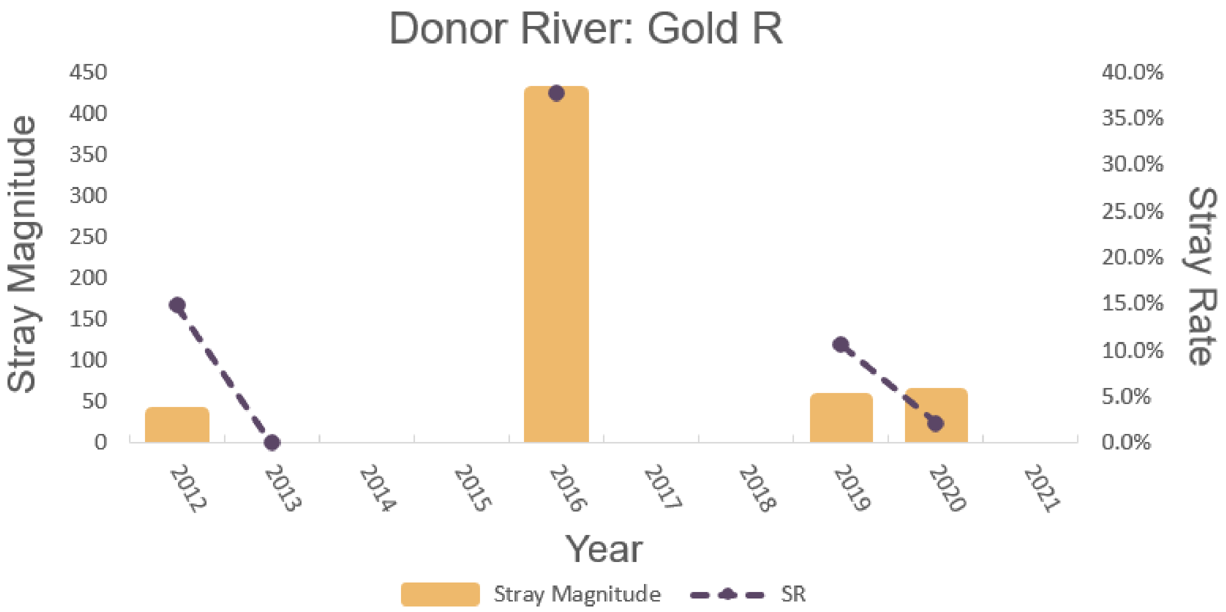

Figure 7.21. Temporal trends in stray rate and magnitude from Gold R Hatchery Chinook (reared at Conuma R Hatchery) calculated from thermal mark recoveries in systems sampled across SBC.

Gold R – Recipient River

Gold R was sampled for thermal mark recoveries since 2005. In almost every years analyzed, $pHOS_{stray}$ was greater than 0.50 (Figure 7.12), and was comprised almost entirely from the outside-CU population of Robertson Cr. In contrast $pHOS_{local}$ only averaged 0.19 (Table E9). These results are similar to those observed by Candy et al. (2009), who described this straying relationship and hypothesized that between 1986 and 2015, a complete replacement of the original Gold R stock may have taken place. This is the most stark individual donor-recipient stray relationship presently known in SBC. Mean PNI_{local} values were 0.62, compared to a *PNI* of 0.26 when strays were included. This indicates that strays are the most significant driver of increased hatchery contribution in Gold R.

Other sporadic instances of strays were observed in the Gold R, however these cases rarely exceed a handful of observations, and rarely represented more than 3% of the return. Other donor rivers included nearby Burman R, with occasional recoveries of Conuma R Chinook. Outside-CU stays beyond Robertson Cr originated from Nitinat R and Sarita R in a couple of years (Table E9).

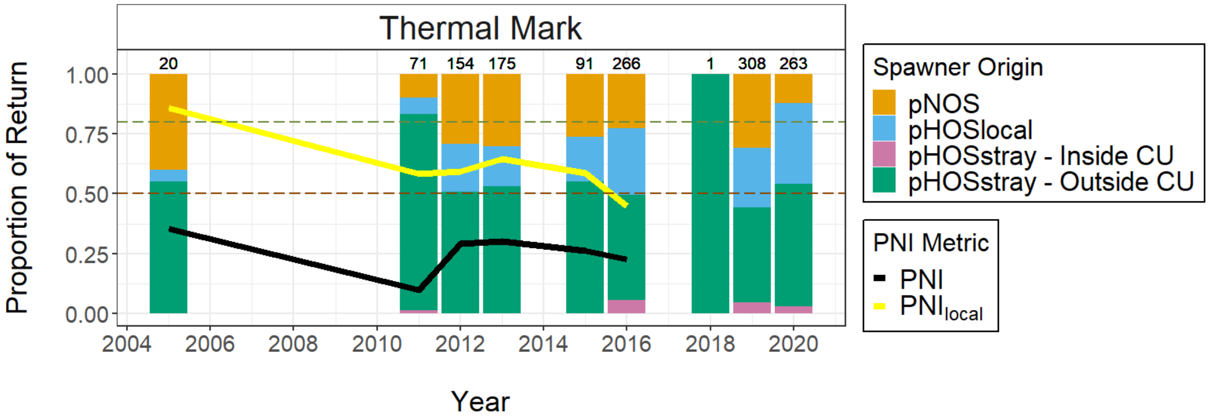

Figure 7.22. Origin of spawners returning to Gold R between 2005 and 2020 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Leiner R – Recipient River

Leiner R was regularly sampled since 2006. In each year, Conuma R Chinook were observed in the escapement, contributing between 6–37% of the return across years. Strays from nearby Tahsis R were also recovered in the Leiner R, but occurred less often than Conuma R recoveries. Other, sporadic within-CU recoveries from Burman R and Sucwoa R were also observed between 2006–2021, but never more than a single recovery in any given year (Table E10).

Outside-CU stray recoveries were observed from Robertson Cr, Nahmint R and Nitinat R stocks between 2006–2021, but were only observed as single recoveries, except in 2016 when two Robertson Cr fish strayed into the Leiner R. Hatchery-origin Chinook regularly comprised more than half of samples taken in Leiner R, with an average *pHOS* of 0.60 (Figure 7.13). Mean PNI_{local} was 0.62, indicating an ‘integrated-transition’ system whereas mean *PNI* was 0.26, indicating an integrated-hatchery system. This result suggests that strayed Chinook may be driving trends in hatchery contribution to the river.

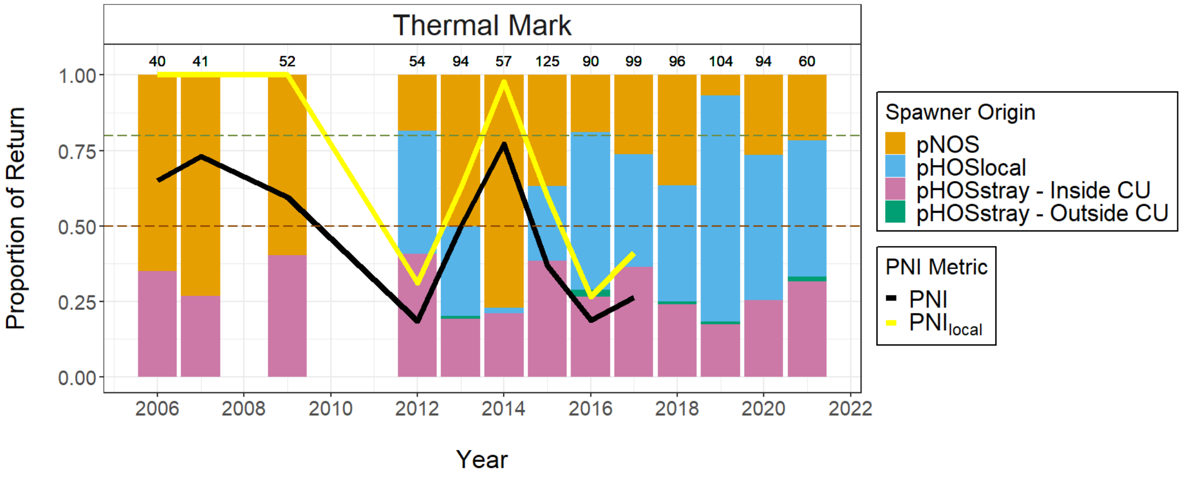

Figure 7.23. Origin of spawners returning to Leiner R between 2006 and 2021 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Tahsis R – Recipient River

Tahsis R was sampled since 2004. Much like Leiner R, Conuma R strays were observed in Tahsis R in nearly every year sampled, but represented a much smaller proportion of the average return (Table E11). The most substantive contribution of hatchery strays into Tahsis R originated from nearby Leiner R. The regular exchange of mature Chinook between Tahsis R and Leiner R exemplifies the ambiguity that arises with the definition of straying at fine geographic scales, and suggests that these populations share a genetic heritage.

Sporadic within-CU recoveries from Gold R and Sucwoa R were also observed in Tahsis R in some years, but no patterns were observed outside of Conuma R input. Outside-CU stray recoveries were detected from Robertson Cr, Sarita R and Nitinat R populations since 2017, but these sporadic recoveries never made up a large proportion of the return (mean $pHOS_{stray,OCU}$ = 0.01). *PNI* values fluctuated between integrated-wild and integrated-hatchery-like systems, but the average for the time series fell below 0.5 (Figure 7.14). In most years, the magnitude of $pHOS_{local}$ drove this pattern, except in 2015–2017, where out-of-system strays contributed substantially to the return, depressing *PNI* values.

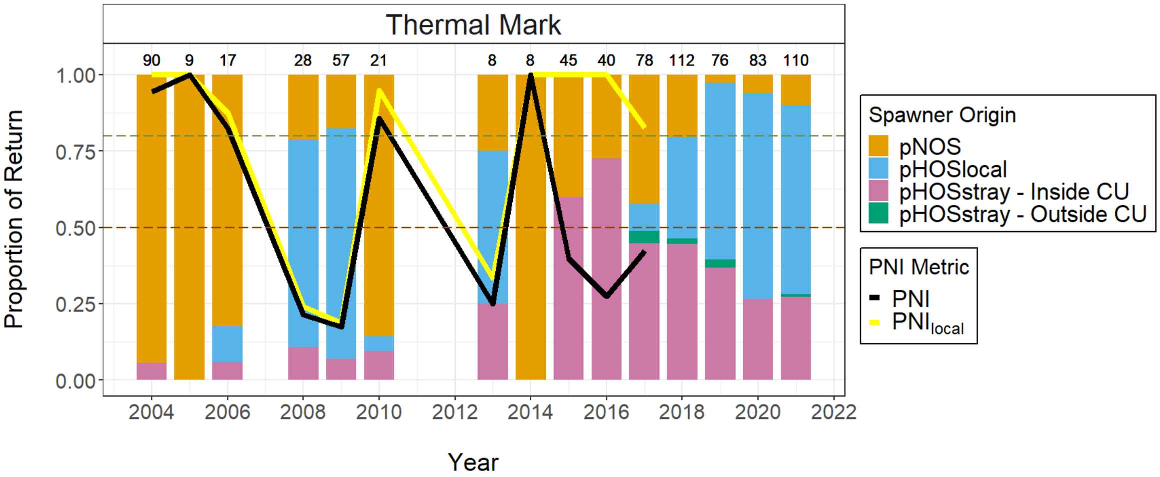

Figure 7.24. Origin of spawners returning to Tahsis R between 2004 and 2021 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners (pHOS$_{local}$), strayed hatchery-origin spawners originating from inside the CU (pHOS$_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU (pHOS$_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI$_{local}$) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Sucwoa R and Tlupana R – Recipient Rivers

Sucwoa R and Tlupana R outflows reside on opposite sides of the estuary that feeds into Conuma R hatchery (Figure 7.3). In both systems, and in most years, *pHOS*$_{stray}$ was greater than *pHOS*$_{local}$ (Figures 7.15, 7.16). The greatest component of *pHOS*$_{stray}$ originated from Conuma R in each year (Tables E11 and E12). A single recovery from Robertson Cr occurred once in each river, and a Burman R Chinook was recovered in Tlupana in 2014.

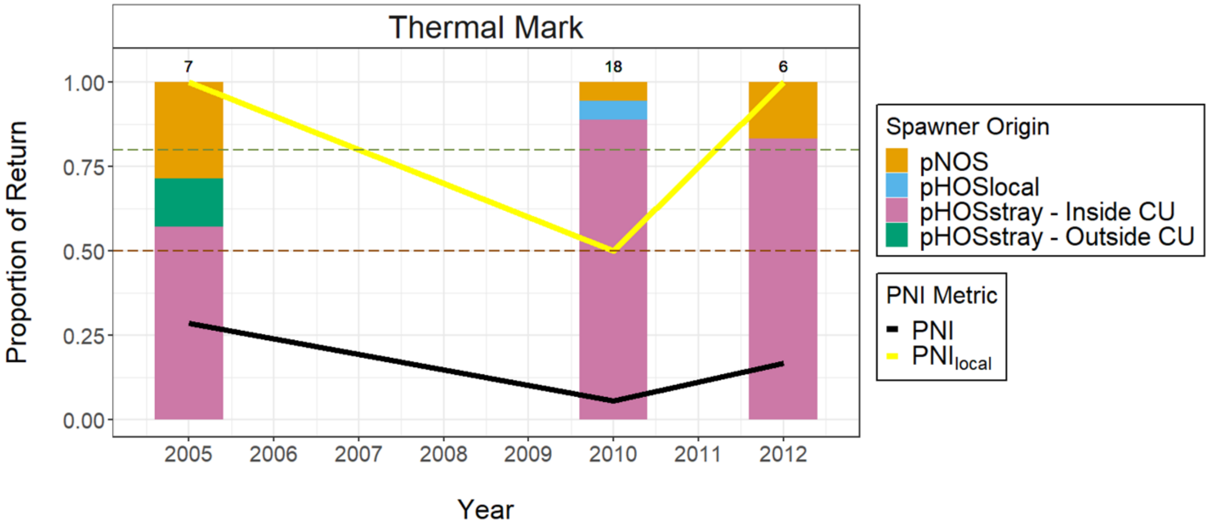

Figure 7.25. Origin of spawners returning to Sucwoa R between 2005 and 2012 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

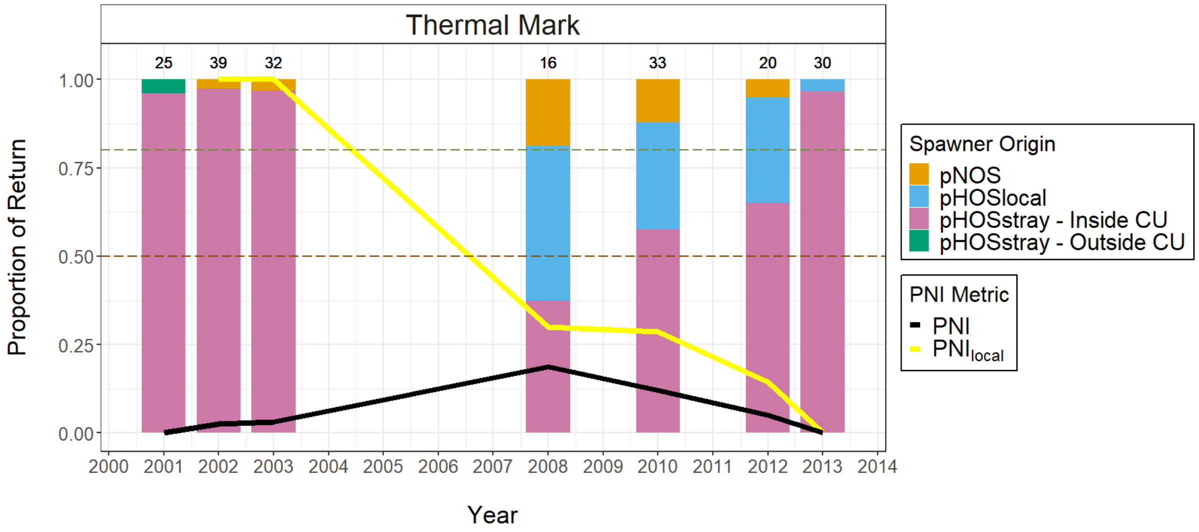

Figure 7.26. Origin of spawners returning to Tlupana R between 2001 and 2013 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Zeballos R – Recipient River

Zeballos R is the northernmost enhanced stock in Nootka Sd and was sampled between 2004 and 2009. Like most other systems in Nootka Sd, Conuma R strays made up a substantial proportion of the return in Zeballos R (Table E14). During this period, *pHOS*$_{\text{stray}}$ averaged 0.10, and *pHOS*$_{\text{local}}$ averaged 0.50 (Figure 7.17). Other within-CU strays were sporadically observed from Gold R and Burman R, however outside-CU strays were more commonly observed. Robertson Cr and Nitinat R hatchery Chinook were observed in 2005 and 2006 straying into Zeballos R, and Sarita R Chinook were observed in 2005, 2006, 2007 and 2009. Sampling efforts should be re-initiated here to determine modern straying trends in this system.

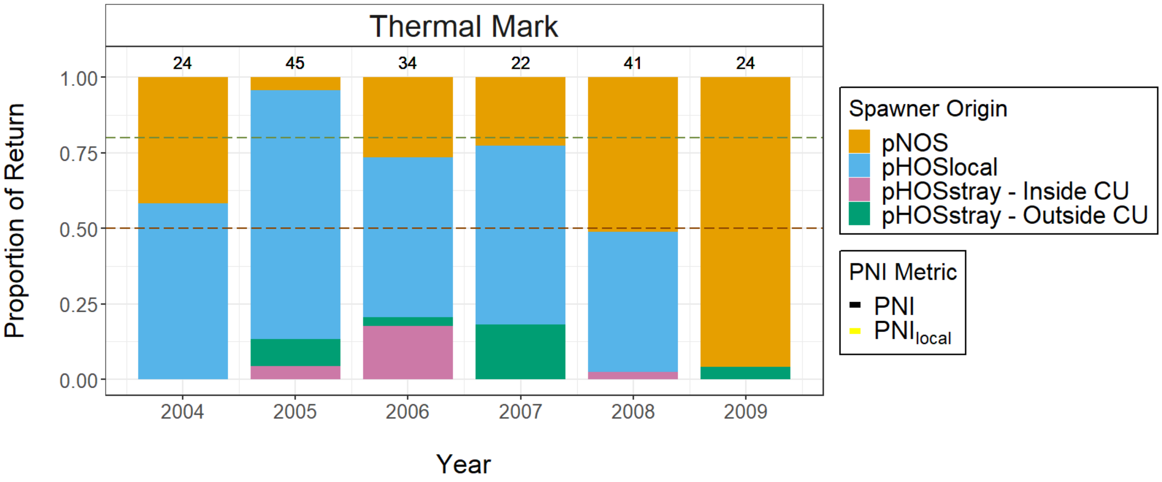

Figure 7.27. Origin of spawners returning to Zeballos R between 2004 and 2009 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners (pHOS$_{\text{local}}$*), strayed hatchery-origin spawners originating from inside the CU (pHOS*$_{\text{stray}}$ *– Inside CU), and strayed hatchery-origin spawners originating from outside the CU (pHOS*$_{\text{stray}}$ *– Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year.*

7.1.3. Conservation Unit: CK-31 – West Vancouver Island-South

CK-31 (West Vancouver Island-South), contains numerous, large, Chinook-bearing rivers, located in two Sounds (Clayoquot Sound and Barkley Sound), and several coastal basins along the Southwest of Vancouver Island (Figure 7.18). The CU contains two large production facilities, Robertson Creek Hatchery and Nitinat River Hatchery. These facilities release upwards of six and three million hatchery-origin Chinook, each year, respectively. On the Northern end of the CU, rivers in Clayoquot Sound remain largely unenhanced, with sporadic hatchery supplementation occurring in some systems. Of 42 river basins where Chinook were regularly observed since 1953, 15 were sampled between 1998–2021, accounting for an estimated 95% of total escapement to the CU. All of these stocks were identified using thermal marks, and four were additionally marked using CWTs during this period. *pHOS*$_{\text{stray}}$ for rivers in CK-31 averaged 0.10, estimated from thermal mark recoveries, and 0.01 estimated from CWTs. *pHOS*$_{\text{stray,OCU}}$ averaged 0.08 based on thermal mark recoveries, and 0.00 based on CWTs. Average *PNI* values were calculable for nine stocks in this CU based on thermal marks and four stocks based on CWTs. Of the nine thermally marked stocks, three had average *PNI* values indicating integrated-wild populations (*PNI* ≥ 0.8), two indicated integrated-transition populations (*PNI* between 0.5 and 0.8), and four indicated integrated-hatchery populations (*PNI* < 0.5). CWT recoveries indicated two integrated-transition stocks, and two integrated-hatchery stocks in the CU.

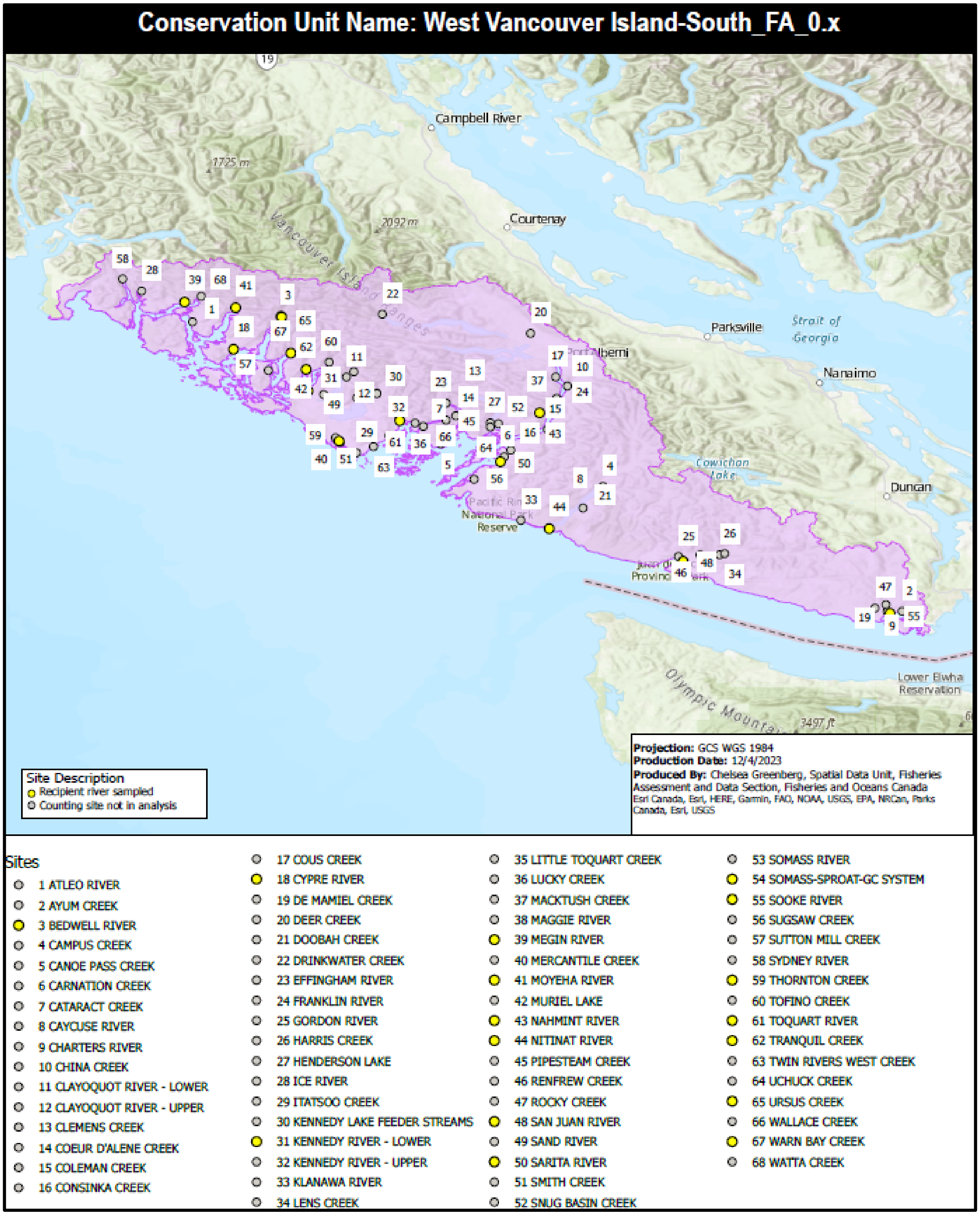

Figure 7.28. Boundary map of the CK-31 Conservation Unit (West Vancouver Island-South) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

7.1.3.1. Clayoquot Sound

Clayoquot Sound contains a number of unenhanced rivers that have historically experienced minimal hatchery input. Since the early 1980s, Thornton Creek Hatchery, a Community and Economic

Development (CEDP) facility, has been enhancing a small number of Chinook populations and currently rears an average of 300,000 fish annually, primarily originating from Toquart R. This facility also supports the local Tofino Hatchery, a Public Involvement Project (PIP) facility, that enhances various rivers throughout Clayoquot Sd with the purpose of rebuilding low escapement populations in the area. The Tofino Hatchery has reared a variety of populations since its inception, and as such, *pHOS* and *PNI* values in Clayoquot Sd rivers have varied depending on which populations were being enhanced in the years preceding escapement sampling. Further, as a result of sporadic enhancement resulting in few broodstock collections, straying estimates are typically calculated from deadpitch or natural spawner samples that are more difficult to obtain and result in small sample sizes for most systems and years. Thus, it is important to note that our estimates of straying in Clayoquot Sd will imprecise until regular, systematic sampling across years can be performed. During our period of analysis, we analyzed samples originating from six river systems within Clayoquot Sd: Megin R, Moyeha R, Cypre R, Bedwell R, Tranquil Cr, and Kennedy R - Lower.

Megin R and Moyeha R – Recipient Rivers

At the northwestern end of the Sound, Megin R and Moyeha R were both sampled sporadically between 2010 and 2017. In Megin R, samples taken in 2015 and 2017 revealed the presence of Conuma R Chinook in the escapement. In 2015, Conuma R Chinook represented two-thirds of the 15 samples taken, and in 2017, one Conuma R Chinook and one Megin R Chinook were observed (Figure 7.19, Table E15).

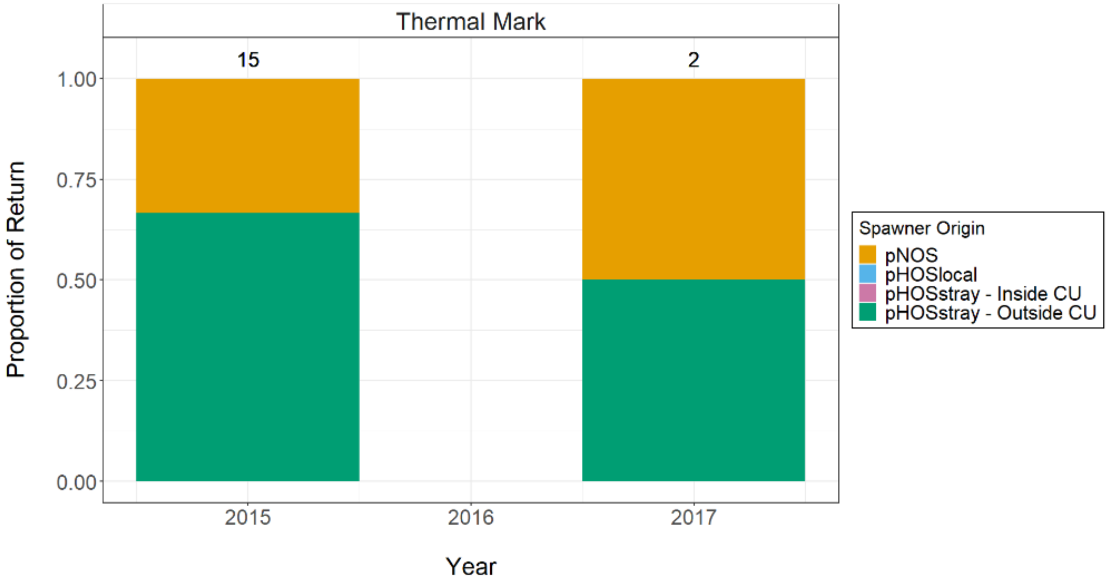

Figure 7.29. Origin of spawners returning to Megin R between 2015 and 2017 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. As this stock is not enhanced, no PNI estimates were calculated.

Moyeha R sampling revealed 6/11 samples taken in 2010 to be of Conuma R origin, but in 2011 and 2017, all fish sampled were of Moyeha R origin (Figure 7.20, Table E16). Both Megin R and Moyeha R are unenhanced systems where no broodstock is taken, thus *PNI* values could not be calculated.

This trend of Conuma R fish straying into Megin R and Moyeha R is supported by genetic baseline data presented in Section 4; Chinook returning to these systems showed low F_{ST} distances that clustered very closely with both historical and recent Conuma R samples. Samples from Megin R were further removed from Conuma R fish on the dendrogram, but still clustered closer to Conuma R Chinook than other Clayoquot Sd populations like Tranquil Cr.

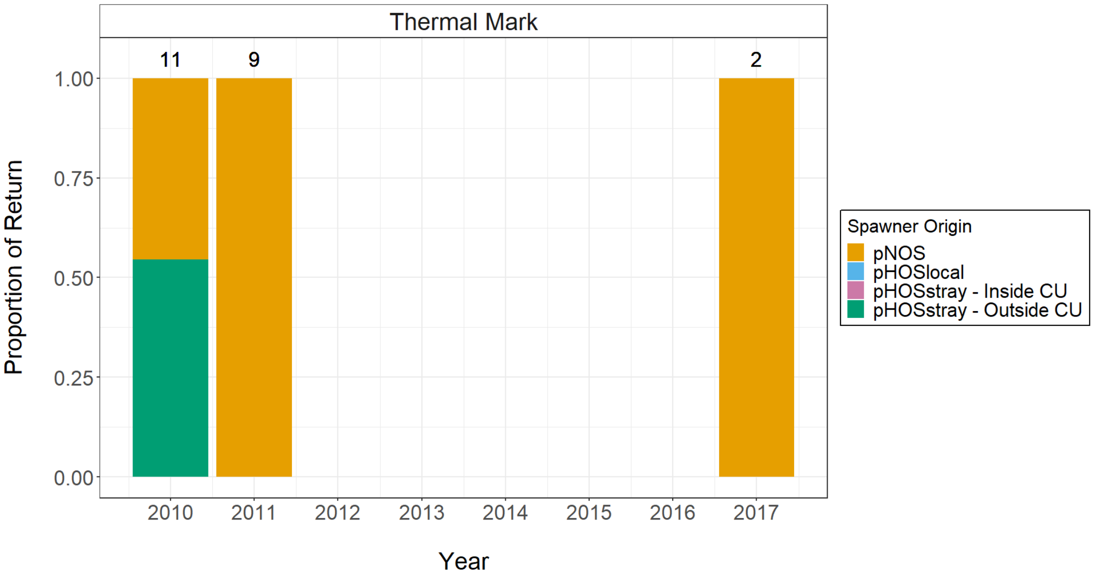

Figure 7.30. Origin of spawners returning to Moyeha R between 2010 and 2017 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. As this stock is not enhanced, no PNI estimates were calculated.

One hypothesis that explains the greater propensity for Conuma R Chinook to stray into Megin R and Moyeha R over other Clayoquot Sd rivers may be a shared water source feeding both Nootka Sd streams and Western Clayoquot Sd. As olfaction of natal stream characteristics is an integral part of correct homing (Keefer and Caudill 2014), source water similarities may be driving this pattern. However, further study into the chemical profiles of streams across the WCVI is needed before any such conclusions can be drawn.

Bedwell R – Recipient Rivers

The Bedwell R is under special management due to its previous categorization as a ‘wild’ escapement indicator in Clayoquot Sound. In 2011, after six consecutive years of returns of less than 100 Chinook Salmon, it was decided to initiate enhancement. The production target was set at 25,000 eggs (approximately 6–8 females), and all local hatchery releases were adipose fin clipped. Since 2013, the return has averaged about 500 Chinook per year.

The population was adipose-clipped and CWT’d, but not marked with a stock-identifying thermal mark, making $pHOS_{local}$ incalculable for this mark type. No strays were observed in CWT samples taken between 2015 and 2019 (Figure 7.22). For thermal mark samples, $pHOS_{stray}$ averaged 0.18 across years, and $pHOS_{stray,OCU}$ averaged 0.06 (Table E17). Strays from Gold R (outside the CU) were regularly observed returning to Bedwell R in 2015, 2016, 2017 and 2019. In addition, in 2018, one stray recovery from Conuma R was observed, and in 2019, stray recoveries were observed from Leiner R (1), and Robertson Cr (5). Other than those mentioned above, thermal mark analyses did not reveal any other stray observations.

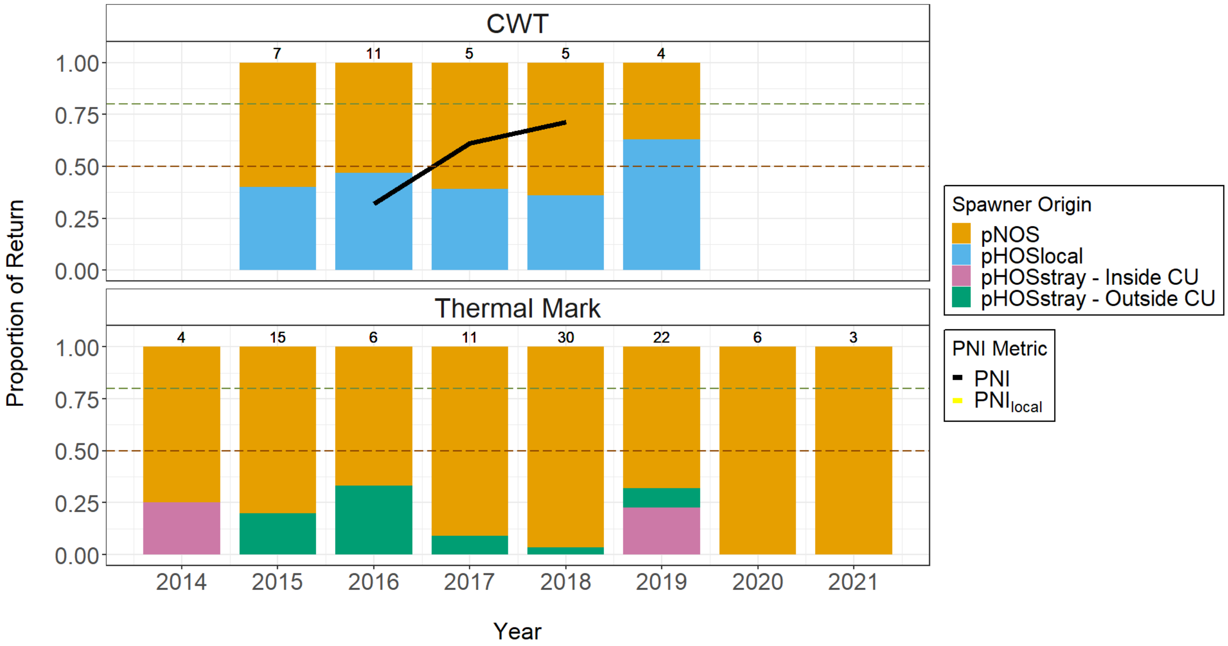

Figure 7.31. Origin of spawners returning to Bedwell R between 2014 and 2021 estimated from CWT and thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs or otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5. As this stock is not thermally marked, no PNI estimates were calculated for this mark type.

Cypre R – Recipient Rivers

Cypre R was sampled in 2011 and again from 2014–2020. In 5/7 years, no strays were observed in thermal mark samples (Figure 7.21). In 2016, one adipose clipped Chinook of unknown origin was observed, representing a $pHOS_{stray}$ of 0.09 (Table E19). In 2019, one Robertson Cr fish was observed, representing a $pHOS_{stray}$ of 0.11. In these, and most other years, sample sizes were low, meaning we lack precise estimates of straying in this system.

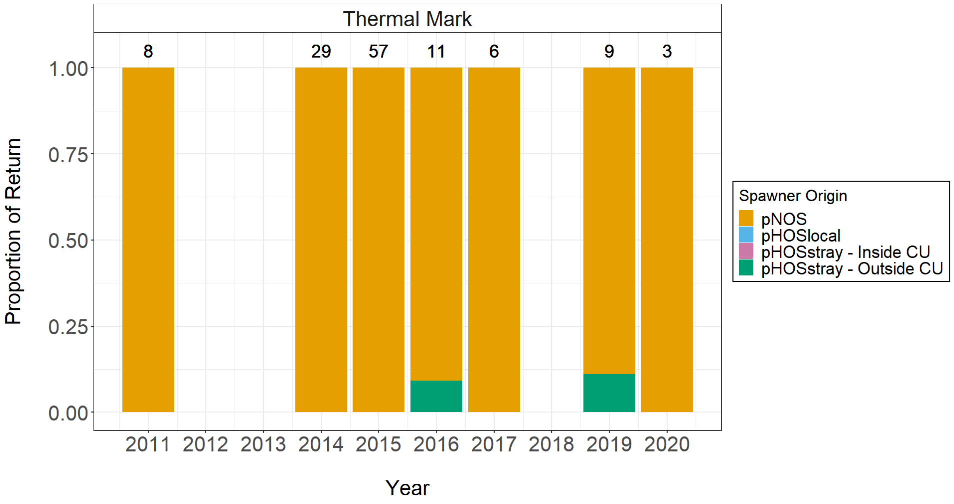

Figure 7.32. Origin of spawners returning to Cypre R between 2011 and 2020 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners (pHOS$_{local}$), strayed hatchery-origin spawners originating from inside the CU (pHOS$_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU (pHOS$_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. As this stock is not thermally marked, no PNI estimates were calculated.

Tranquil Cr and Kennedy R – Recipient Rivers

At the eastern end of Clayoquot Sd, Tranquil Cr and Kennedy R were the most abundant source of Chinook analyzed for thermal marks in the area. Samples in Tranquil Cr were taken in 2011 and between 2014–2021 and in all years, except for 2019, no thermal marks indicating hatchery strays were observed (Figure 7.23). In 2019, six samples were analyzed from Tranquil Cr, of which two originated from Robertson Cr Hatchery (Table E20).

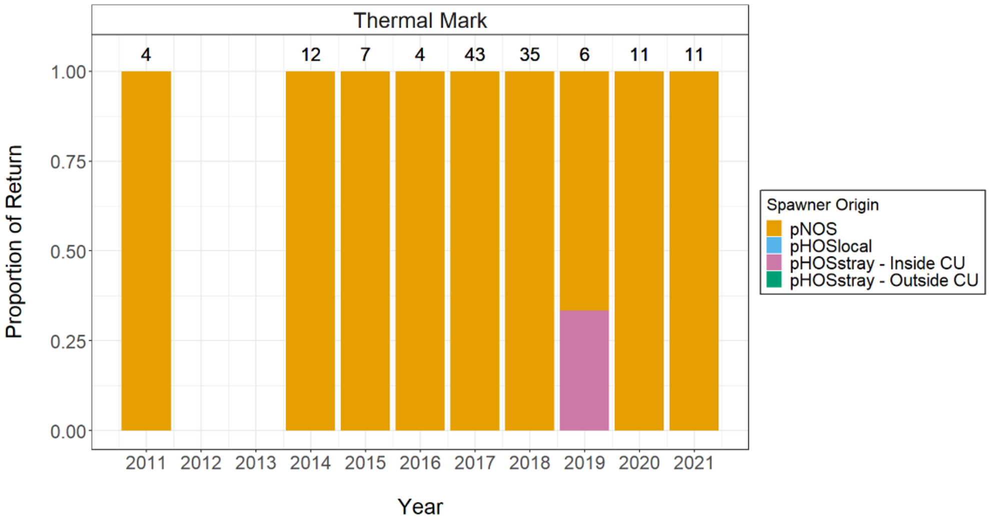

Figure 7.33. Origin of spawners returning to Tranquil Cr between 2011 and 2021 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners (pHOS$_{local}$), strayed hatchery-origin spawners originating from inside the CU (pHOS$_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU (pHOS$_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. As this stock is not thermally marked, when enhanced, no PNI estimates were calculated.

In nearby Kennedy R, samples from 2015–2017 revealed no hatchery strays in the system (Figure 7.24). Sampling in 2004 in Kennedy R revealed a single stray in 49 samples originating from Robertson Cr (Table E21).

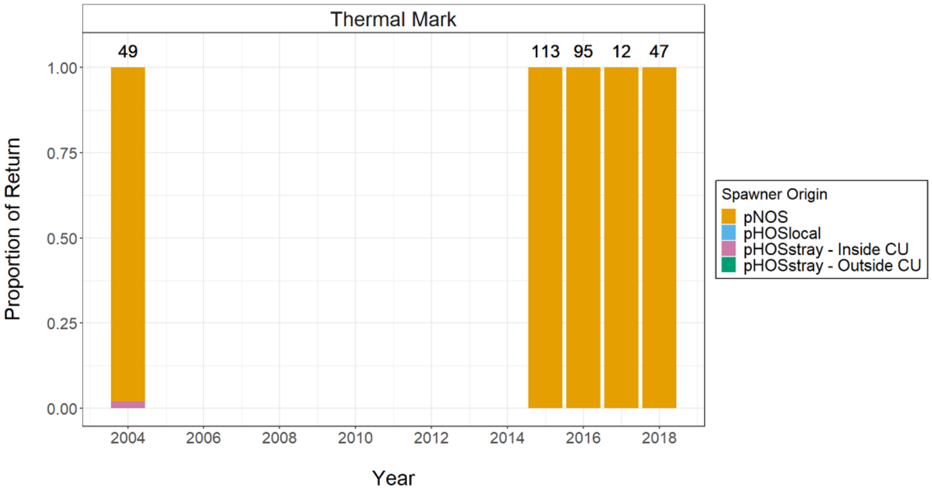

Figure 7.34. Origin of spawners returning to Kennedy R - Lower between 2004 and 2018 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners (pHOS$_{local}$), strayed hatchery-origin spawners originating from inside the CU (pHOS$_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU (pHOS$_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. As this stock is not enhanced, no PNI estimates were calculated.

7.1.3.2. Barkley Sound – WCVI

Barkley Sound contains several Chinook bearing rivers, as well as one of the largest Chinook-rearing hatchery facilities in BC—Robertson Creek. This facility is located on Stamp R near Great Central Lake within the larger Somass R drainage basin, which also contains Sproat Lake and several smaller streams. Prior to the 1970s, escapement of adult Chinook to systems in Barkley Sd, including the Somass R, averaged over 12,000 individuals per year. Since enhancement at Robertson Cr began in the early 1970s, average escapement values to the Sound have increased to an average of >50,000 individuals with some years seeing as many as 148,000 spawners. In addition to the Somass System, four other Chinook producing rivers in Barkley Sd were sampled for thermal marks and CWTs between 1998 and 2017: Sarita R, Nahmint R, Toquart R, and Thornton Cr.

Robertson Creek Hatchery – Somass / Robertson Cr donor stock

Robertson Cr hatchery, has been enhancing salmon since the early 1970s, and presently releases the most Chinook of any facility in the Pacific Region; upwards of seven million individuals per year. A subset of Chinook reared at this facility are marked with CWTs as an indicator for the WCVI Stock Management Unit. Thermal marks have also been applied to Chinook since the 1993 brood year. Robertson Cr Hatchery is one of the few systems in SBC that has marking programs for both thermal mark and CWT mark types from 1998 to the present.

For this investigation, all Chinook returning to the Somass System were grouped into one basin, although fine-scale straying likely exists within reaches of this drainage. The genetic similarity of these populations, as well as their substantial hatchery composition, makes the classification of these spawners as one large meta-population reasonable.

CWT recoveries of Robertson Cr Chinook in SBC showed a low average stray rate of 0.5%, with outside-CU straying occurring at a rate of 0.4% (Table D5). These strays were recovered within a similar geographic range as was seen for thermal mark results, but to fewer recipient systems. This difference may be due to the greater detectability of thermal marks compared to CWTs, which are typically only applied at a rate of 10–15% in CWT marked populations in SBC. The average magnitude of strays detected via CWTs was 152 across years, but reached a high of 1,388 individuals in 2020 (Table D5).

Thermal mark data revealed an average stray rate from Robertson Cr Hatchery of 2.0% between 1998 and 2021 (Table D6). Since 2011, annual stray rates were substantially greater than were observed between 1998–2010 (Figure 7.25), with the largest observations a result of straying into Gold R. Robertson Cr also exhibits the highest outside-CU stray rate of the three WCVI OPS facilities with observations frequent in occurrence, but often small in magnitude (Table D6). Robertson Cr strays were recovered as far away as Chilliwack R in 2004 and 2006, where five and one recoveries respectively were expanded to represent an estimated 448 and 117 Chinook strays to the river. The mean outside-CU stray rate from Robertson Cr was similar to the total stray rate, averaging 1.8%, which was expected as most strays were recovered in Gold R.

The magnitude of strays estimated from thermal marks originating from Robertson Cr Hatchery averaged 152 Chinook per year between 1998 and 2021 (Table D6). However, since 2012, regular annual estimates of > 1,000 strayed Chinook originating from Robertson Cr have been commonplace, a trend which may warrant investigation and intervention to limit this increasing tendency.

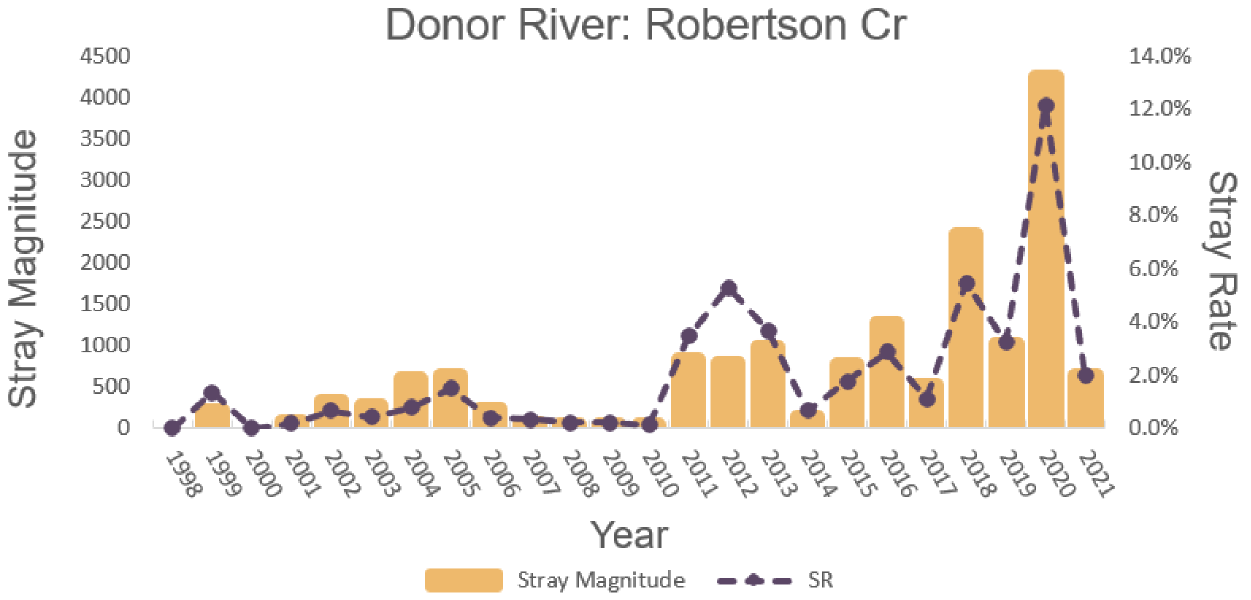

Figure 7.35. Temporal trends in stray rate and magnitude from Robertson Cr Hatchery Chinook calculated from thermal mark recoveries in systems sampled across SBC.

For both thermal mark and CWT recoveries from Robertson Cr Hatchery, the greatest number of strays were observed returning to Gold R. In most years when Gold R samples were taken, the return was dominated by Robertson Cr hatchery strays. Other authors found similar results, with genetic cluster analyses suggesting that Gold R Chinook have been more similar to Robertson Cr and other Barkley Sound Chinook since the mid-1980s, and projecting that the original Gold R population may have been fully supplanted by the Robertson Cr stock during this time (Candy et al. 2009). This observation may not be the direct result of hatchery production, but has certainly been exacerbated by it. In fact, when strays into Gold R were removed from the donor straying calculations, Robertson Cr stray rates dropped to <1%. Robertson Cr hatchery typically releases more Chinook than any other hatchery in BC—upwards of seven million smolts annually. Additionally, this facility mixes rearing water from ground-fed sources with surface water during early rearing, which may affect imprinting in juveniles. However, Robertson Cr Hatchery has an ample flow buffer in the Great Central Lake Dam that controls flows to reduce the impact of droughts on upstream migration. Thus, besides the specific propensity for

Robertson Cr Chinook to stray into the Gold R, the genetic impact of straying from Robertson Cr hatchery fish on natural-origin populations appears to be low.

Somass/Robertson Creek – Recipient River

Robertson Cr hatchery and the Somass System were analyzed between 1998 and 2021. The majority of these samples were taken at either Stamp R, Sproat R, or directly at the hatchery, with occasional sampling taking place in other tributaries within the drainage. Thermal mark analysis of these Chinook revealed that in each year since 1998, >99% of returns were of Somass System/Robertson Cr origin (both of natural- and hatchery-origin; Figure 7.26). Average $pHOS_{\text{stray}}$ and $pHOS_{\text{stray,OCU}}$ both approximated 0.00 over the time series. However, strays from nearby Nahmint R were regularly observed returning to the Somass System throughout the sampling period. As Chinook from Nahmint R are typically reared at Robertson Cr, this result is unsurprising. Sporadic annual recoveries from other basins in the WCVI were also observed in the Somass System including Chinook from Nitinat R, Gold R, and Burman R (Table E22). Results from CWT recoveries mirrored what was observed in the thermal mark analyses, with close to 100% Robertson Cr/Somass System Chinook present in all years. Sporadic recoveries of Nahmint R, as well as Marble R and Sarita R Chinook were occasionally observed in CWT samples, but average $pHOS_{\text{stray}}$ and $pHOS_{\text{stray,OCU}}$ were 0.00 (Table E23). As Robertson Cr has operated as a major production facility since the early 1970s, thermal mark derived *pHOS* values during our study period ranged between 0.8 and 1.0, as expected. *PNI* values were typically close to 0, indicating an integrated-hatchery system.

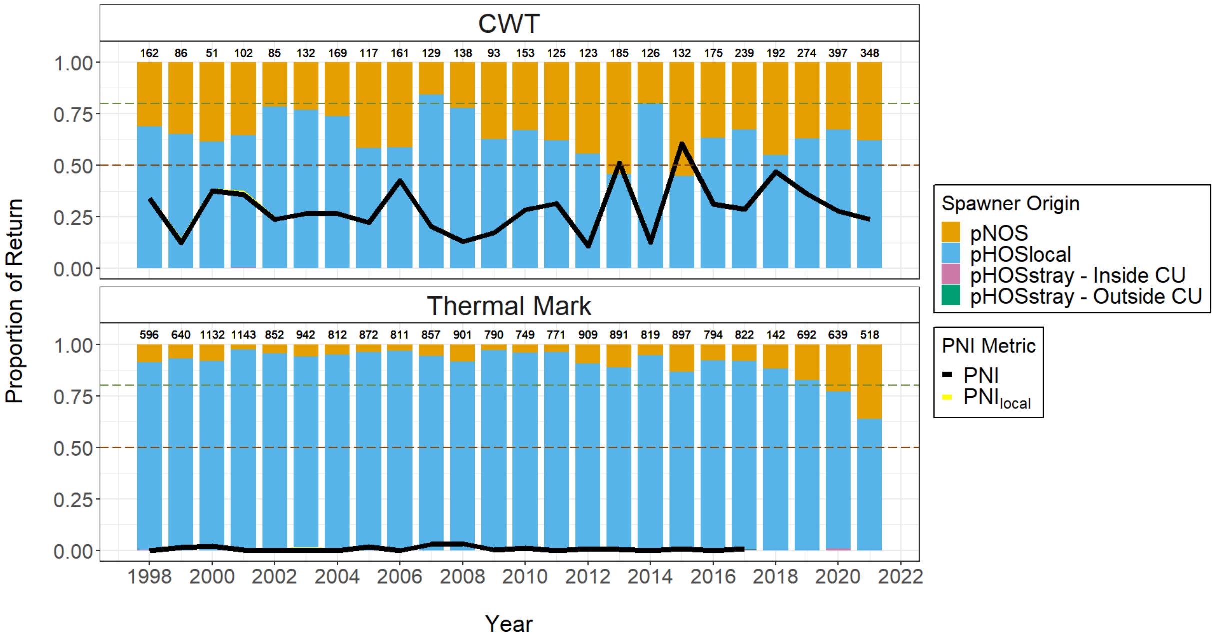

Figure 7.36. Origin of spawners returning to Robertson Cr/Somass System between 1998 and 2021 estimated from CWT and thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs or otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Robertson Cr Hatchery - Nahmint R donor stock

Nahmint R Chinook have been supplemented by Robertson Cr Hatchery since 1982 and are currently marked with both CWTs and thermal marks. CWT recoveries in SBC between 2002 and 2021 showed an average stray rate of 4.2% for Nahmint R, with the majority of stray recoveries observed in Robertson Cr (Table D7), the hatchery where they are reared. Recoveries from Nahmint R were observed straying outside the CU into Burman R in 2017, and into Big Qualicum R in 2015.

Thermally marked otolith recoveries showed a high, but variable stray rate from Nahmint R, averaging 17.7%, with annual stray rates as high as 50.3% (Figure 7.27). The majority of these strays were recovered in Robertson Cr, returning to the facility in which they were reared. Only in 2015 and 2019 were Nahmint R Chinook recovered in other rivers, with observations in Sarita R and Leiner R respectively (Table D8).

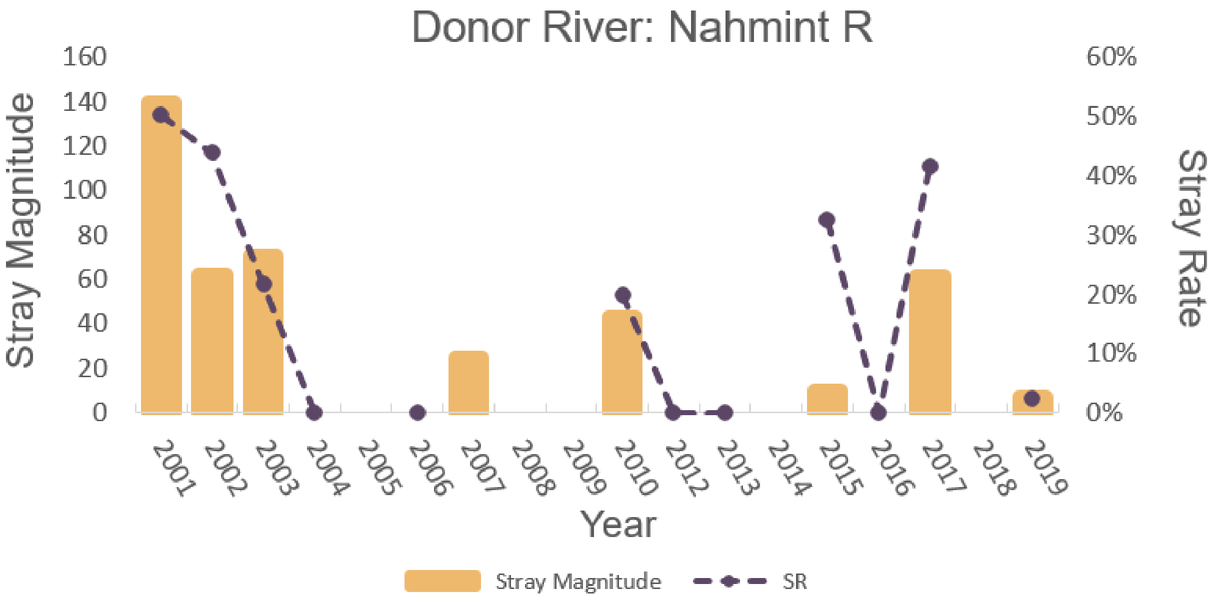

Figure 7.37. Temporal trends in stray rate and magnitude from Nahmint R Hatchery Chinook (reared at Robertson Cr Hatchery) calculated from thermal mark recoveries in systems sampled across SBC.

Artificially high stray rates observed in some years may be produced from the expansion process used for thermal marks. In years when escapement is high relative to sampling effort, strays may be overexpanded in recipient systems. Additionally, if escapement is low, or sampling effort is high in the donor system, the contribution of homed individuals in H_{TOT} may be low relative to the contribution of expanded strays. This may be occurring in Nahmint R, where in many years, a high proportion of the escapement was sampled. Strays into Robertson Cr were also regularly expanded from a few individuals to larger number of recoveries, with an average escapement of over 40,000 Chinook during our period of analysis, and an average sampling rate of only 2.2%.

The magnitude of strays originating from Nahmint R averaged 18 individuals across years calculated from CWTs (Table D7), and 32 individuals calculated from thermal mark recoveries (Table D8). As the direction of straying in this case is from a natural-origin to a hatchery dominated system, the genetic risk of straying from Nahmint R still appears quite low.

Nahmint R – Recipient River

Nahmint R Chinook have been enhanced at the Robertson Cr facility since the early 1980s in years where sufficient broodstock is available in the river. Sampling for thermal marks in this system has occurred since 1999 (Table E24). The most consistent trend of straying into Nahmint R is the regular occurrence of Robertson Cr fish in the escapement. Strays from Robertson Cr range from lows of 1% in many years to a high of 54% in 2002, when 111 of 205 samples were determined to be of Robertson Cr origin. Strays from Sarita R were also commonly observed as strays – occurring in 2002, 2003, 2006, 2010, 2012, 2015, 2016, and 2017. These fish represented between 1–4% of samples in most years, but accounted for 8% of the return in 2012. Other sporadic stray recoveries were observed originating from Conuma R, Nitinat R, and Gold R in several years throughout the sample period, with Conuma R Chinook making up anywhere from 2–9% of returns from 2015–2017.

Nahmint R is enhanced with the goal of conservation and rebuilding via broodstock collection in the river and rearing at Robertson Cr. As such, hatchery Chinook are regularly observed in the majority of escapement samples—a sign of success for these types of programs before natural-origin Chinook can be managed at a higher level when returns are improved. From 2001 to 2006, *pHOS* was >50%, with moderate levels of straying. Since 2006, *pHOS* values have dipped below 50% in many years, and *PNI* has been managed at a level between 0.50 and 0.80, indicative of an integrated-transition hatchery system that ensures natural-origin Chinook dominate (Figure 7.28). However, during this time of reduced hatchery-influence, strays from outside the CU have increased, with $pHOS_{\text{stray,OCU}}$ reaching a high of 0.13 in 2015. The result of this straying can be visualized from the difference between PNI_{local} and *PNI* values in the latter half of our time series (Figure 7.28). Thus, while Nahmint R has seen a greater proportion of natural-origin Chinook in recent years, straying into this system from hatchery populations like Conuma R, Gold R, and others may be hindering a more substantial natural-origin return.

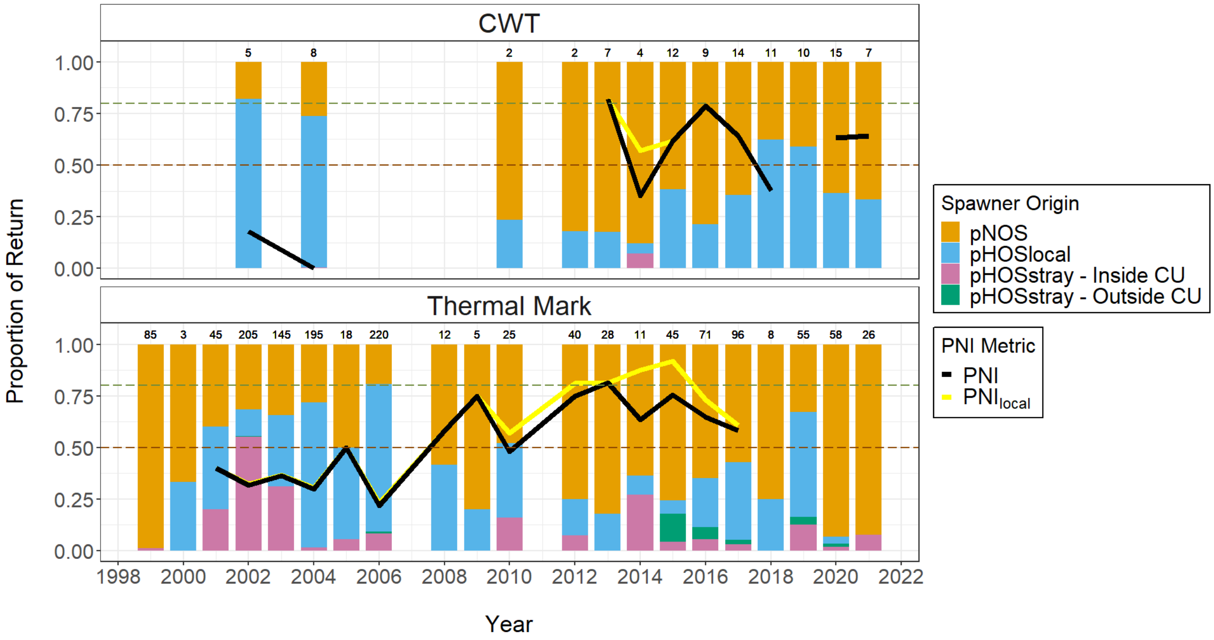

Figure 7.38. Origin of spawners returning to Nahmint R between 1998 and 2021 estimated from CWT and thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs or otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Nitinat R Hatchery – Sarita R donor stock

Sarita R, located on the Eastern side of Barkley Sd, has been enhanced since the early 1990s via Nitinat R hatchery to provide a harvest surplus and maintain a self-sustaining natural population in the river. CWT data, available for 11 years between 1998–2021, reveals an average annual stray rate of 2.3%. All CWT recoveries originating from Sarita R were recovered in large, hatchery-dominated systems within the CU; in Robertson Cr and Nitinat R (Table D9).

Thermal mark data between 1998 and 2021 show a moderate average stray rate of 3.1% (Table D10). The two largest observed values, in 2017 and 2020 (Figure 7.29), were due to a number of Sarita R

Chinook straying into the Nitinat R system, where their rearing facility is located. Strays from Sarita R were observed in Nitinat R in 50% of years sampled. Sarita R Chinook were also regularly observed straying into Nahmint R. This trend is particularly interesting as no other river in Barkley Sd received strays from Sarita R according to the thermal mark data.

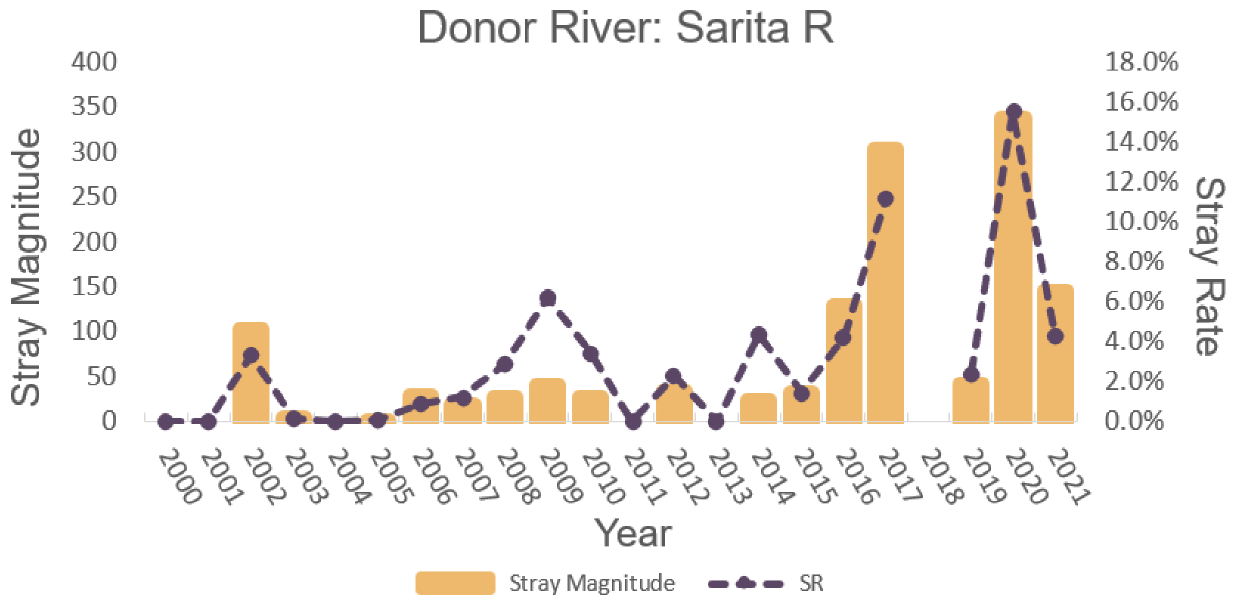

Figure 7.39. Temporal trends in stray rate and magnitude from Sarita R Hatchery Chinook (reared at Nitinat R Hatchery) from thermal mark recoveries in systems sampled across SBC.

The magnitude of strays originating from Sarita R was low and consistent, notwithstanding the outlying years described above. An average magnitude of 71 strays was observed, mostly within the CU (92%). Sporadic stray recoveries were observed in Nootka Sd, with consistent recoveries observed in Zeballos R, Tahsis R and Conuma R. Further North, an outlying recovery of Sarita R Chinook in Kauok R represented an expanded 24 individuals in 2014. Overall, straying from the Sarita R stock into SBC systems appears to be minimal, and poses little risk to natural-origin populations, beyond a potential increased propensity to stray into nearby Nahmint R.

Sarita R – Recipient River

Chinook recoveries from Sarita R were analyzed for thermal marks between 1998–2021. $pHOS_{local}$ made up the majority of recoveries in all years after 1999 (Figure 7.30). Average $pHOS_{stray}$ and $pHOS_{stray,OCU}$ was 0.11, and 0.00 respectively. In all years except for 2007, 2008, and 2016, Nitinat R hatchery strays were observed in Sarita R and accounted for an average of 3.2% of returns in those years (Table E26). Prior to 2003, between 0.3% and 78% of returns were determined to be of hatchery-origin, but contained thermal marks that were not identifiable to a specific hatchery. In these instances, it was assumed that these Chinook originated from Nitinat R Hatchery, as no other hatchery contributed to Sarita R escapement with regularity in subsequent years. A single Robertson Cr stray recovery was observed in samples taken in each of 2003, 2010, 2014, 2015, and 2016. Beyond these regular occurrences, sporadic stray recoveries were observed throughout our period of analysis originating from Conuma R, Nahmint R, and Tlupana R, but never exceeded 1% of escapement samples.

CWT samples were analyzed for several periods between 1998 and 2021. In these samples, Nitinat R strays were observed in each of 1999, 2004, and 2018; Conuma R strays were observed in 2004; and Nahmint R strays were observed in 2018 (Table E27).

pHOS values estimated from thermal marks were consistently high, and *PNI* values were low, indicative of an integrated-hatchery system. These data suggest that the genetic pressure on natural-origin spawners in the Sarita R is predominantly from local hatchery-origin spawners as opposed to out-of-system strays. Based on our findings, we would recommend the continued management of local enhanced Chinook to buffer hatchery risk in this system.

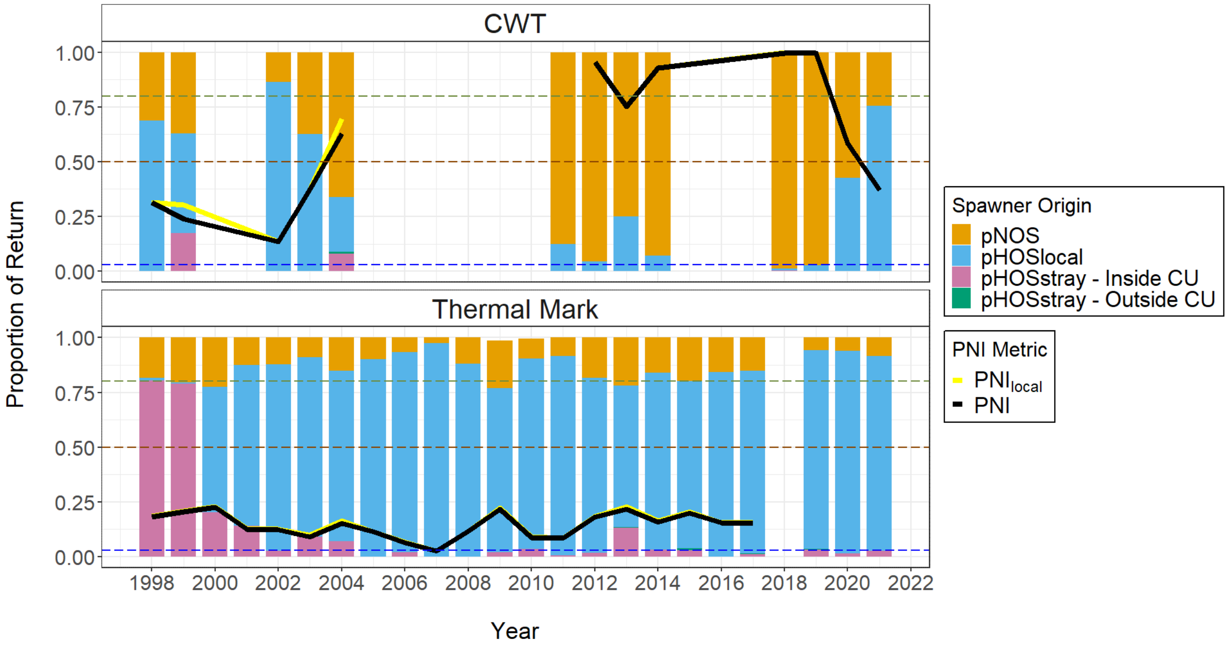

Figure 7.40. Origin of spawners returning to Sarita R between 1998 and 2021 estimated from CWT and thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners (pHOS$_{local}$), strayed hatchery-origin spawners originating from inside the CU (pHOS$_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU (pHOS$_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs or otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI$_{local}$) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Toquart R – Recipient River

The Toquart R Chinook population has been enhanced historically, founded from Nitinat R stock and reared out of the nearby Thornton Cr Hatchery. Sampling in 2015 and 2016 did not reveal any strays from Nitinat R, however Conuma R Chinook were observed representing 7% and 5% of the annual return, respectively (Figure 7.31). Genetic sampling performed in 2015 by Withler et al. (2017), revealed that the Toquart R population had become genetically distinct from earlier Toquart R samples as well as Nitinat R samples that founded the population. This may be due to the influence of the natural Toquart population, or straying from other Clayoquot populations. DNA samples collected in 2015 aligned with thermal mark data, but also suggested that an unmarked Chinook observed was genetically of Robertson Cr stock. Genetic results from populations like Toquart R reveal the complex nature of determining genetic heritage of adult Chinook after multiple years of transplanting and straying (both natural and hatchery) among rivers on the WCVI.

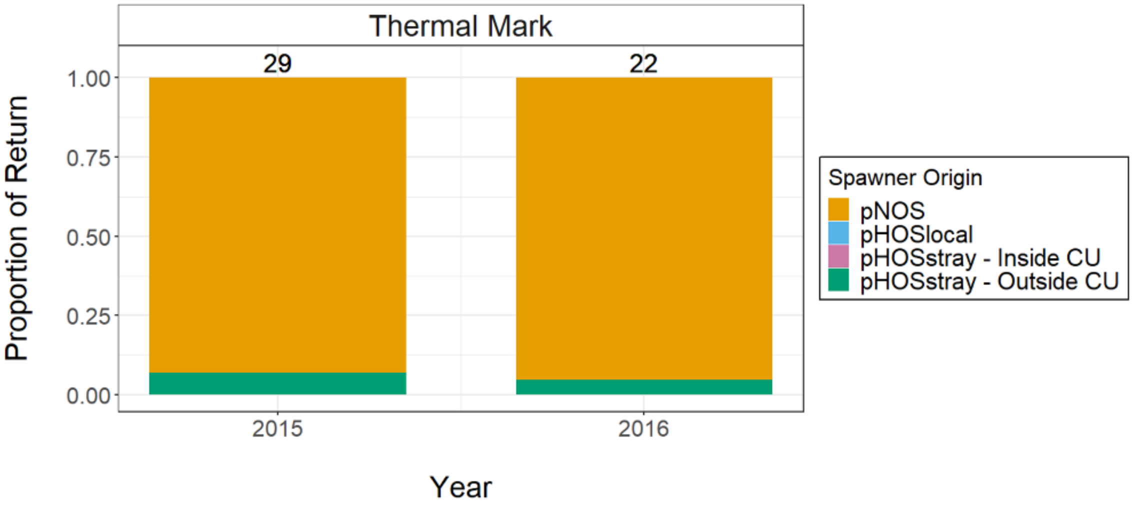

Figure 7.41. Origin of spawners returning to Toquart R between 2015 and 2016 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. As this stock is not thermally marked, no PNI estimates were calculated.

Thornton Cr – Recipient River

Thornton Cr hatchery, based in Ucluelet Inlet, was founded from Robertson Cr hatchery stock in 1982, and was perpetuated through natural returns to Thornton Cr. Release targets from the early 2010s were typically around 300,000 smolts, with the goal of providing harvest opportunities to ocean fisheries as well as a terminal fishery in the Inlet. While no CWT or thermal mark data exist for this population during our time period, genetic analysis of nearby rivers revealed a high stray rate by Thornton Creek Chinook.

7.1.3.3. Nitinat to Sooke (NIT-SKE) – WCVI

The southwestern tip of Vancouver Island—between Nitinat and Sooke Rivers—contains a small number of Chinook Salmon producing rivers, supplemented by local hatcheries. The largest facility, Nitinat R Hatchery, was built in 1980 on the Nitinat River just upstream of Nitinat Lake to enhance various salmon populations for commercial, recreational, and First Nations fisheries. Nitinat R Hatchery also satellite rears Chinook for release in nearby Sarita R and Sooke R. A small CEDP facility—Four Mile Creek—operates on the San Juan R and has supplemented the Chinook populations there since the early 1980s.

Nitinat R Hatchery – Nitinat R donor stock

Between 1998–2021, Chinook reared at Nitinat R Hatchery were primarily identified by thermal marks, but CWTs were used until the 2002 brood year.

CWT recoveries of Nitinat R Chinook were only observed between 1998–2006, following the cessation of CWT marking in 2002. Strays were rarely observed during this period, with the only recoveries being observed in1999 in Robertson Cr and Sarita R, and in 2004, when Nitinat R Chinook were observed in the distant Campbell/Quinsam R system (Table D11).

Thermal mark recoveries of Nitinat R fish across SBC were notably lower than any other facility on the WCVI between 1998 and 2021. The average stray rate for this system was 0.9%. Trends in overall stray rate did not fluctuate substantially over the time period (Figure 7.32), and recoveries were mostly confined to the same CU, with an average outside-CU stray rate of 0.1% (Table D12). This stray rate was far below what was observed for other major production facilities on the WCVI. It is possible that strong environmental homing cues help Chinook home more precisely in this system that flows out to a large brackish, tidal-influenced lake before meeting the ocean, although further work into the role of water chemistry in homing on SBC rivers is necessary to confirm this hypothesis.

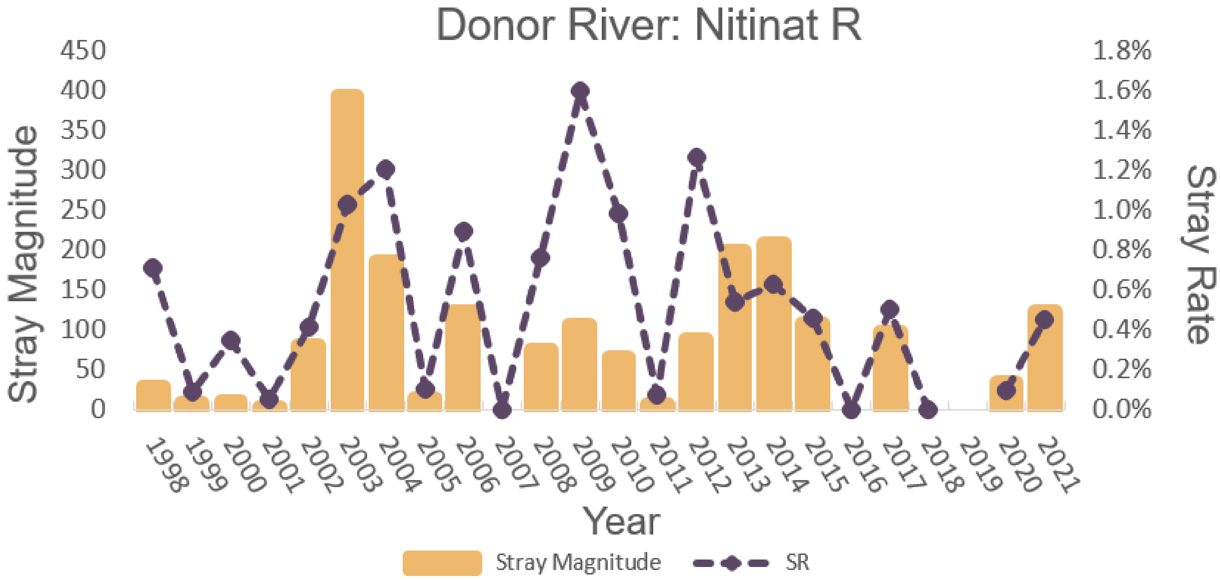

Figure 7.42. Temporal trends in stray rate and magnitude from Nitinat R Hatchery Chinook from thermal mark recoveries in systems sampled across SBC.

Despite releasing between two and three million Chinook annually, thermally marked recoveries suggested that Nitinat R Hatchery only produced an average of 85 strays per year between 1998 and 2021. Of those strays, the majority across years (64%) were recovered in nearby Sarita R, with an additional 15% observed in San Juan R. Beyond these regularly occurring donor-recipient relationships, strays from Nitinat R were rarely, and sporadically observed in low numbers returning to rivers in Nootka Sd, and Barkley Sd (Table D12). Although straying was very low at Nitinat R Hatchery, a few aberrant stray recoveries on the ECVI and adjacent Coastal Inlets were observed—straying to Campbell/Quinsam R, Nanaimo R, and Salmon R/JNST.

Nitinat R – Recipient River

Otolith samples for thermal marks are obtained as a part of the broodstock capture program in Nitinat Lake as well as from in-river sampling and hatchery swim-ins. Additional samples are obtained from terminal fisheries on 'Excess Salmon to Spawning Requirement' (ESSR) licenses in Nitinat Lake.

Annual sample sizes ranged from 48–1,012 during our period of analysis, with an average of 561 Chinook examined for thermal marks each year. Strays were observed returning to Nitinat R in most years of sampling, but $pHOS_{stray}$ rarely exceed 0.01, averaging 0.00 over the time-series (Figure 7.33). Sarita R Chinook were the most regularly observed stock recovered in the Nitinat R, occurring in 9 out of 20 years (Table E29). Straying from the Sarita R stock was expected since rearing of this stock takes place at Nitinat R hatchery nearby; in fact, this level of straying is quite low compared to other populations on the WCVI that employ satellite rearing. Strays from Robertson Cr were also observed in 7 out of 20 years. The only other instance of straying detected by thermal mark in Nitinat R were single recoveries of Chilliwack R hatchery Chinook in 2011 and 2013. These recoveries were anomalous, but represent some of the longest straying distances between donor and recipient populations in our study area. Like Conuma R and Robertson Cr hatcheries on the WCVI, Nitinat is also a large-scale production facility and as such, sees predictably high *pHOS* values year over year. Thermal mark data between 1998 and 2018 revealed *pHOS* values ranging from 0.76–1.00 and *PNI* values ranging from 0.00–0.24, firmly placing Nitinat R Chinook in the Integrated-hatchery designation (Figure 7.33).

Between 1998 and 2006, several Chinook with thermal marks could not be not linked to any hatchery, but were similar to the intended mark applied by Nitinat R hatchery. These Chinook were assumed to have homed correctly due to their high abundance in the return during these early years, and their absence in future years. These recoveries highlight one drawback in using thermal marks as an hatchery-identification tool—the unintended application of an alternate otolith mark.

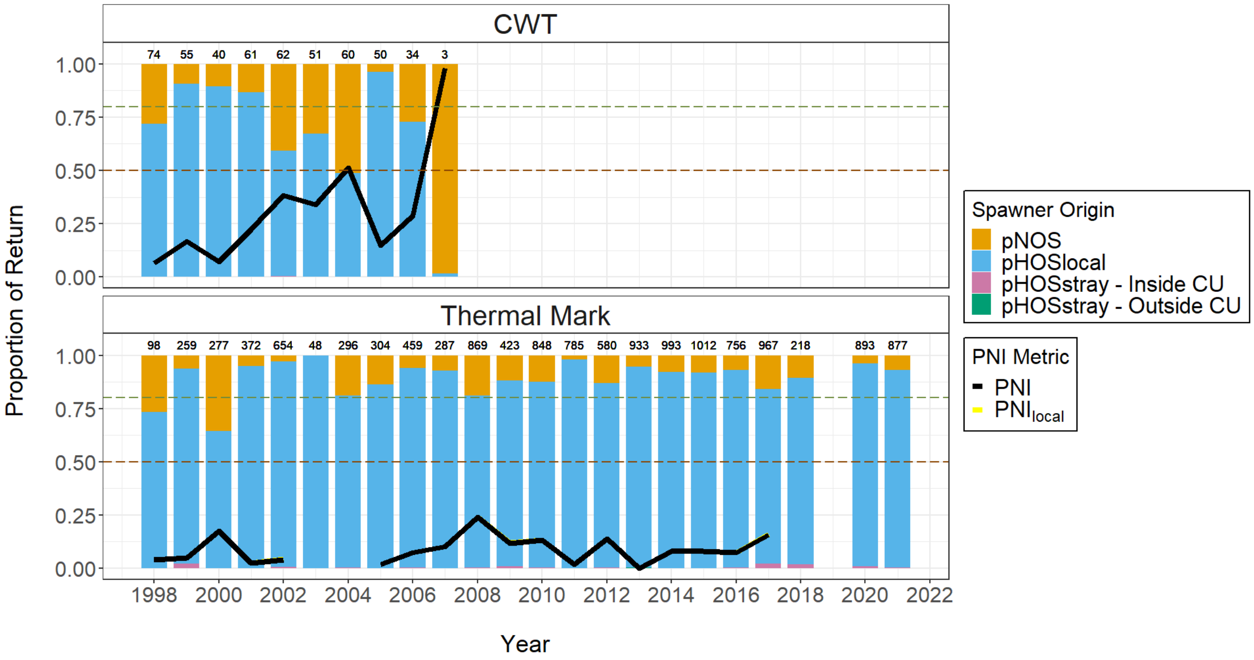

Figure 7.43. Origin of spawners returning to Nitinat R between 1998 and 2021 estimated from CWT and thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs or otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

San Juan R – Recipient River

Four Mile Creek Hatchery is a small CEDP facility that aims to restore historic Chinook populations to San Juan River. Sampling for thermal marks occurred sporadically since 2004, and were primarily obtained in broodstock sampling. In-river sampling for San Juan R Chinook only occurred in 2015 during our period of analysis. In all years, except for 2017, strays were observed returning to San Juan R (Figure 7.34). $pHOS_{stray}$ averaged 0.05 during this time, however this average was driven by an outlying year in 2019 when a reported 344 strays from Spius Cr were allegedly recovered in San Juan R. While this may be possible, the more plausible scenario was that an error in thermal mark application or reading created a spurious result. With this outlying year removed, average $pHOS_{stray}$ in the San Juan R falls to 0.02.

The most commonly observed strays in the San Juan R originated from Nitinat R Hatchery, occurring in five of eight years (Table E31). A single Robertson Cr recovery was observed in 2005 and 2014, and Conuma recoveries were observed in 2006 and 2015. Overall, hatchery strays contributed at low levels to the escapement. *pHOS* values for San Juan R ranged widely from 0.01–0.91 among years, but averaged 0.51 across years. *PNI* values were calculable between 2004–2014, where they averaged 0.58, indicative of an integrated-transition system.

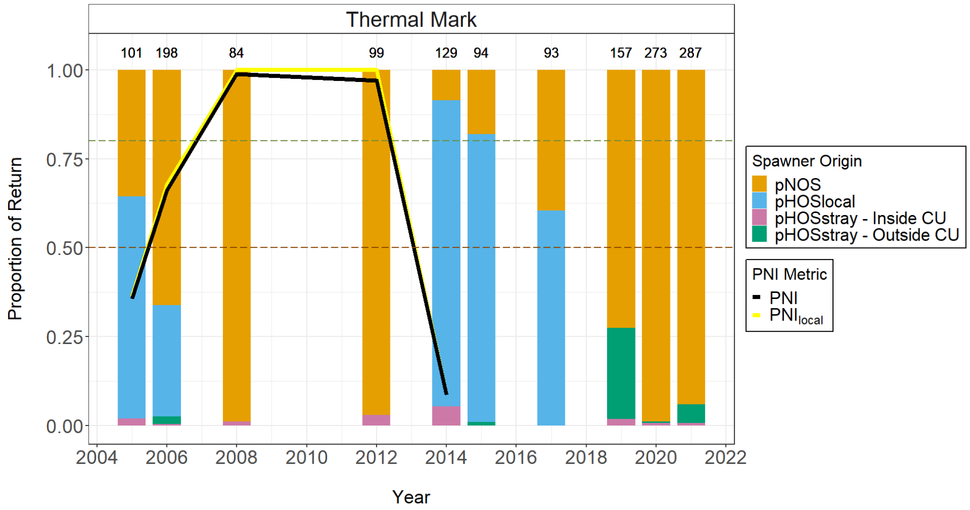

Figure 7.44. Origin of spawners returning to San Juan R between 2015 and 2016 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners (pHOS$_{local}$), strayed hatchery-origin spawners originating from inside the CU (pHOS$_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU (pHOS$_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI$_{local}$) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Sooke R – Recipient River

Sooke R Chinook is a previously extirpated population that is currently enhanced for harvest and rebuilding purposes with Nitinat R-origin fish. Brood are transferred as eggs into the river, or reared as subyearlings in a seapen in Sooke Harbour until their release. Thermal mark samples were collected sporadically between 2005–2016, with consistent annual sampling occurring since 2017. In all years, hatchery-contribution estimates were derived from broodstock samples, as natural escapement to the river remains low. Average *pHOS*$_{stray}$ values for this system were 0.05, and all strays originated from inside the CU (Figure 7.35). Nitinat R strays were observed in 6/8 years sampled, and Robertson Cr strays were observed in 4 years (Table E32).

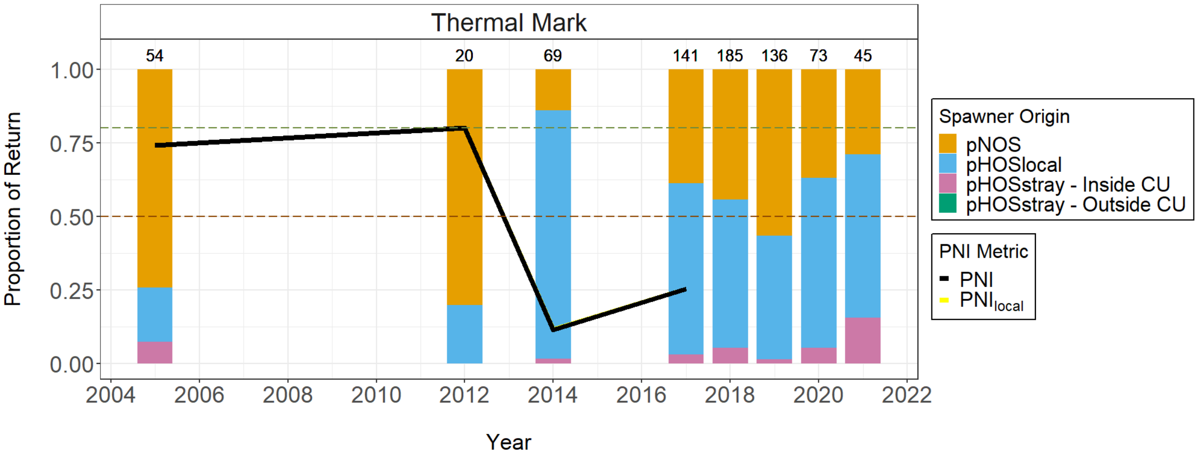

Figure 7.45. Origin of spawners returning to Sooke R between 2004 and 2021 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

7.2. STOCK MANAGEMENT UNIT: LOWER GEORGIA STRAIT CHINOOK SALMON

7.2.1. Conservation Unit: CK-22 – East Vancouver Island-Cowichan & Koksilah

In CK-22 (East Vancouver Island-Cowichan & Koksilah), Chinook occur primarily in the Cowichan and Koksilah Rivers and their tributaries (Figure 7.36). In this analysis, we report recoveries for only the Cowichan R stock, which represents ~98% of the total average return to the CU. Cowichan R is the southern-most enhanced system on the ECVI. The hatchery facility originated in 1978 in partnership with Cowichan Tribes for enhancement, stock assessment, and economic purposes in the region, with an annual egg-target of 3 million. They are marked using both thermal and CWT methods. $pHOS_{stray}$ and $pHOS_{stray,OCU}$ for this CU both averaged 0.02 (based on thermal mark results), and *PNI* values for indicated an integrated-transition population (*PNI* between 0.5 and 0.8).

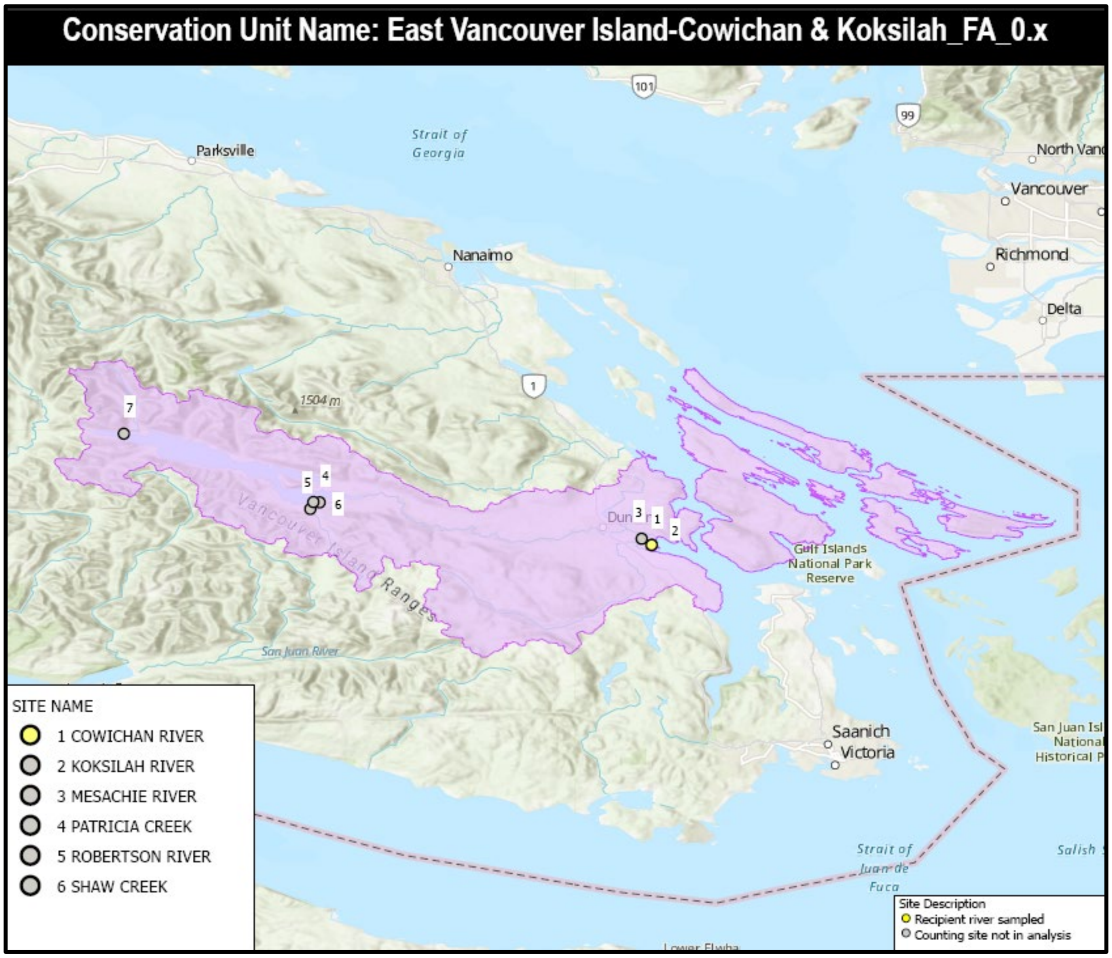

Figure 7.46. Boundary map of the CK-22 Conservation Unit (East Vancouver Island-Cowichan & Koksilah), including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

Cowichan R Hatchery – Cowichan R donor stock

Cowichan R Chinook have been enhanced for over four decades and are currently listed as an indicator stock for Chinook in the Lower Georgia Strait. CWT results for Cowichan R Hatchery Chinook suggest that straying occurred at an average rate of 7.2% across years, with individual years as high as 29.2% (Table D13). However, since 2016, stray rates have declined, falling to an average of 1% between 2016–2021 (Figure 7.37).

Thermal mark recoveries from 2001–2021 show a low rate of straying at 1.5%, driven solely by stray recoveries from Nanaimo R in 2009, 2010, 2016 and 2017 (Table D14). However, using thermal mark results to assess straying from ECVI hatcheries like Cowichan R may be inappropriate as most facilities do not thermally mark their releases, and as such do not sample for them. Thus, on the ECVI, CWT results provide the most accurate indication of stray rate and contribution.

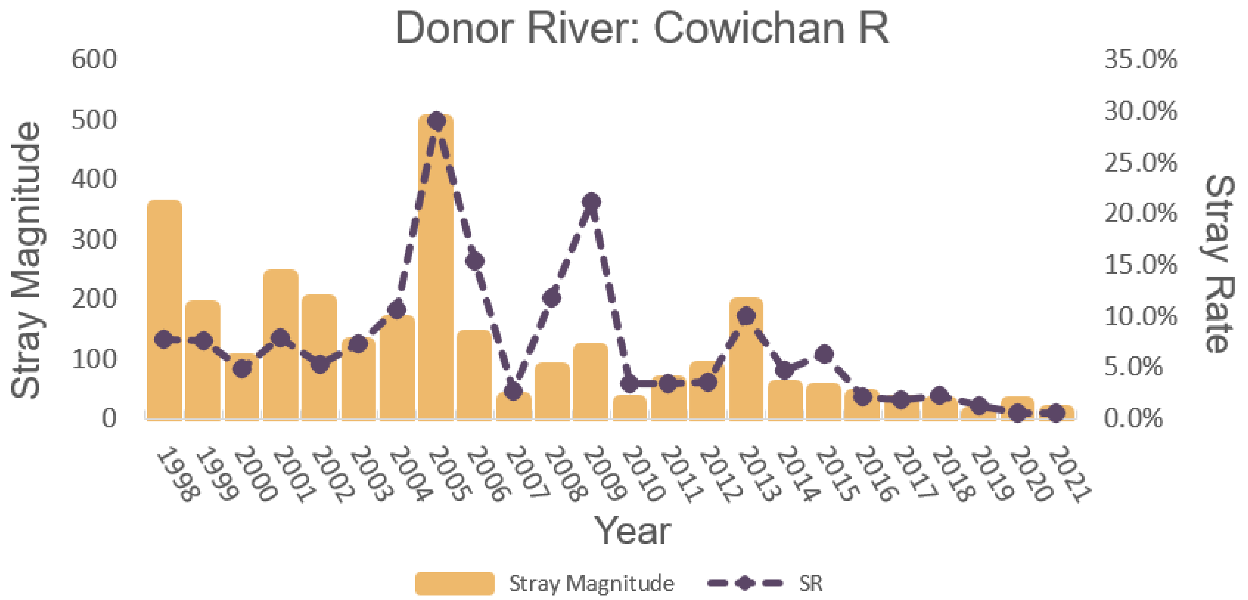

Figure 7.47. Temporal trends in stray rate and magnitude from Cowichan R Hatchery Chinook calculated from CWT recoveries in systems sampled across SBC.

The magnitude of Chinook hatchery strays from Cowichan R, estimated from CWTs, averaged 118 individuals between 1998–2021 (Table D13). The greatest number of strays occurred in 2005, with an expanded 497 individuals sampled across the ECVI region. Cowichan R strays were observed returning to Big Qualicum R in every year sampled, and ranged from 6 to 232 expanded individuals. Strays were also observed returning to Little Qualicum R in almost every year until sampling stopped following the cessation of marking for Little Qualicum R Chinook in 2002. Puntledge R also saw regular recoveries of Cowichan R hatchery Chinook throughout the time series, although recent years showed much fewer strays in the escapement compared to years 1998–2006. Sporadic sampling in Lower and Middle Fraser systems also revealed Cowichan R strays, although detections were not common (Table D13).

While Cowichan R hatchery has seen a recent drop in stray rates, rearing and hatchery practices may have led to historically high straying from this facility. The most notable practice that may have driven increased straying from this facility is groundwater use during early rearing. This practice is suggested to impair sequential imprinting of juveniles (Labelle 1992), and is employed at this facility. Further, research has shown that the presence of copper and heavy metals in rearing water may inhibit olfactory capabilities and affect the ability to imprint correctly (Baldwin et al. 2011). It is possible that the proximity of Cowichan R to a nearby pulp and paper mill may have resulted in a degree of olfactory failure from increased exposure to heavy metals during early rearing, although a more in-depth analysis of rearing water quality is needed to confirm this.

Cowichan R – Recipient River

CWT recovery data from 1998 to 2021 indicated that an average of 99% of returning Chinook sampled were of Cowichan R-origin (Figure 7.38). Despite this low proportion, regular stray recoveries, small in magnitude were observed (Table E34). Chinook from the Chemainus R stock (only ~30 km from Cowichan R) were the most regularly observed stray population, occurring in 8/24 years. Recoveries from Big Qualicum R and US hatcheries made up the next most regular observance of strays, occurring in seven and six years respectively.

Thermal mark results provided similarly low average *pHOS*$_{\text{stray}}$ values, albeit slightly higher at 0.02, compared to 0.01 for CWT recoveries. Strays originating from the WCVI were more commonly observed in thermal mark recoveries, which is expected as it is the principal mark applied in this region.

Strays from Robertson Cr were observed in 2005, 2008, 2012, and 2014–2016 in the thermal mark data and a single Burman R fish was recovered in 2010 (Table E33). Outside of these occurrences, all stray recoveries in the thermal mark data were of ECVI origin.

Long-term averages of *PNI* derived from either CWT or thermal mark data are indicative of an integrated-hatchery system (*PNI* between 0.50 and 0.80), however recent CWT data suggests that *PNI* has been > 0.80, indicative of an integrated-wild population, in each year since 2015. This, along with near-zero $pHOS_{\text{stray}}$ values since 2016, suggests that Cowichan R is very minimally influenced by hatchery-origin Chinook.

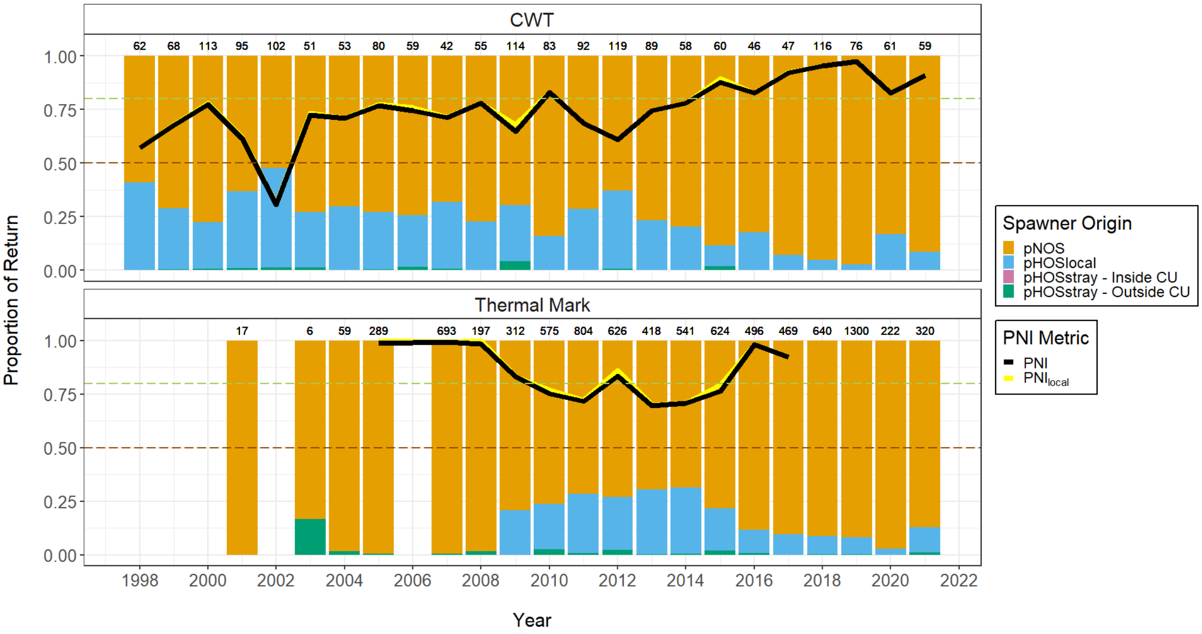

Figure 7.48. Origin of spawners returning to Cowichan R between 1998 and 2021 estimated from CWT and thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs or otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

7.2.2. Conservation Unit: CK-25 – East Vancouver Island-Nanaimo & Chemainus

In CK-25 (East Vancouver Island-Nanaimo & Chemainus), Chinook occur primarily in the Nanaimo R (fall run only), and Chemainus R, among other smaller tributaries (Figure 7.39). In this analysis, we report on both of these stocks, which represent an estimated 98% of the average escapement to the CU. The Nanaimo R contains a CEDP hatchery facility initiated in the late 1970s to provide harvest opportunities to local fishers, and presently aims to release upwards of 400 000 smolts annually. Populations in this CU are marked with thermal marks, but have historically been marked with CWTs. $pHOS_{\text{stray}}$ and $pHOS_{\text{stray,OCU}}$ for this CU averaged 0.08 and 0.00 respectively (based on thermal mark results), and *PNI* values—calculable only for the Nanaimo R—indicated an integrated-hatchery population (*PNI* < 0.5).

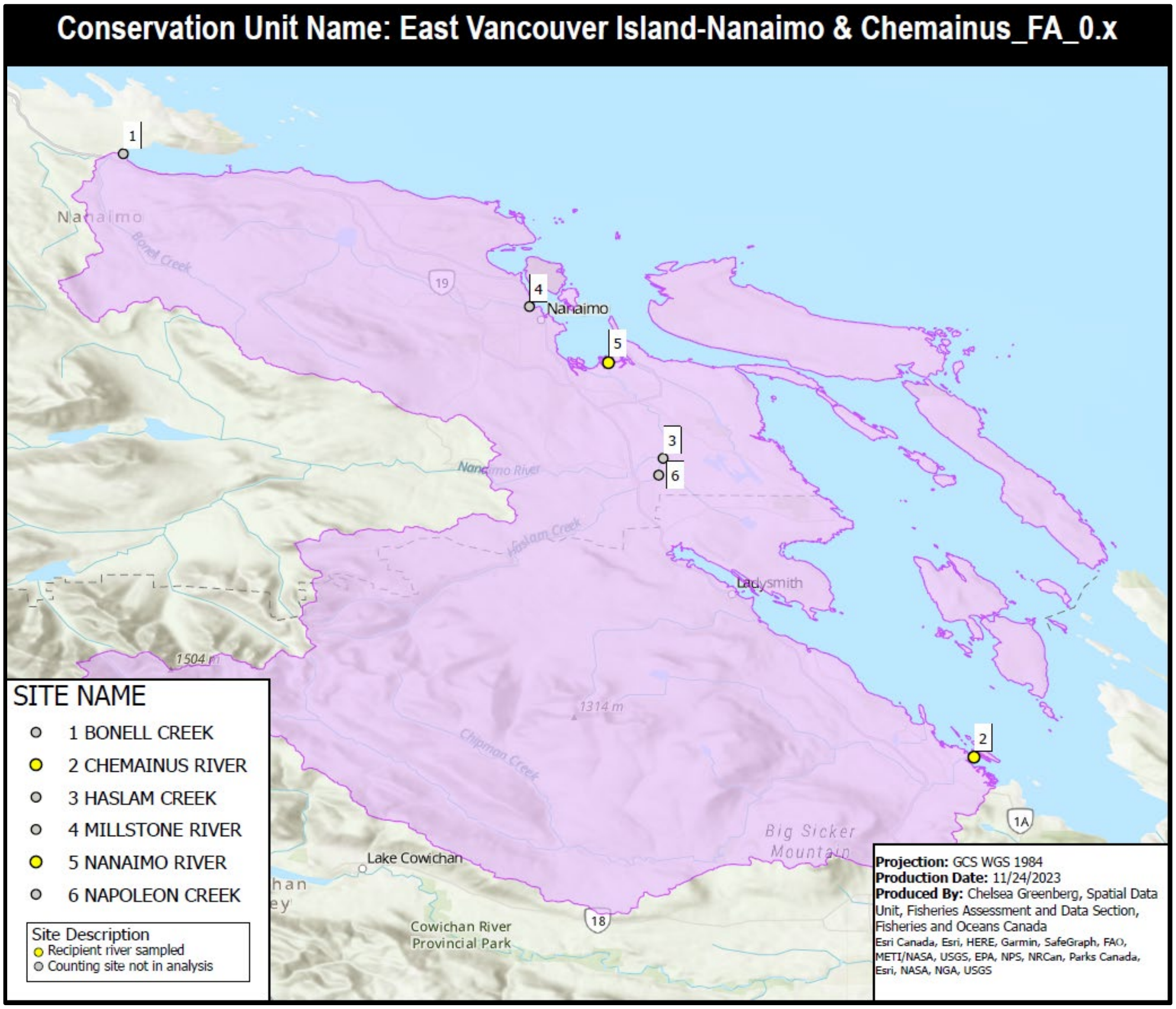

Figure 7.49. Boundary map of the CK-25 Conservation Unit (East Vancouver Island-Nanaimo & Chemainus), including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

Nanaimo R Hatchery – Nanaimo R donor stock

Nanaimo R is one of two systems on the ECVI with two enhanced, temporally distinct populations encompassing the fall and summer run. While some ‘temporal straying’ does occur (summer run fish returning in the fall or vice versa), it is not the core focus of this work. Chinook that returned to their home river as part of a different run-timing were included as homed salmon in this analysis, although the magnitude of recoveries across run-timing is still described. Nanaimo R was CWT marked up until the mid-2000s, before switching to thermal marks, so results are presented for both data types.

Fall-run population

For the fall-run population, CWT recovery data from 1998 to 2008 suggested an average stray rate of 4.0% across years, all of which occurred outside the CU of origin. Straying magnitude averaged 32 individuals across years, with the most consistent recoveries observed in Puntledge R, another hatchery-supplemented system roughly 100 km from the home river (Table D15). As is commonly observed in other ECVI systems, sporadic stray recoveries across the region were detected, but no other consistent trends year-over-year were observed.

Thermal mark data available between 2009 and 2018 revealed a low average stray rate of 0.7% (Figure 7.40), with all strays recovered outside the CU of origin. Strays to Cowichan R were observed in seven years over the time series (Table D16), but only exceeded 1% of H_{TOT} in 2010 and 2012. Stray recoveries were only detected in systems that regularly sample for thermal marks. Thus, strays into systems that do not sample otoliths (e.g., Big Qualicum R and Puntledge R) may be under-represented during this period.

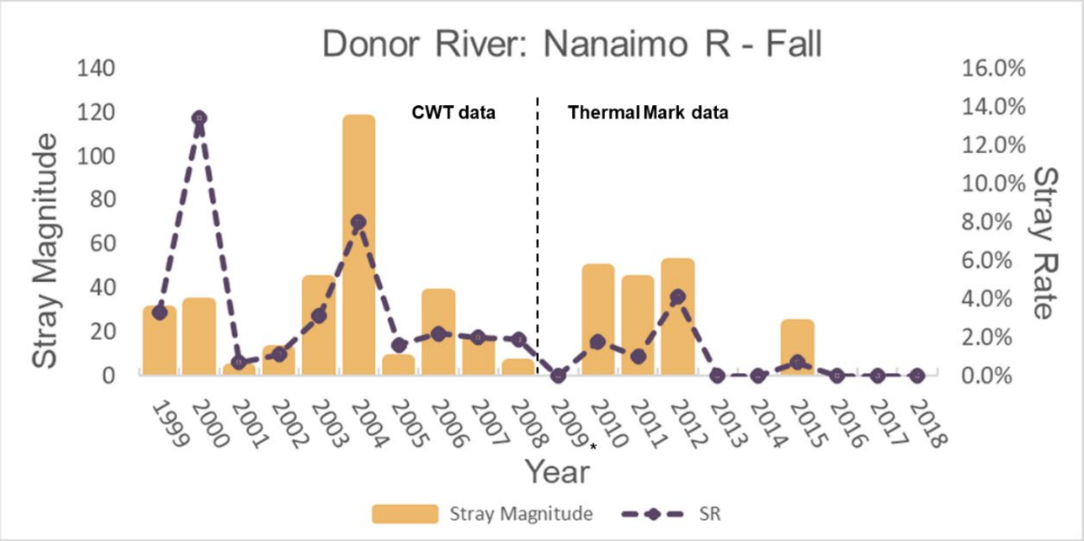

*Figure 7.50. Temporal trends in stray rate and magnitude from Nanaimo R - Fall Hatchery Chinook sampled in systems sampled across SBC calculated from CWT recoveries between 1998–2008, and from thermally marked otolith recoveries between 2009–2018. * indicates the switch from CWT to thermal mark data used.*

Nanaimo R – Recipient River

Fall-run population

CWT data available from 1998 to 2008 showed an average $pHOS_{stray}$ of 0.05 between 1998–2008, with maximum values occurring in 2005 and 2008 of 0.12 and 0.08 respectively (Figure 7.41, Table E36). Like Cowichan R, Chinook of Chemainus R-origin were the most commonly observed as strays, occurring in 7 of 11 years sampled. Cowichan R and Big Qualicum R hatchery strays were also common. Overall, CWT data suggested that straying into the Nanaimo R may have occurred at a slightly elevated rate compared to other, nearby systems between 1998 and 2008.

Thermal mark recoveries from 2004 to 2018 suggest that strayed Chinook rarely made up more than 1% of total samples returning to Nanaimo R (Table E35). An expanded 74 Robertson Cr fish in 2004, and 55 Nitinat R strays observed in 2008 are the only occasions in which WCVI strays were recorded returning to Nanaimo R. Other than a few sporadic detections from ECVI systems in 4/15 years, the rest of the escapements were all of Nanaimo R – Fall origin.

PNI estimates derived from CWT data averaged 0.58 between 1998–2008, indicative of an integrated-transition system. Recent thermal mark estimates however, suggest the Nanaimo R – Fall population may now fall under an integrated-hatchery designation, with values averaging 0.25 between 2009–2018 (Figure 7.41).

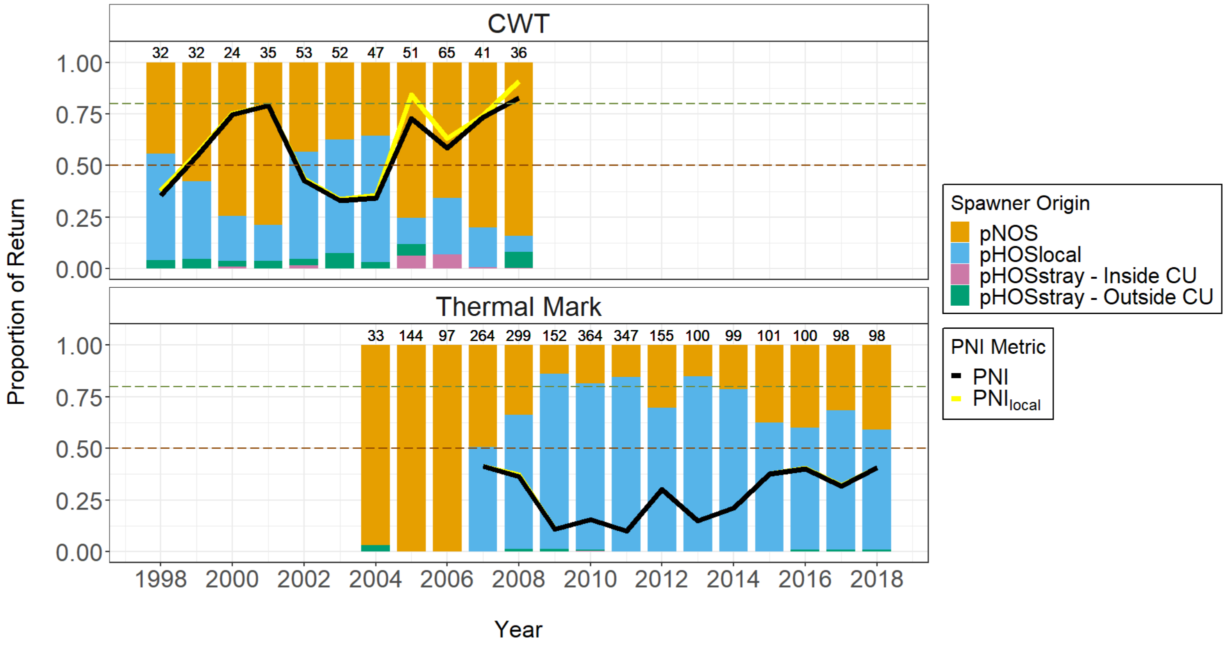

Figure 7.51. Origin of spawners returning to Nanaimo R (Fall Run) between 1998 and 2018 estimated from CWT and thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs or otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

7.3. STOCK MANAGEMENT UNIT: MIDDLE GEORGIA STRAIT CHINOOK SALMON

7.3.1. Conservation Unit: CK-20 – Southern Mainland-Georgia Strait

In CK-20 (Southern Mainland-Georgia Strait), Chinook occur in many coastal systems, very few of which are regularly monitored by DFO. Of 40 sample sites listed in NuSEDS for this CU (Figure 7.42), we report recipient river data for four, as well as Capilano R, a transplanted population that is enhanced within the bounds of this CU. Based on average escapements for rivers in the CU, we estimate that these systems account for 42% of the total escapement to the CU—a significant data gap. Stocks that spawn in the Squamish River watershed are all reared at Tenderfoot Creek Hatchery, and between 1998–2021, sampling occurred only sporadically, on the natural spawning grounds. As most sampling events took place on natural spawners, we do not report *PNI* values, and caution the use of these data to inform trends in straying.

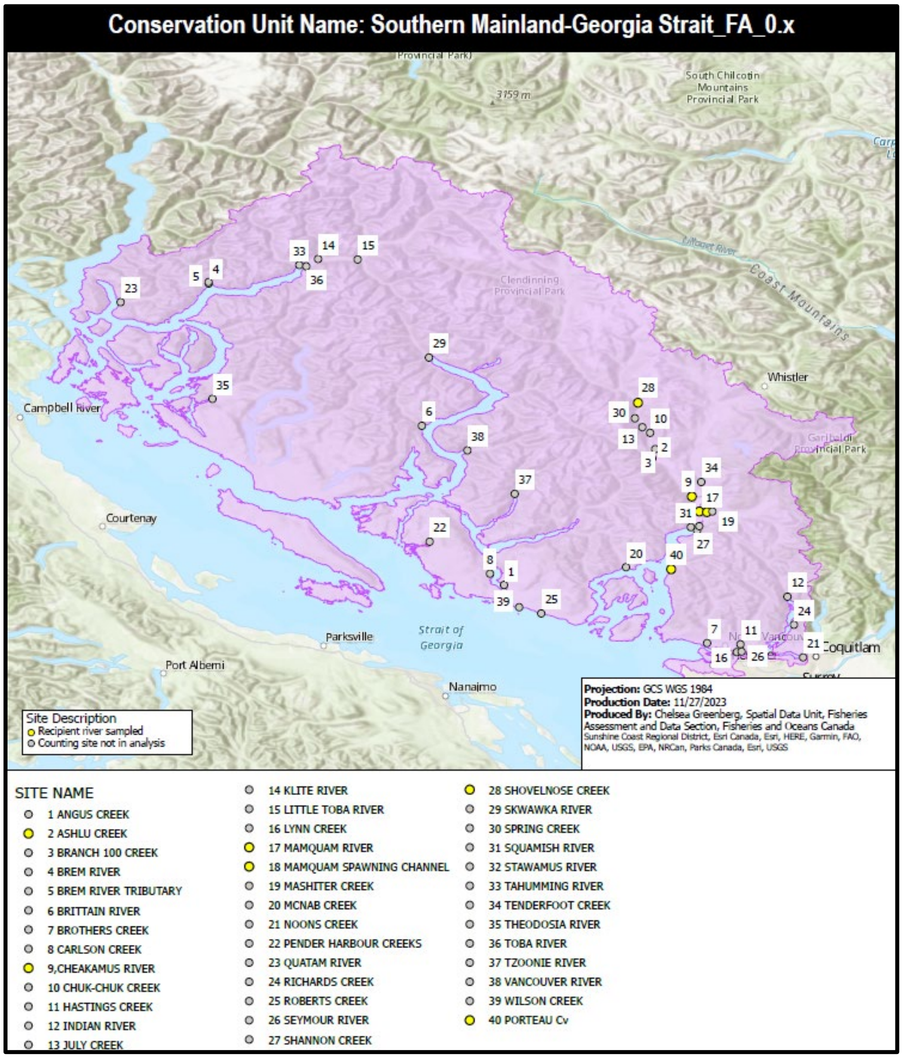

Figure 7.52. Boundary map of the CK-20 Conservation Unit (Southern Mainland Georgia Strait) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

Tenderfoot Cr Hatchery – Squamish R donor stocks (Ashlu Cr, Cheakamus R, Mamquam R, Shovelnose Cr)

The Squamish R system contains four enhanced Chinook stocks: Ashlu Cr, Cheakamus R, Mamquam R, and Shovelnose Cr. Chinook from these stocks were not observed as strays in SBC between 2009 and 2021, except for one observation in Capilano R in 2020. Mixed stock Squamish R releases from Tenderfoot Hatchery reared in the Porteau Cove seapen were observed straying into Campbell/Quinsam R and Capilano R in 2001, with a stray rate of 3.4% in that year. No other Chinook reared in this seapen group were observed as strays between 1998–2001, when the Porteau Cv seapen was in operation.

Squamish R – Recipient Rivers (Ashlu Cr, Cheakamus R, Mamquam R, and Shovelnose Cr)

In accordance with the definition of hatchery straying outlined in Section 2, a Chinook that originated and returned to any of Ashlu Cr, Cheakamus R, Mamquam R, or Shovelnose Cr would not be considered strays. Escapement sampling for CWT-marked fish in these rivers has occurred since 2018, and some data exist for earlier years in Cheakamus R and Mamquam R.

Between 2018 and 2021, Ashlu Cr sampling revealed no CWT recoveries from outside of the Squamish R system. Recoveries from rivers the Squamish R system were observed originating from Cheakamus

R and Shovelnose Cr Chinook, but not Mamquam R. *pHOS* values ranged between 0.31 and 0.62 between 1998 and 2021, alternating annually between high and low values. Sampling in Shovelnose Cr between 2018 and 2021 revealed no strays from outside the Squamish R system. Similarly to Ashlu Cr, occasional recoveries originating from Cheakamus R and Ashlu Cr were observed returning to Shovelnose Cr, but not from Mamquam R. *pHOS* alternated between high and low values in Shovelnose Cr, but showed the opposite pattern to Ashlu Cr, with low hatchery contributions in 2018 and 2019 (0.36 and 0.24 respectively) compared to higher values in 2019 and 2021 (0.66 and 0.64 respectively). Mamquam R sampling between 2017 and 2021 revealed one Cheakamus R-origin fish in each year except 2021. *pHOS* values in Mamquam R ranged between 0.17 and 0.68, but did not show the same oscillatory pattern observed in Ashlu Cr and Shovelnose R.

Sampling in Cheakamus R occurred between 2009–2011, and from 2016–2021. Strays from the Porteau Cv release group, a mixed-stock Squamish-origin population reared at Tenderfoot Cr Hatchery, were observed returning to Cheakamus R between 2009 and 2011, and comprised the majority of expanded CWT recoveries during that time. Historical escapement sampling of this system revealed that the Porteau Cv rearing group, being of multiple origins and reared in a seapen, were the most substantial source of stock intermixing between 1988 and 1992, likely due to extensive hybridization and low affinity to the natal site (Schubert 1993). The last seapen-reared cohort from Porteau Cv was released in 2012, and the last CWT-marked group was released in 2007, explaining why recoveries from this stock were not observed in Cheakamus R after 2011. The only outside-CU stray recovery observed in this system originated from Puntledge R in 2017, representing an expanded two fish in the escapement. *pHOS* values for Cheakamus R were relatively low between 2009–2011 averaging 0.29, compared to an average of 0.62 between 2017–2021.

Overall, the genetic impact of strays on Squamish R stocks appears to be low, however low sampling rates in these rivers historically means that uncertainty of estimates is high. Low returns and a high hatchery contribution in most Squamish R tributaries suggests that genetic and selective broodstock management will be important facets of rebuilding these populations. Continued and expanded escapement monitoring for these populations is also recommended to further assess the risk posed by both local and stray hatchery fish to the Squamish R system.

Capilano R Hatchery – Capilano R / Chilliwack R donor stock

Capilano R, is a coastal system located outside of Metro Vancouver, and has not historically sustained a notable return of natural-origin Chinook. However, since the 1970s, a naturalized population founded from Big Qualicum R stock have been reared at Capilano R Hatchery to support local marine and freshwater fisheries in the region. CWT marking of this population has occurred in two periods, between 1998–2004, and from 2013–present. In both periods, all Capilano R strays were recovered in the Lower Fraser region straying into Chilliwack R, Harrison R and Stave R. The annual magnitude of strays originating from Capilano R averaged 52 individuals across our time-series, but reached a high of 119 expanded recoveries in 2021 (Table D17). CWT recoveries since 2015 suggest an increased average stray rate, occurring regularly above 4% (Figure 7.43). This trend may be expected given the genetic heritage shared by these populations. The potential genetic impacts to the Chilliwack R are low, itself being a transplanted Harrison R population, however the implications of Capilano R Chinook straying into the Harrison R, a primarily natural-origin population, may be more significant. Continued monitoring of both donor and recipient populations and the removal of strays will be important to minimize future negative impacts from Capilano R strays.

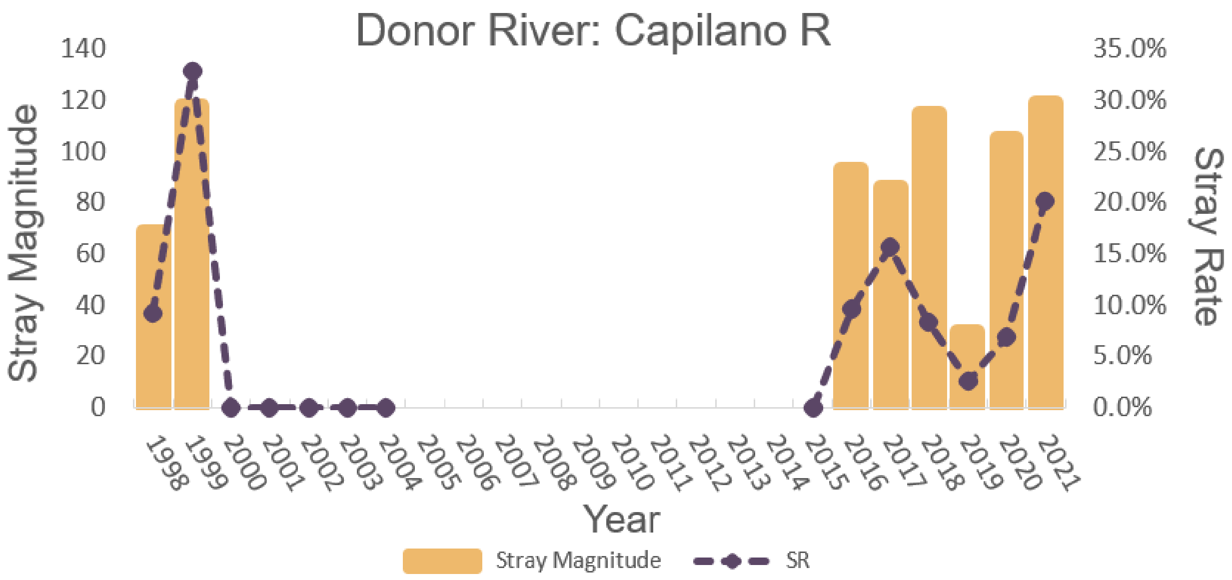

Figure 7.53. Temporal trends in stray rate and magnitude from Capilano R Hatchery Chinook calculated from CWT recoveries in systems sampled across SBC.

Capilano R – Recipient River

CWT sampling for Chinook in Capilano R occurred either during broodstock sampling or natural spawner enumeration below the dam. In addition to the naturalized Capilano R stock, Chilliwack R transplants were released with CWTs during this time. As per the definition of straying outlined in the literature (Candy and Beacham 2000), and described in Section 2, any Chinook released in the Capilano R system would be considered to have homed correctly if it returned to spawn there regardless of its stock of origin. CWT sampling occurred in two periods: 1998–2004 and 2015–2021 (Figure 7.44). During the earlier period, two stray recoveries from Cowichan R were observed in 1998, representing an expanded 48 Chinook, and in 1999, one stray from Nanaimo R and two from Porteau Cv were observed, representing an expanded 1 and 22 Chinook respectively (Table E38). The remainder of Chinook that returned in these years were either of naturalized Capilano R-origin, or were transplants from the Chilliwack R stock. Strays were recovered in 3/7 years in the second period of CWT sampling in Capilano R. In 2015, two stray recoveries from each of Robertson Cr and Big Qualicum R were recovered representing an expanded 13 and 6 fish respectively. In 2016 one Cowichan R Chinook stray was recovered, and in 2020 two Cheakamus R Chinook were observed in Capilano R sampling as strays. Other than these observations, all recoveries made in Capilano R since 1998 either originated from the original Capilano R transplanted population, were of Chilliwack R stock released into the Capilano R or were released from the Sandy Cv seapen (located < 10 km from the outlet of the river).

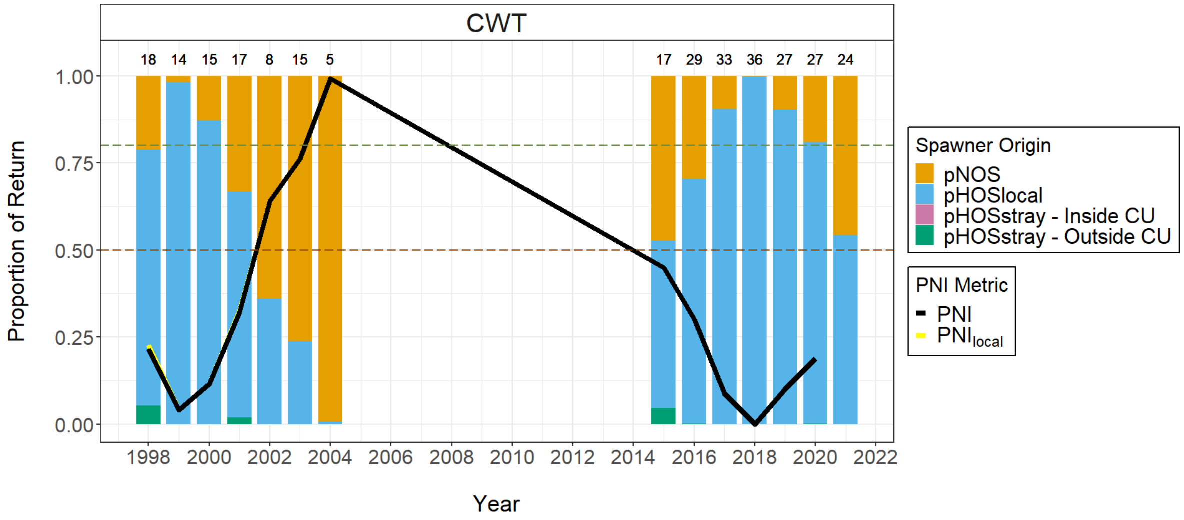

Figure 7.54. Origin of spawners returning to Capilano R between 1998 and 2018 estimated from CWT recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

7.3.2. Conservation Unit: CK-27 – East Vancouver Island-Qualicum & Puntledge

In CK-27 (East Vancouver Island-Qualicum & Puntledge), Chinook occur primarily in three systems: Big Qualicum R, Little Qualicum R, and Puntledge R, all of which are enhanced, representing approximately 96% of average escapement to the CU. Two major OPS facilities, Big Qualicum R Hatchery and Puntledge R Hatchery, release a combined 4.65 million Chinook smolts annually in this area. Both of these hatcheries CWT mark their releases and do not employ thermal marks. $pHOS_{stray}$ and $pHOS_{stray,OCU}$ for this CU averaged 0.02 and 0.01 respectively, and average *PNI* values for each system (n=3) indicated integrated-hatchery populations (*PNI* < 0.5).

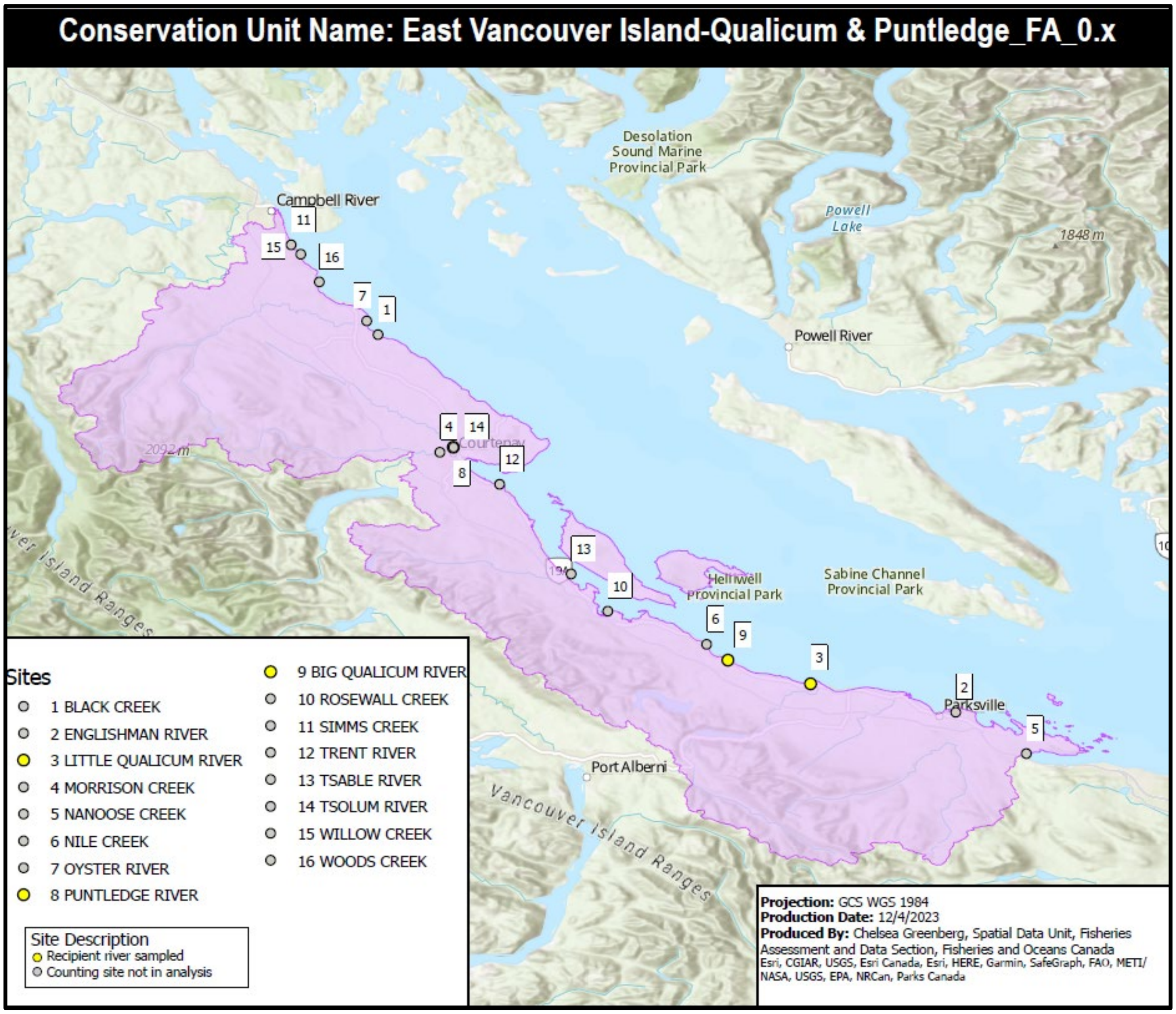

Figure 7.55. Boundary map of the CK-27 Conservation Unit (East Vancouver Island-Qualicum & Puntledge) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

Big Qualicum R Hatchery – Big Qualicum R donor stock

Expanded CWT recoveries from Big Qualicum R Hatchery Chinook across SBC revealed an average annual stray rate of 1.6% (Figure 7.46).

Strays were most often observed in nearby rivers that occupy the same CU, namely Little Qualicum R and Puntledge R (Table D18). The majority of strays were observed in Little Qualicum R prior to the ending of marking there in 2002. This donor-recipient stray relationship may be expected given that Little Qualicum R Chinook were originally founded from Big Qualicum R brood. Marking of the Little Qualicum R population stopped in 2002 due to an observed overlap with Big Qualicum R population dynamics, which suggested that it would be redundant to mark this stock for assessment purposes. In recent years, Little Qualicum R Hatchery has resumed CWT marking and sampling of the stock, and strays are once again being observed (Table D15). Due to the close genetic relationship of these two populations, the potential impacts that this straying relationship pose are minimal.

Outside-CU straying occurred at a rate of 0.7% averaged across years. The majority of these strays were recovered in the ECVI region at hatcheries with high sampling rates (Campbell/Quinsam R, Nanaimo R and Cowichan R) with two instances of recoveries occurring outside of the ECVI in each of 1999 and 2015 (Table D18). The magnitude of strays observed originating from Big Qualicum R averaged 76 individuals across years. Given that Big Qualicum R is a large production facility that releases nearly 3 million Chinook annually, it is notable that they have maintained such a low stray rate in most years since 1998.

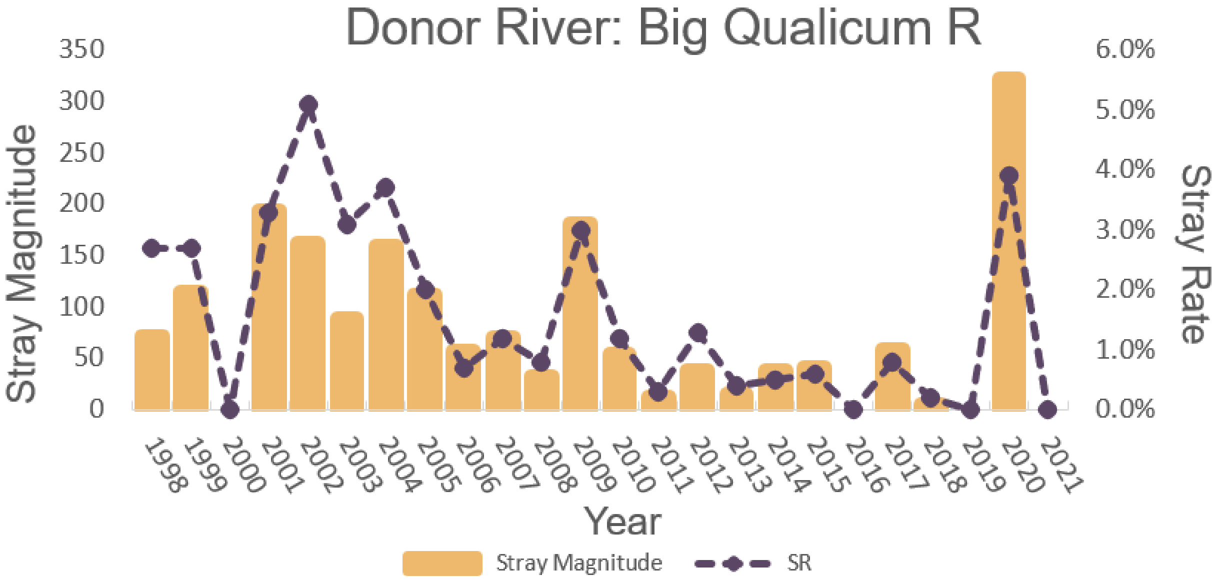

Figure 7.56. Temporal trends in stray rate and magnitude from Big Qualicum R Hatchery Chinook calculated from CWT recoveries in systems sampled across SBC.

Big Qualicum R – Recipient River

Big Qualicum R is home to one of the earliest enhancement projects undertaken in BC and has been producing hatchery Chinook since 1970. A portion of the population is marked with CWTs each year, and no thermal mark application or sampling has taken place.

pHOS and *PNI* estimates for Big Qualicum R indicated an integrated-hatchery system in all years sampled between 1998–2021 (Figure 7.47). Between 1998–2005, $pHOS_{stray}$ was high, averaging 0.09, with strays originating mostly from Little Qualicum R (Table E39). In contrast, between 2006–2021, $pHOS_{stray}$ fell to an average of 0.01, however, $pHOS_{local}$ remained high. One potential explanation for the decline in $pHOS_{stray}$ may be the cessation of CWT marking in Little Qualicum R during the mid-2000s. It is possible that recoveries of Little Qualicum R Chinook continued after 2006, but could not be identified. Thus, the true value of $pHOS_{stray}$ to Big Qualicum R may be higher than reported here.

It should also be noted that between 2000–2002, several CWTs from the stock ‘Big Qualicum + Little Qualicum” were observed, indicating a cross between Little and Big Qualicum populations. In this analysis, these fish were determined to have homed correctly if they returned to either system. Strays from Cowichan R were observed in Big Qualicum R in every year sampled, but averaged only 1% of the total escapement. Strays from US hatcheries were recovered in 21/24 years sampled, but represented only 0.1% of total escapement (Table E39). Strays from Campbell/Quinsam R were also recovered in most (19/24) years, representing 0.8% of escapement, followed by strays from Puntledge R and Chemainus R which accounted for an average of 0.4% and 0.1% of annual escapements respectively.

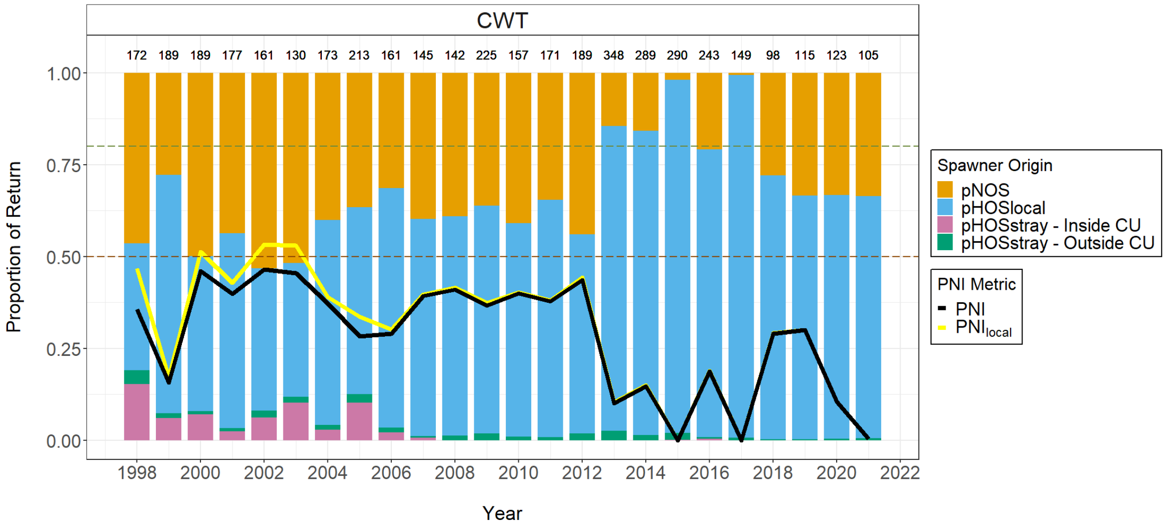

Figure 7.57. Origin of spawners returning to Big Qualicum R between 1998 and 2021 estimated from CWT recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Little Qualicum R – Recipient River

Little Qualicum R has been enhanced since 1979, founded from transplanted Big Qualicum R brood. Returning adults are enumerated annually in a spawning channel on the river. CWT marking was employed until the early 2000s, and marks were recovered until 2006.

$pHOS_{stray}$ was consistently low between 1998–2007, averaging 0.02 (Figure 7.48). Average $pHOS_{stray,OCU}$ was 0.00, and when observed, was comprised mostly of Cowichan R strays (Table E40). Similar to Big Qualicum R, returns that originated from crosses between Big and Little Qualicum Rs were deemed to have homed correctly. These crosses accounted for 2–21% of the total return between 2000 and 2003. Big Qualicum R strays were observed in each year sampled, except for 2000, but never exceeded 4% of total escapement. Sporadic stray recoveries were detected from all other ECVI hatcheries between 1998–2006, but no system other than Big Qualicum R ever accounted for >1% of samples. In 2001 and 2002, CWTs were recovered from US hatcheries, and in 2001, an expanded 10 Chinook from San Juan R on the WCVI were observed, but apart from these observations, no Chinook from outside the ECVI were detected.

PNI estimates between 1998–2004 designated Little Qualicum R as an integrated-hatchery system (<0.50), however estimates between 2005–2006 were much higher. This was likely the result of eliminating CWT-marking in the mid-2000s and is not indicative of an actual increase in natural-origin influence.

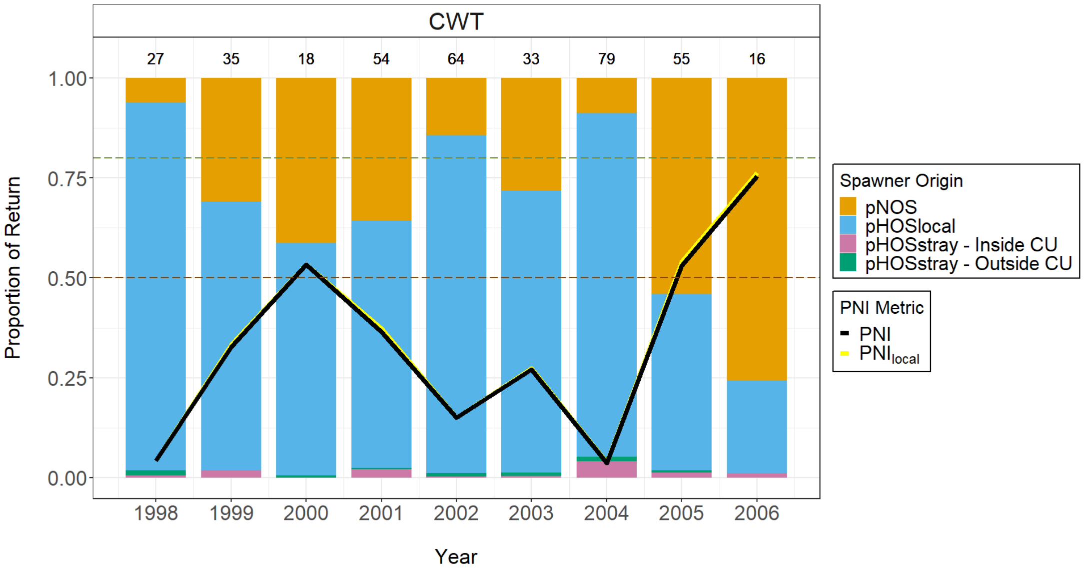

Figure 7.58. Origin of spawners returning to Little Qualicum R between 1998 and 2020 estimated from CWT recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners (pHOS$_{local}$), strayed hatchery-origin spawners originating from inside the CU (pHOS$_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU (pHOS$_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI$_{local}$) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Puntledge R Hatchery – Puntledge R donor stock

Puntledge R supports multiple species of Pacific salmon, including two temporally and genetically distinct runs of Chinook that return in either the Fall or Summer. The Puntledge R hatchery was initiated to rebuild both of these populations following historic low abundances occurring as a result of damming at the outlet of Comox Lake in 1912.

Fall-run population

Puntledge R Hatchery enhances both fall and summer runs of Chinook Salmon and marks a portion of both populations with CWTs. Fall-run Chinook recoveries revealed an average stray rate of 1.2% between 1998–2021, with abnormally high stray rates occurring in 2007, 2008, and 2010 (Figure 7.49). Outside-CU stray rates were nearly identical to total stray rates, with most recoveries occurring in Nanaimo R and Campbell/Quinsam R (Table D19).

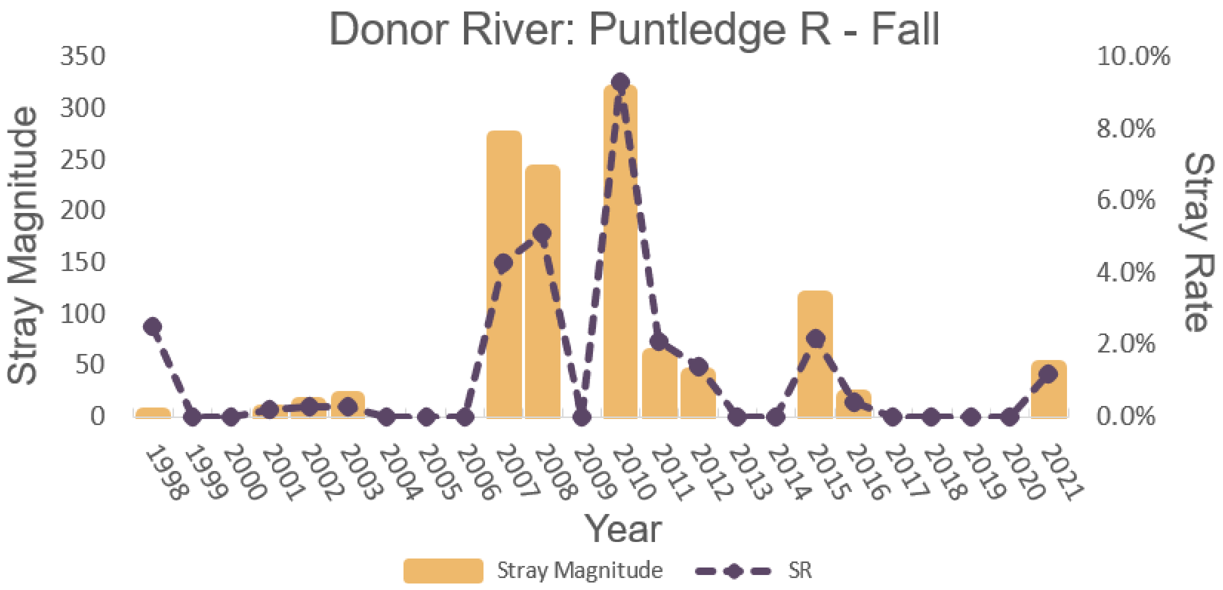

Figure 7.59. Temporal trends in stray rate and magnitude from Puntledge R - Fall Hatchery Chinook calculated from CWT recoveries in systems sampled across SBC.

Puntledge R – Recipient River

Fall-run population

Average *pHOS*$_{\text{stray}}$ from Puntledge R (Fall run) was very low at 0.01; strays only occurred as a high proportion of the escapement in 1998 and 1999 (Figure 7.50). *pHOS*$_{\text{stray,OCU}}$ was also low, as most strays observed in Puntledge R escapements originated from outside the CU.

Strays recovered in 1998 and 1999 originated from all ECVI hatcheries, as well as from distant facilities like Kitimat R and Conuma R (Table E41). Like other ECVI systems, a consistent, low level of stray contribution from Cowichan R was observed across the time-series, but only accounted for an average of 1% of the total average return. Puntledge R, Summer-run Chinook were regularly recovered in fall sampling. These recoveries accounted for an average of 3% of escapements between 1998–2021. Strays from outside the ECVI were also observed straying into Puntledge R with occasional, sporadic recoveries from Robertson Cr, Chilliwack R, and US hatcheries over the time series.

Average *PNI* for the Puntledge R Fall run was 0.31, and in all years except 2021, the population was designated as an integrated-hatchery system.

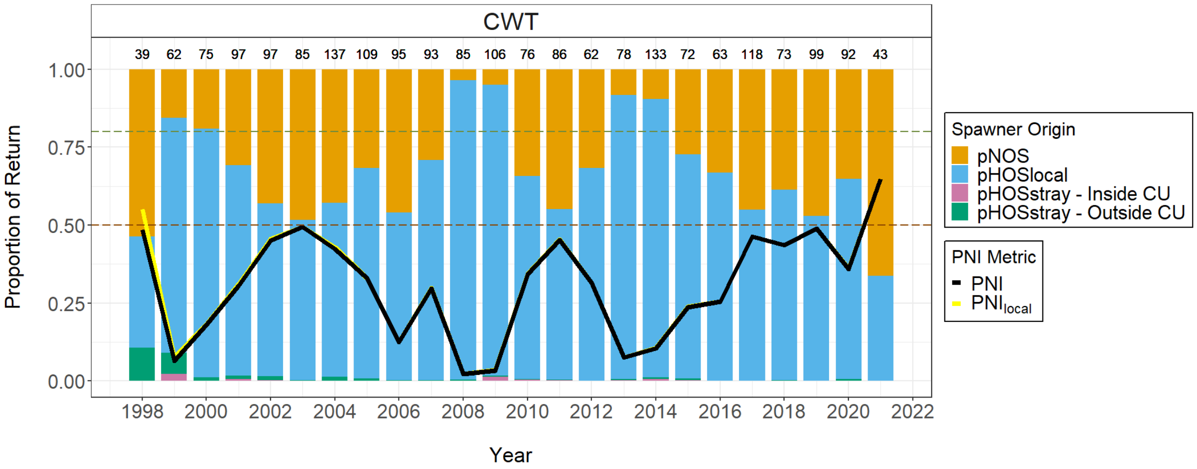

Figure 7.60. Origin of spawners returning to Puntledge R (Fall Run) between 1998 and 2021 estimated from CWT recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

7.3.3. Conservation Unit: CK-83 – East Vancouver Island-Georgia Strait

In CK-83 (East Vancouver Island-Georgia Strait), Chinook occur in two distinct basins on the ECVI that share a summer-run life history. The Puntledge and Nanaimo R hatcheries both enhance these runs at their respective facilities, and aim to release 500,000 and 225,000 smolts respectively each year. Straying is limited in this CU, with $pHOS_{stray}$ and $pHOS_{stray,OCU}$ both averaging 0.00 since 1998. Average *PNI* values between 1998–2021 for rivers in this CU indicated one integrated-hatchery population (*PNI* < 0.5), and one integrated-transition population (*PNI* between 0.50 and 0.80).

*Figure 7.61. Boundary map of the CK-83 Conservation Unit (East Vancouver Island-Georgia Strait) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow. *note that in this figure, sample sites are described at the mouth of the river, however spawning grounds are located inland, within the bounds of the CU.*

Nanaimo R Hatchery – Nanaimo R donor stock

Summer-run population

CWT recoveries for summer-run, Nanaimo R Chinook were observed between 1998 and 2005, with an average stray rate of 2.9% across years (Figure 7.52). Recoveries were only found in nearby Puntledge R, returning as part of both fall and summer runs (Table D20). Thermal mark recoveries of summer-run Naniamo R Chinook were observed between 2008–2021, with regular recoveries observed in Cowichan R between 2010–2013 (Table D21).

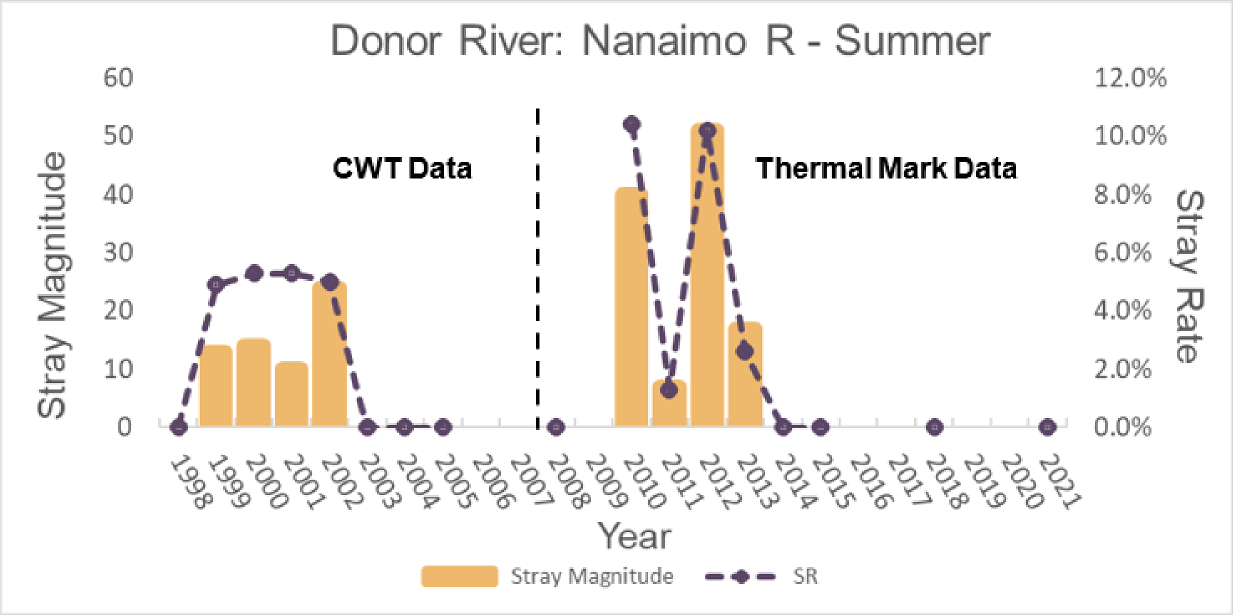

*Figure 7.62. Temporal trends in stray rate and magnitude from Nanaimo R - Summer Hatchery Chinook sampled in systems sampled across SBC calculated from CWT recoveries between 1998–2005, and from thermally marked otolith recoveries between 2008–2021. * indicates the switch from CWT to thermal mark data used.*

Nanaimo R – Recipient River

Summer-run population

Summer-run Chinook returning to the Nanaimo R were sampled for CWTs between 1998 and 2005. During this time, no strays were detected (Table E43, Figure 7.53). Thermal mark sampling between 2004–2018 indicated an expanded 3 and 13 Robertson Cr Chinook straying to Nanaimo R in 2005 and 2016 return years respectively (Table E42). No other strays were observed during this period. Nanaimo R – Summer run *PNI* fluctuated greatly between 1998–2018, but in most years indicated an integrated-transition or integrated-wild designation. Average *PNI* for this system was 0.65 based on thermal mark recoveries.

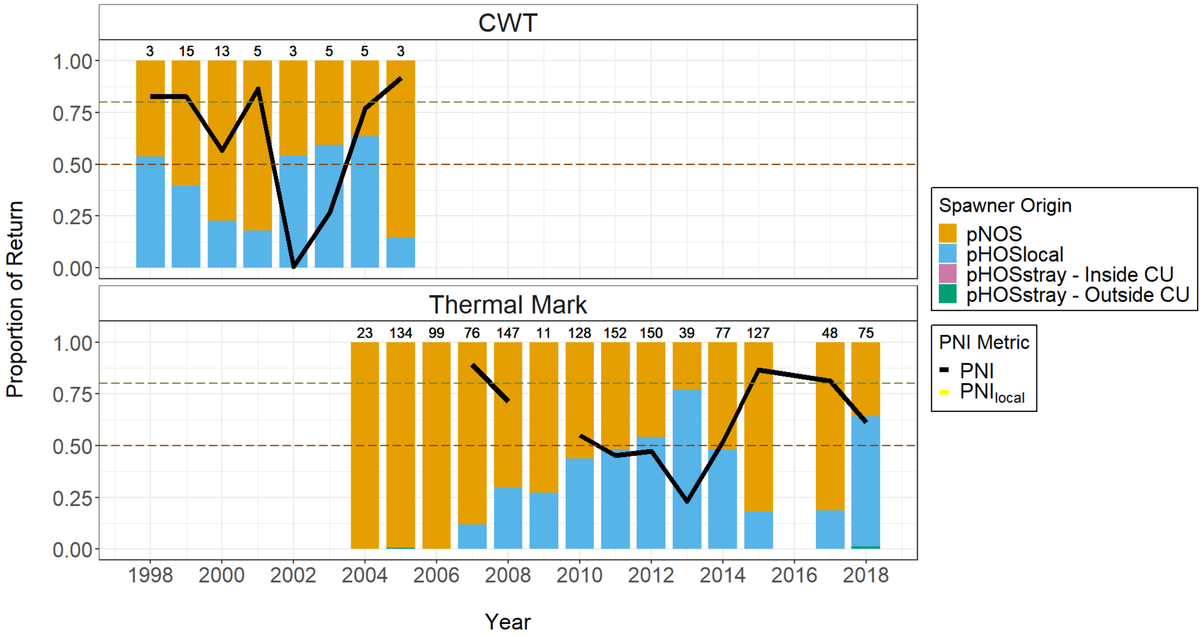

Figure 7.63. Origin of spawners returning to Nanaimo R (Summer Run) between 1998 and 2018 estimated from CWT and thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs or otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Puntledge R Hatchery – Puntledge R donor stock

Summer-run population

Both total and outside-CU stray rates for Summer-run Chinook originating from Puntledge R were 0.2%, with stray recoveries observed in three years between 1998–2021 (Figure 7.54). Similar to the Fall-run population, stray recoveries were observed returning to Nanaimo R and Campbell/Quinsam R (Table D22).

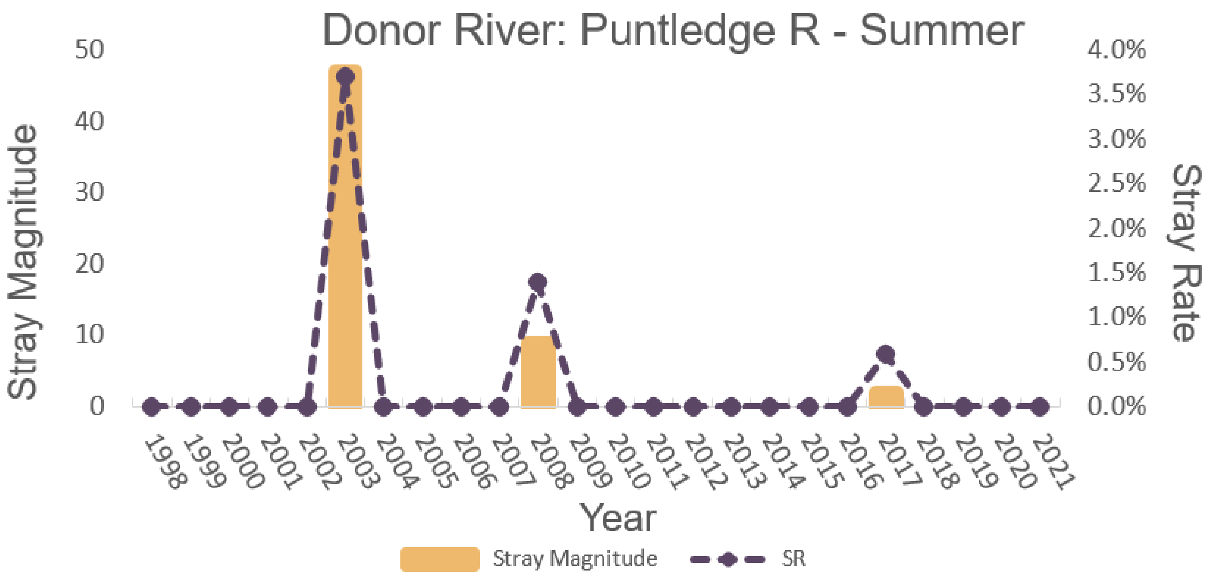

Figure 7.64. Temporal trends in stray rate and magnitude from Puntledge R - Summer Hatchery Chinook calculated from CWT recoveries in systems sampled across SBC.

Puntledge R – Recipient River

Summer-run population

Puntledge R – Summer-run escapement was much lower than the Fall-run, however stray dynamics were similar. Like the Fall run, most stray observations were observed between 1998–2002, with average $pHOS_{\text{stray}}$ values of 0.03 before 2002, and average $pHOS_{\text{stray}}$ values of 0.00 afterwards (Figure 7.55). Average $pHOS_{\text{stray,OCU}}$ values were nearly identical to total $pHOS_{\text{stray}}$ estimates. Strays originated from all ECVI hatcheries, however the most common recoveries were of US-hatchery origin (Table E44).

Average *PNI* for Puntledge R – Summer Chinook was low at 0.24 indicative of an integrated-hatchery system.

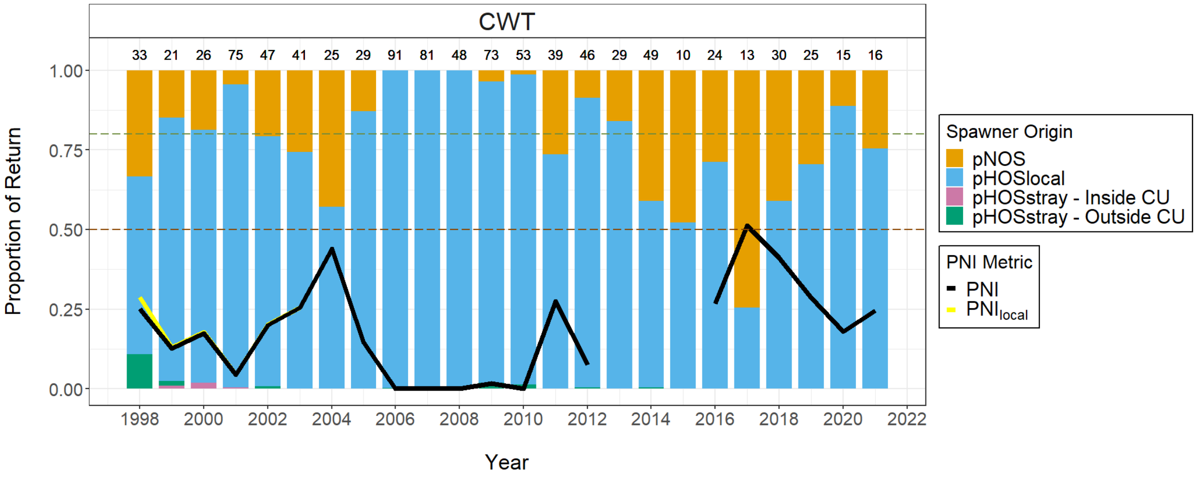

Figure 7.65. Origin of spawners returning to Puntledge R (Summer Run) between 1998 and 2021 estimated from CWT recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

7.4. STOCK MANAGEMENT UNIT: MAINLAND INLET CHINOOK SALMON

7.4.1. Conservation Unit: CK-28 – Southern Mainland-Southern Fjords

In CK-28 (Southern Mainland-Southern Fjords), Chinook have been recorded in NuSEDS occurring at 26 unique sites (Figure 7.56). For this analysis, we have data only for the Phillips R, representing an estimated 9% of total escapement to this CU—a significant data gap in SBC. Average $pHOS_{stray}$ and $pHOS_{stray,OCU}$ values were both 0.03 for this system, and average *PNI* values indicated an integrated-transition population (*PNI* between 0.50 and 0.80).

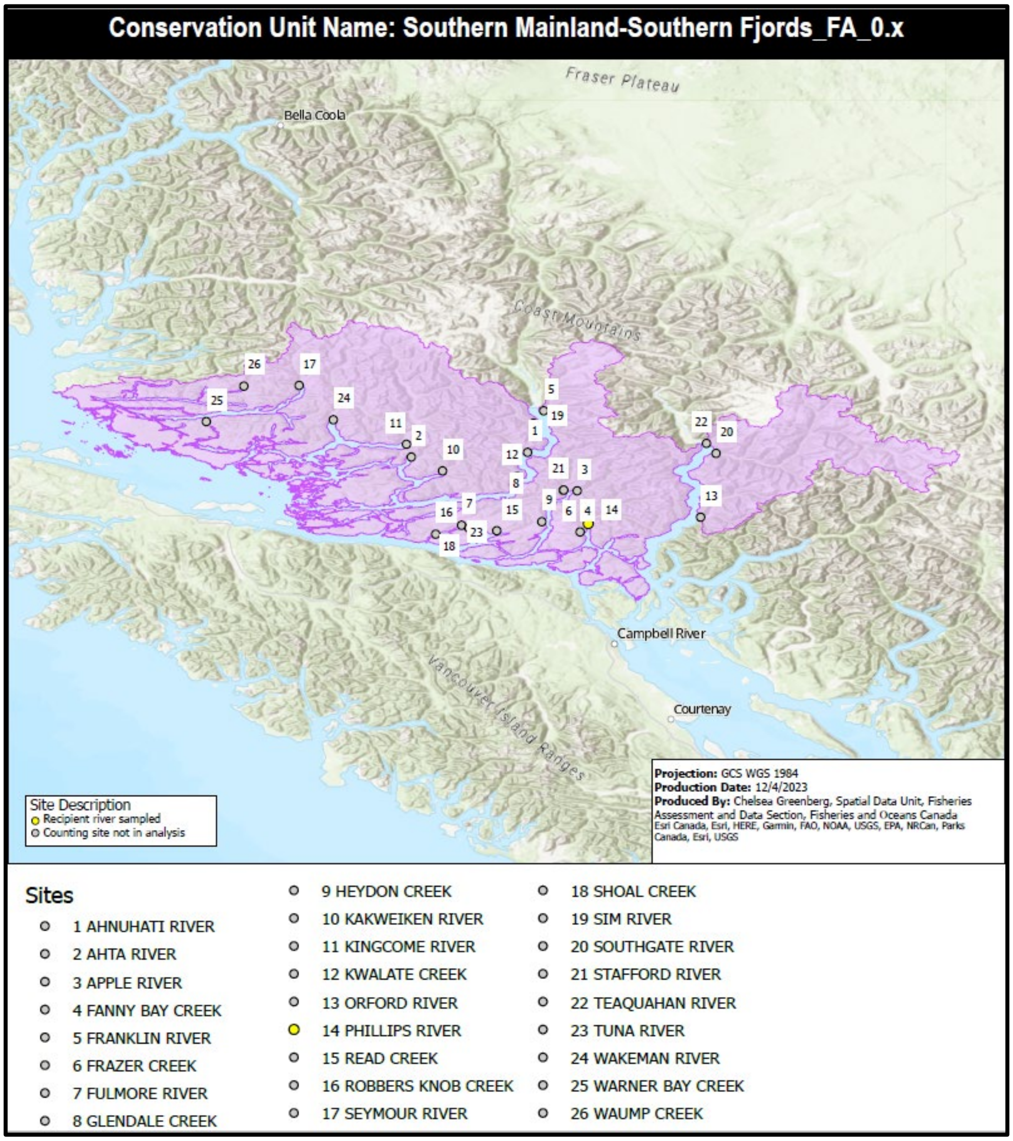

Figure 7.66. Boundary map of the CK-28 Conservation Unit (Southern Mainland-Southern Fjords) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

Phillips R was sampled regularly between 2009–2021, and during this time, $pHOS_{\text{stray}}$ and $pHOS_{\text{stray,OCU}}$ averaged 0.03. Strays were recovered sporadically, and did not occur at all in 9/13 years (Figure 7.57). Strays originated from Puntledge R in two years and Campbell/Quinsam R and US Hatcheries in one year each (Table E45).

Average *PNI* for Phillips R Chinook was 0.53 over our time period, indicative of an integrated-transition system.

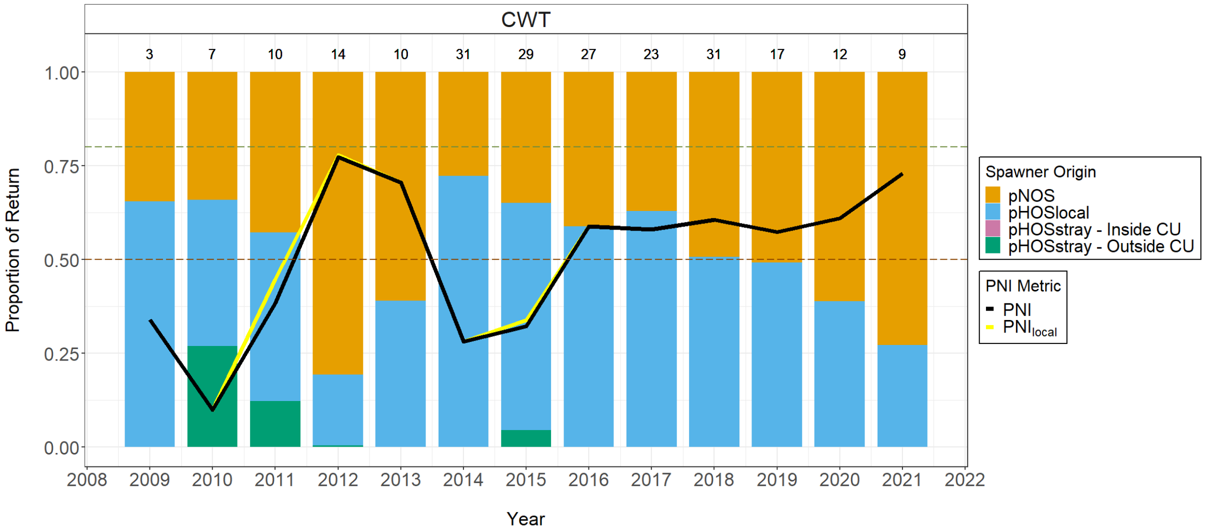

Figure 7.67. Origin of spawners returning to Phillips R between 2008 and 2021 estimated from CWT recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

7.5. STOCK MANAGEMENT UNIT: UPPER GEORGIA STRAIT CHINOOK SALMON

7.5.1. Conservation Unit: CK-29 – East Vancouver Island-North

In CK-29 (East Vancouver Island-North), Chinook have been recorded at 19 unique sampling sites since 1953 (Figure 7.58). However, most of the total escapement to the CU occurs in four systems, all included in this analysis: Campbell R, Quinsam R, Nimpkish R, and Salmon R/ JNST. These systems account for an estimated 91% of total escapement to the CU. A major-OPS facility on the Quinsam R enhances local Campbell and Quinsam R stocks, as well as satellite rearing the Salmon R/JNST population. All enhanced populations in this CU use thermal marking; Campbell/Quinsam R uses thermal marks and CWTs. $pHOS_{stray}$ and $pHOS_{stray,OCU}$ for this CU both averaged 0.01, and average PNI values indicated one integrated-hatchery population ($PNI < 0.50$), and two integrated-wild populations ($PNI > 0.8$) in the CU.

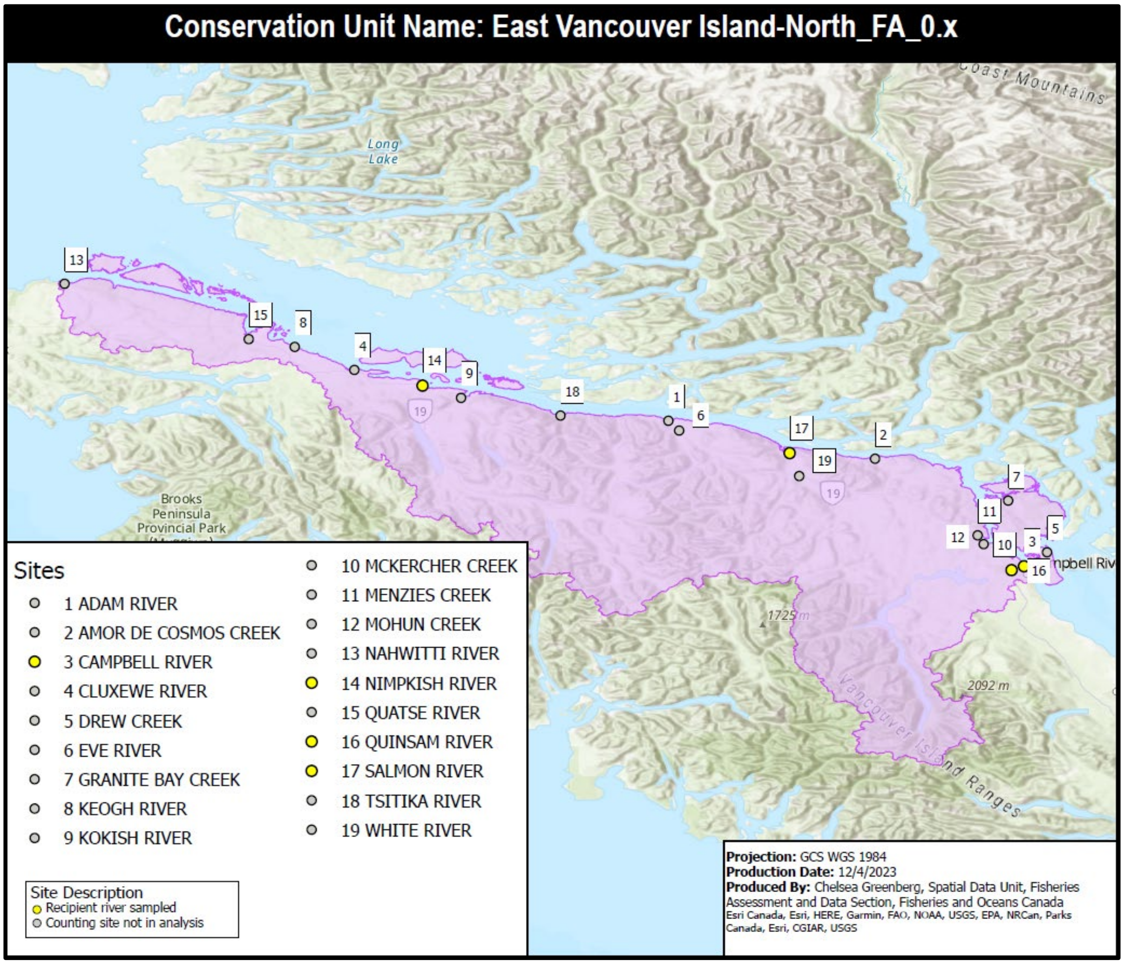

Figure 7.68. Boundary map of the CK-29 Conservation Unit (East Vancouver Island-North) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

Quinsam R Hatchery – Campbell R & Quinsam R donor stocks

The Campbell and Quinsam River system is located at the north end of the Strait of Georgia and contains a large-production facility (Quinsam R Hatchery) that has enhanced Chinook for harvest and assessment since 1974. Since both populations are proximate in geography, and are enhanced and enumerated at the same facility, they are treated as one metapopulation in this analysis.

CWT samples across SBC revealed an average stray rate of 1.2% for Campbell/Quinsam R Chinook, all of which occurred outside the CU. Strays were primarily recovered in enhanced systems where populations are regularly marked and sampled for CWTs. Straying from this system was greatest between return years 2009–2015, before falling to near 0% after 2016 (Figure 7.59). The average magnitude of strays based on expanded CWT recoveries was 43 individuals (Table D23), mostly driven by consistent recoveries in Big Qualicum R. Other, less frequent stray observations were detected in Puntledge R, Phillips R and Little Qualicum R over the time-series.

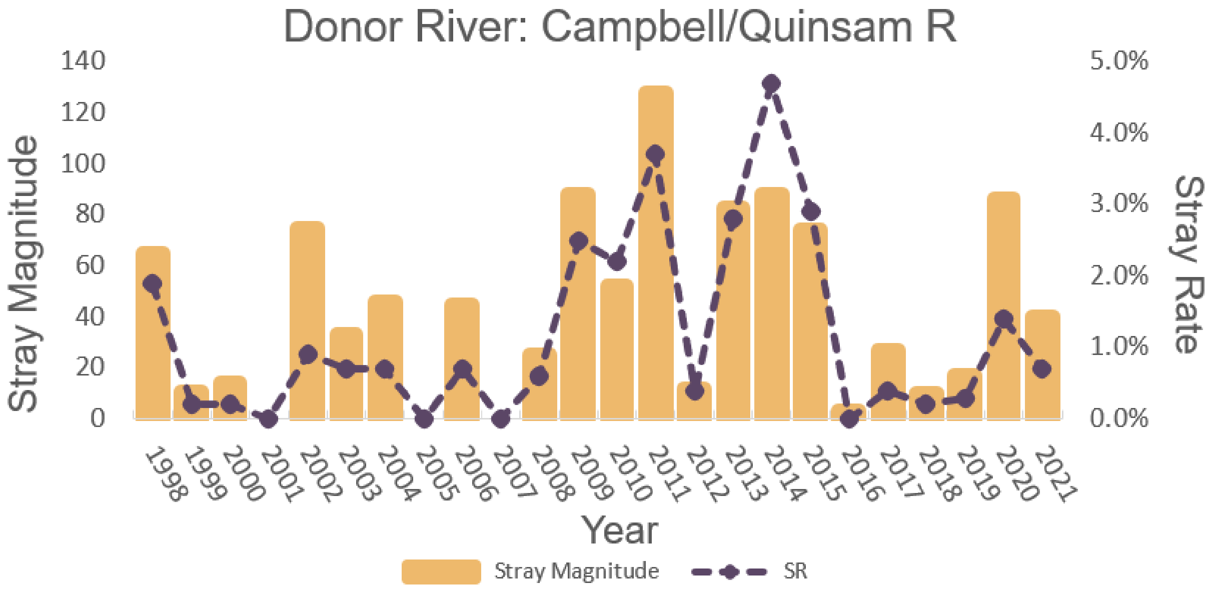

Figure 7.69. Temporal trends in stray rate and magnitude from Campbell/Quinsam R Hatchery Chinook calculated from CWT recoveries in systems sampled across SBC.

Thermal mark results showed an average stray rate of 0.3% across years, with most recoveries observed within the same CU, straying into Salmon R/JNST (Table D24), a population that is reared at Quinsam Hatchery, before being released in the home river. In 2003 and 2004, Chinook were observed straying outside the CU, into Cowichan R.

Results from both CWT and thermal mark recoveries suggest that the potential genetic impacts of straying from the Campbell/Quinsam R stocks are quite low.

Campbell/Quinsam R – Recipient Rivers

Both CWT and thermal mark data between 1998–2021 showed similar results for recipient stray contribution (Figure 7.60). CWT data suggested that between 1998 and 2021, average $pHOS_{\text{stray}}/pHOS_{\text{stray,OCU}}$ was 0.01. All ECVI hatcheries donated strays over the 24-year period, but all occurred sporadically, never making up more than 2% of the total return in any one year (Table E47). The most common observation was of US Hatchery Chinook occurring in 9/24 years. Of the ECVI systems, Campbell/Quinsam R saw the most strays originating from distant donor populations, with sporadic detections of Chinook from Robertson Cr, San Juan R, Porteau Cv, Nitinat R, Harrison R and Chilliwack R.

Thermal mark results from 1998–2021 suggested average $pHOS_{\text{stray}}/pHOS_{\text{stray,OCU}}$ was negligible; 0.00 (Table E46). Similar, sporadic detections of strays from distant systems occurred from Nitinat R, Robertson Cr, Chilliwack R.

PNI estimates derived from both CWT and thermal mark data indicated that Campbell/ Quinsam R has maintained an integrated-hatchery designation for the past 24 years.

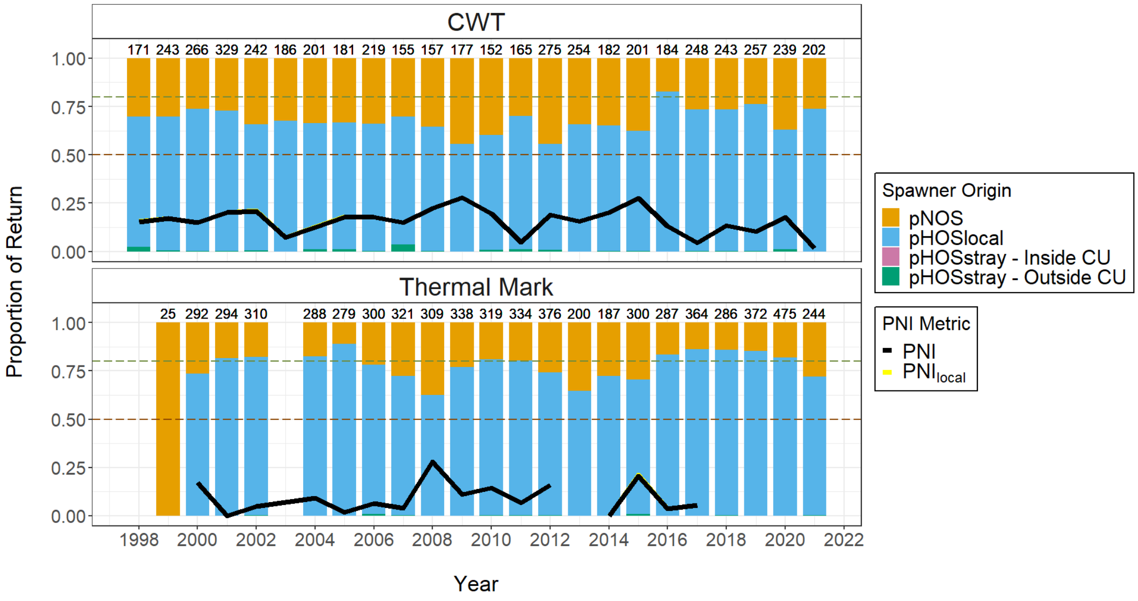

Figure 7.70. Origin of spawners returning to Campbell and Quinsam Rs between 1998 and 2021 estimated from CWT and thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs or otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Salmon R/JNST – Recipient River

Salmon R Chinook (identified in DFO reports as Salmon R/JNST), that enter marine waters near Sayward, have been enhanced since 1984; reared at Quinsam R Hatchery and transported to Sayward for imprinting before release. The population was thermally marked since the early 2000s, and thermal marks have been recovered in brood samples since 2006.

Strays were regularly observed in the earlier period of the time series, but were not recovered since 2014 (Figure 7.61). Average $pHOS_{stray}$ was 0.03, with most strays originating from Campbell/Quinsam R (Table E48). $pHOS_{stray,OCU}$ was 0.01, driven by sporadic stray recoveries of Robertson Cr in 2008 and Nitinat R in 2009.

Average *PNI* for Salmon R/JNST was 0.81 over the time series, indicative of an integrated-wild population, however *PNI* was depressed by an increased stray contribution from 2007–2010, with significant deviations between PNI_{local} and total *PNI* (Figure 7.61).

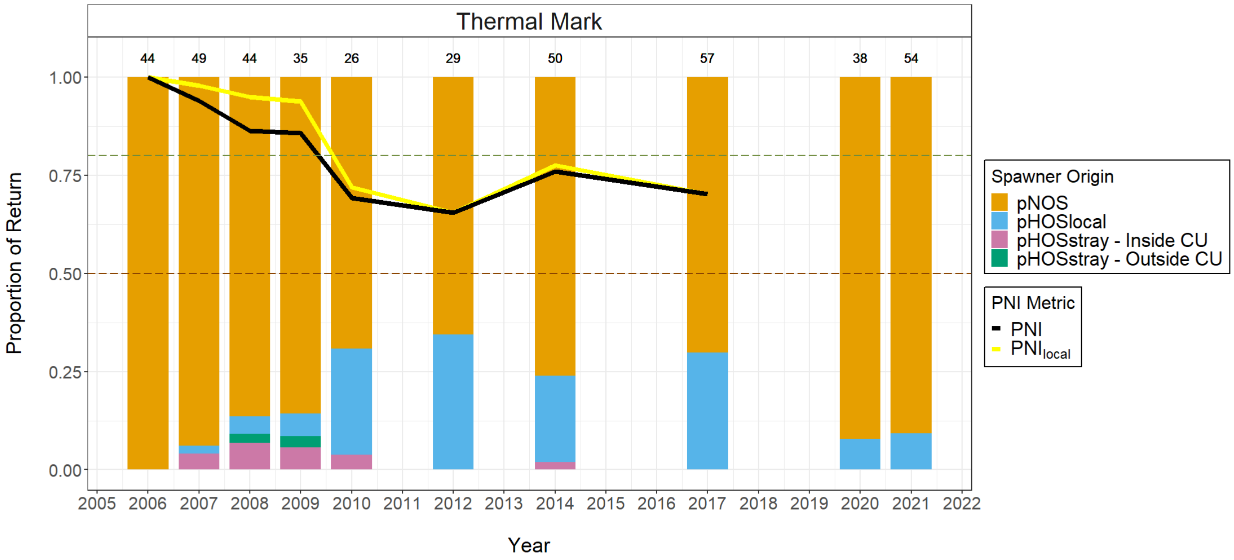

Figure 7.71. Origin of spawners returning to Salmon R/JNST between 2006 and 2021 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Nimpkish R – Recipient River

Chinook from the Nimpkish R and Woss R are enhanced through a CIP facility operated by the Namgis First Nation. This population was thermally marked since 2014, and during our analysis, no strays were recovered (Figure 7.62, Table E49). Average *PNI* was 0.82 over the time-series, indicative of an integrated-wild system.

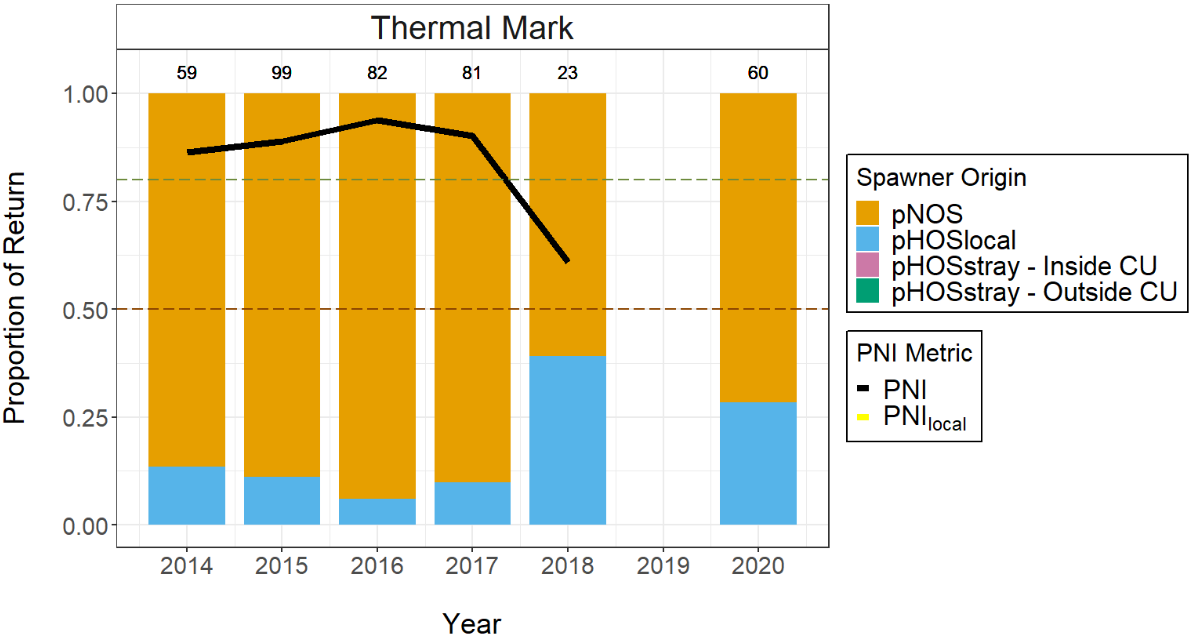

Figure 7.72. Origin of spawners returning to Nimpkish R between 2014 and 2020 estimated from thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

7.6. STOCK MANAGEMENT UNIT: FRASER FALL RUN 4_1 CHINOOK SALMON

7.6.1. Conservation Unit: CK-03 – Lower Fraser River-Fall Run

CK-03 (Figure 7.63) contains the Harrison R, the largest individual run of Chinook Salmon in the Fraser River. The population serves as an abundance indicator for ‘Fall-Run 4_1’ Fraser Chinook and regularly sees natural spawners escapements between 50,000–100,000. The population is enhanced for assessment by Chehalis R hatchery. $pHOS_{stray}$ and $pHOS_{stray,OCU}$ for this CU both averaged 0.01, and average *PNI* values indicated that the Harrison R was designated an integrated-wild system (*PNI* > 0.8).

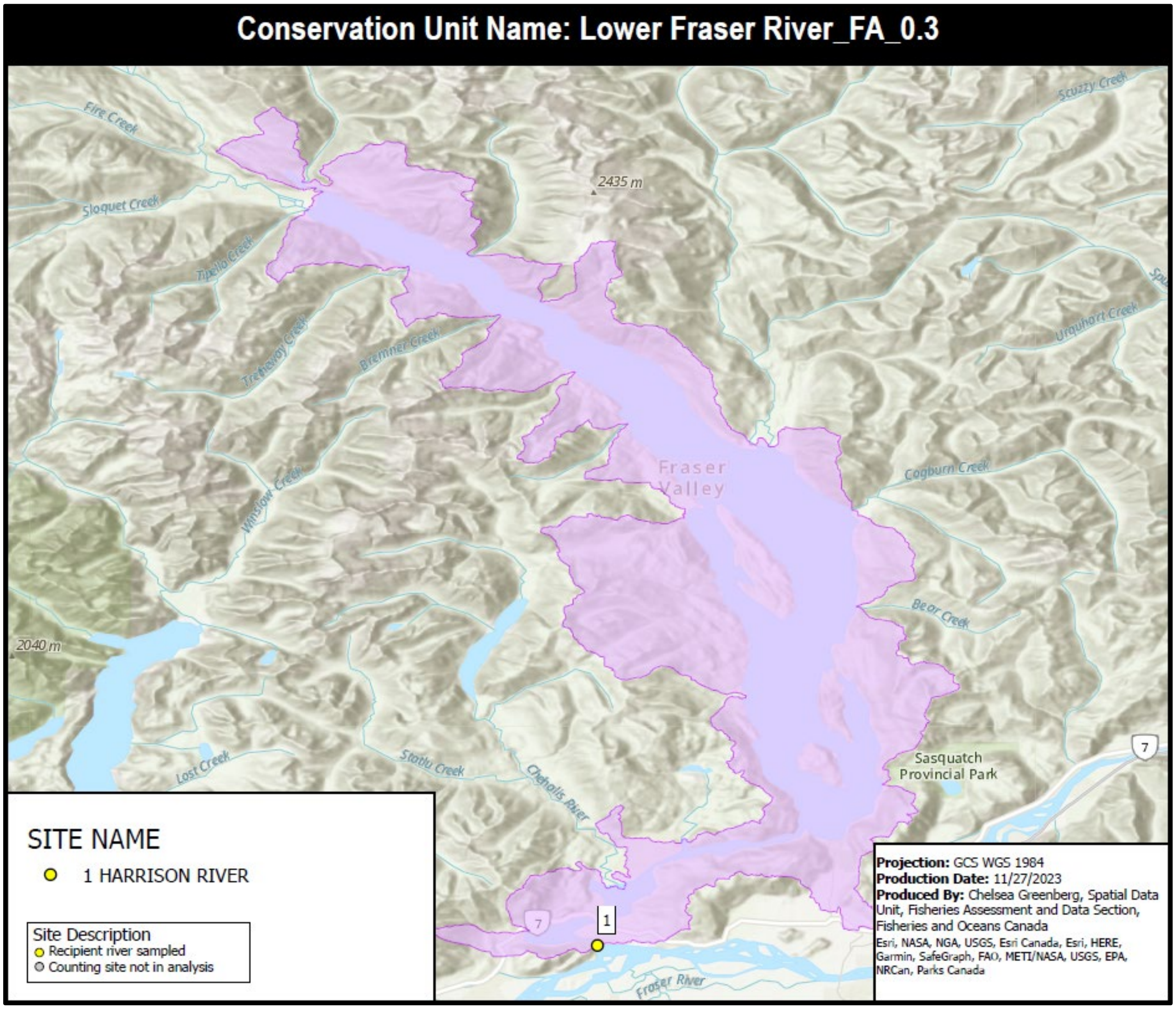

Figure 7.73. Boundary map of the CK-03 Conservation Unit (Lower Fraser River-Fall Run) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

Chehalis R Hatchery – Harrison R donor stock

The Chehalis R Hatchery primarily enhances Chehalis R and Harrison R Chinook stocks. Harrison R Chinook are enhanced and identified by CWTs only. Expanded CWT recoveries from this population revealed an average stray rate of 0.4% between 1998–2021 (Figure 7.64). As a single-site CU, all strays from Harrison R were considered outside-CU strays. Strays from Harrison R were observed in nearby Chilliwack R throughout the study period and in Stave R before 2004 (Table D25). A single stray from the Harrison R hatchery stock was recovered in Campbell/Quinsam R in 2010, but otherwise no strays outside of the Fraser R system were detected. The magnitude of strays originating from Harrison R averaged 19 expanded recoveries per year, suggesting that the potential impacts from straying in this population are negligible.

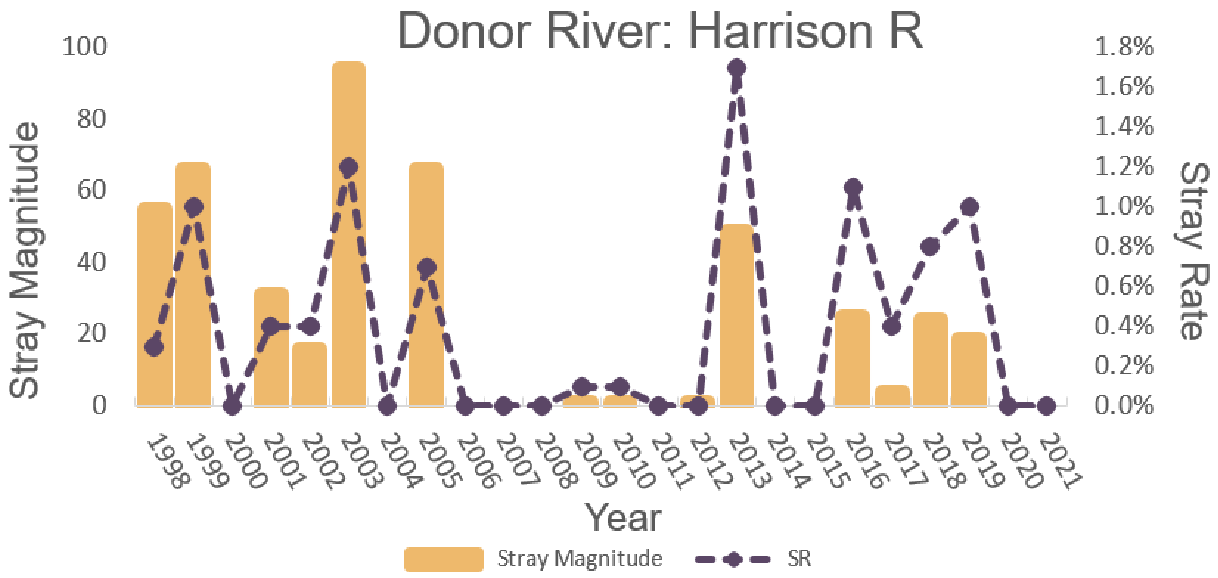

Figure 7.74. Temporal trends in stray rate and magnitude from Harrison R Hatchery Chinook calculated from CWT recoveries in systems sampled across SBC.

Harrison R – Recipient River

CWT sampling in the Harrison R between 1998 and 2021 indicated low average *pHOS*$_{\text{stray}}$ values of 0.01, with 67% of years showing *pHOS*$_{\text{stray}}$ values of 0.00 (Figure 7.65). Consistent annual recoveries of Chilliwack R Chinook were observed in the Harrison R (Table E51). This trend may be expected as Harrison R Chinook comprised the original founding population for the Chilliwack R Fall Run. Transplanted Capilano R Chinook also strayed into the Harrison annually from 2016–2021, reaching a high of 89 expanded recoveries in 2016. Strays from nearby Stave R between 2000–2005, accounted for 2–11% of hatchery recoveries in those years.

Strays from Vancouver Island systems were recovered in four years. Strays from Cowichan R were observed in 2013, 2016 and 2018. Additionally, an expanded 194 strays were estimated to have strayed from Robertson Cr into Harrison R in 2017, although these expanded values were based on only two CWT recoveries. Despite these sporadic observations, the potential genetic impact on the recipient population is likely low. As the largest natural-origin spawning population in BC, Harrison R has maintained a consistently high *PNI*, ranging from 0.86 to 0.99, with an average of 0.95, indicative of an integrated-wild population.

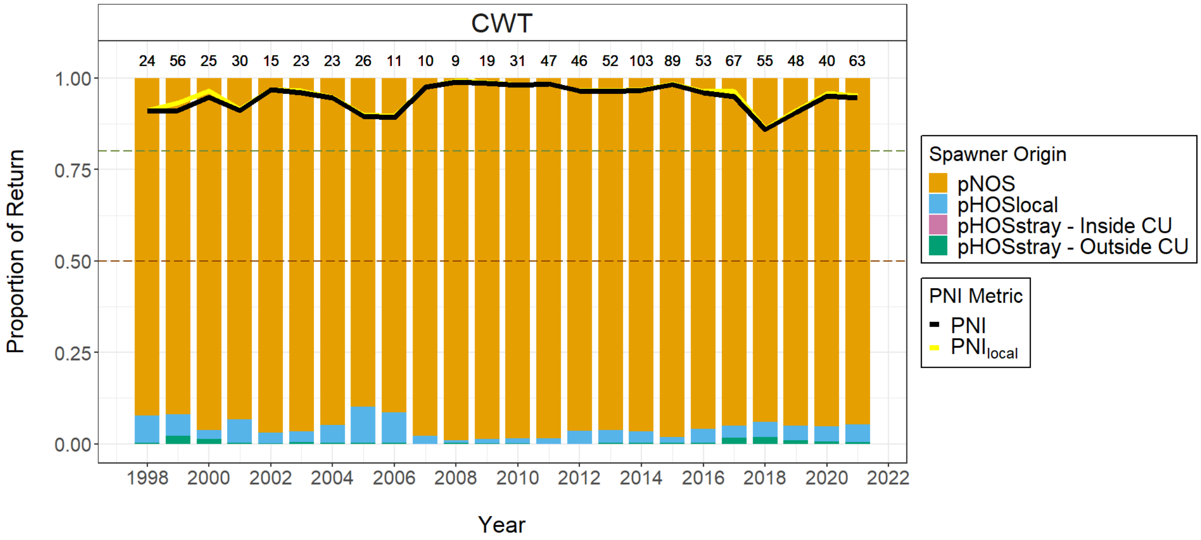

Figure 7.75. Origin of spawners returning to Harrison R between 1998 and 2021 estimated from CWT recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

7.6.2. Conservation Unit: CK-9006 – Fraser-Cross CU Supplementation

Two small Lower Fraser systems were enhanced sporadically between 1998–2021 as cross-CU transplant populations: Chehalis R and Stave R. These populations fall within a distinct CU (CK-9006), as their genetic heritage is tied to other populations in SBC. A small subset of years in which CWTs were recovered are reported here.

Chehalis R was sampled in three years: 2014, 2017, and 2020. In each of these years, no stray recoveries were observed, and *PNI* averaged 0.35 indicative of an integrated hatchery population (Table E52).

The Stave R was sampled between 1998–2003, and saw straying during this time. Harrison R strays were recovered in 4/6 years, and in 1999, strays from Cowichan R, Capilano R and Chilliwack R were also observed (Table E53). Average $pHOS_{stray}/pHOS_{stray,OCU}$ was 0.04 and *PNI* in all years indicated an integrated hatchery population.

7.6.3. Conservation Unit: CK-9008 – Fraser-Harrison Fall Transplant

The CK-9008 (Fraser-Harrison Fall Transplant) conservation unit consists of the Chilliwack R transplant population founded from Harrison R Fall Chinook (Figure 7.66). The population is sustained through continued enhancement by Chilliwack R Hatchery and is marked with both CWTs and thermal marks. $pHOS_{stray}$ and $pHOS_{stray,OCU}$ for this population/CU averaged 0.00, and average *PNI* values indicated an integrated-hatchery population (*PNI* < 0.50).

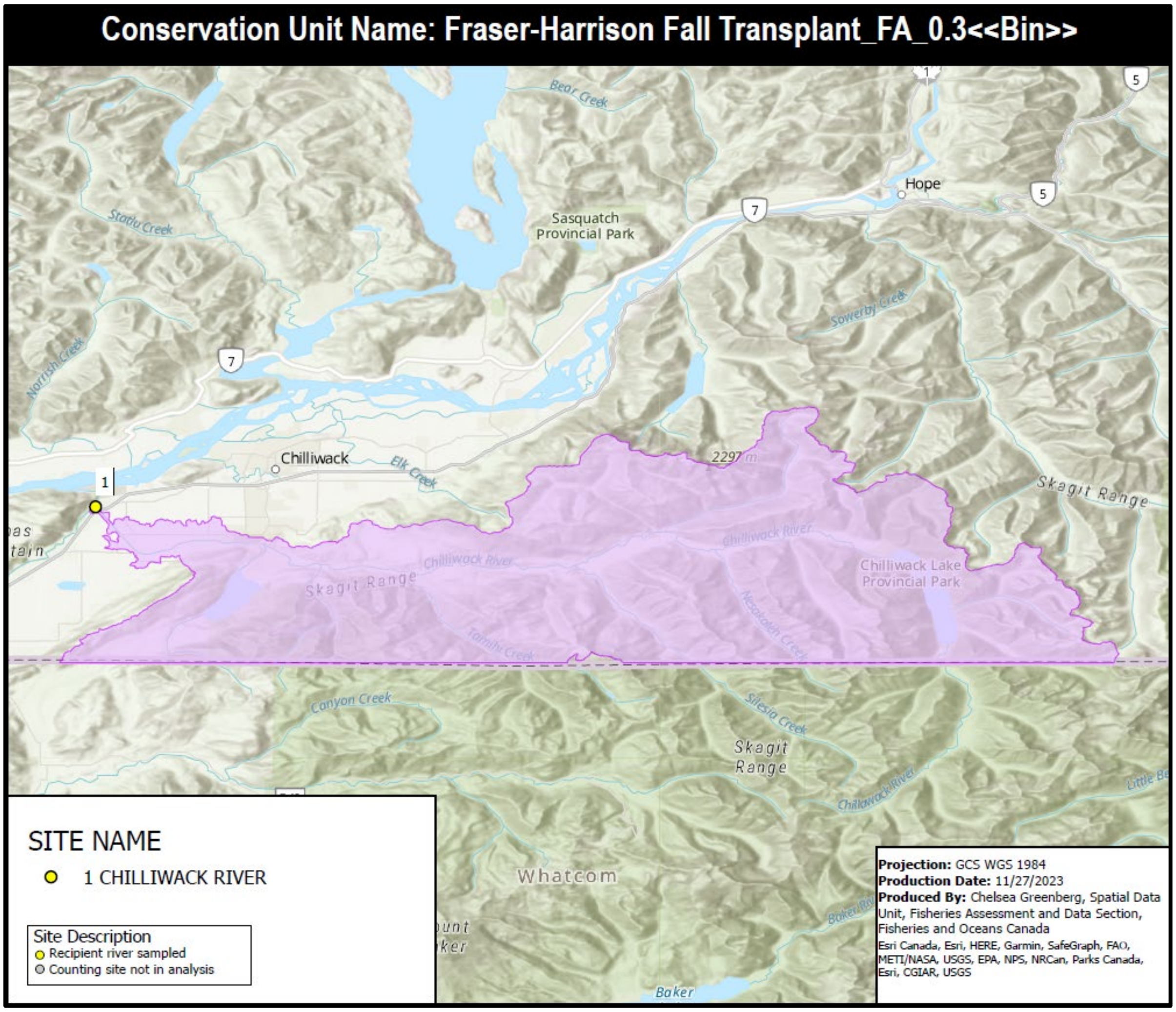

Figure 7.76. Boundary map of the CK-9008 Conservation Unit (Fraser-Harrison Fall Transplant) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

Chilliwack R Hatchery – Chilliwack R donor stock

Fall-run population

Chilliwack R, 4_1, Fall Chinook are enhanced for assessment purposes and to provide increased harvest opportunities for marine and freshwater fisheries. The population was marked using both CWT and thermal marks historically, but CWT data were available for the entire study period.

CWT data from 1998–2021 revealed a low average stray rate of 0.7%, with large magnitudes of straying occurring prior to 2004 (Figure 7.67). Most of these strays were recovered in nearby Harrison R (Table D26). As these strays were observed in their genetic founding population, and Harrison R sees consistently large natural-origin returns, the potential impacts of this hatchery straying relationship are likely low. The magnitude of strays observed from CWT-marked Chilliwack R Chinook averaged 174 per year. Stray recoveries were observed returning to Campbell/Quinsam R in 2007 and 2008, in Puntledge R in 2007 and in Stave R between 1998–2000. No other Chilliwack R strays were observed in CWT samples from 1998–2021.

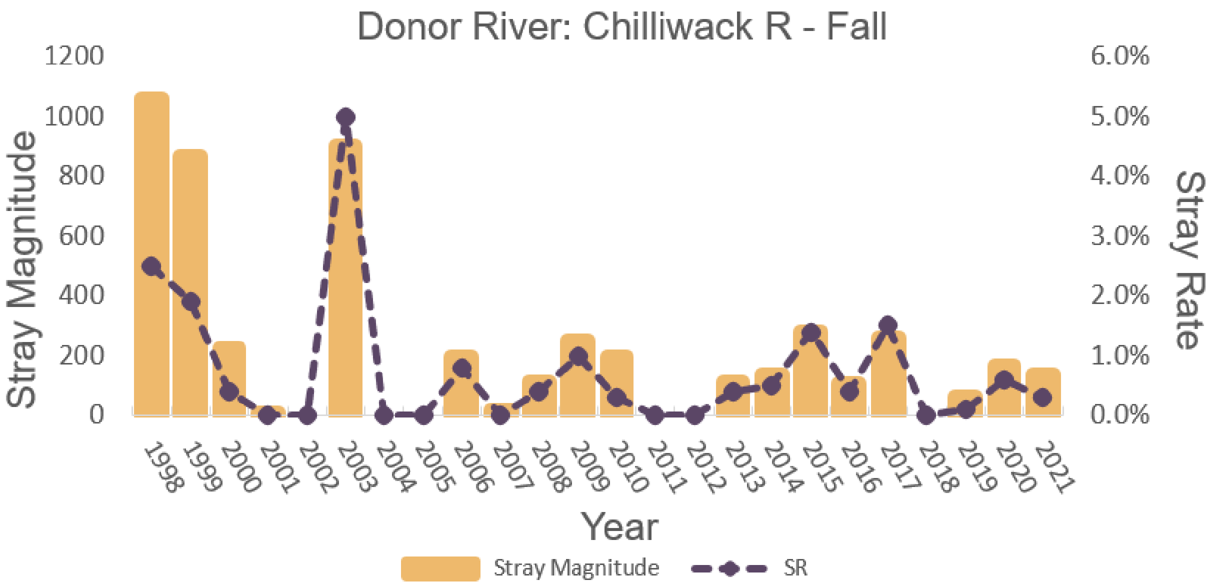

Figure 7.77. Temporal trends in stray rate and magnitude from Chilliwack R – Fall Hatchery Chinook calculated from CWT recoveries in systems sampled across SBC.

Thermal mark recoveries from 1998–2013 revealed only three years in which Chilliwack R – Fall Chinook were recovered as strays (Table D27), occurring in Campbell/Quinsam R in 2007, and into Nitinat R in 2011 and 2013. In each of these cases, only a single Chilliwack R stray was observed and expanded.

Summer-run population

In addition to the transplanted Fall run of Chinook, Chilliwack R Hatchery enhances a 5_2 transplanted Chinook population founded on broodstock collected in several Upper Fraser streams (including Quesnel R, Chilko R, Slim Cr, Bowron R, and Finn Cr). This population is enhanced to provide freshwater, recreational harvest opportunities along the Vedder R and Chilliwack R. During our period of analysis, this population was not marked with CWTs or thermal marks and thus, we cannot describe trends in stray rate. This presents a source of risk that is currently unaccounted for in SBC rivers, and future marking and monitoring of this population is advised. Transplanted Chinook likely stray at greater rates than non-displaced populations (Candy and Beacham 2000). However, recent advances in genetic stock identification using single-nucleotide polymorphisms can now differentiate the summer-run population from its Upper Fraser founding stocks with a 90% assignment success (Beacham et al. 2021). Further, PBT marking of summer-run Chilliwack R broodstock has occurred since the 2019 brood year, and potential strays will be identifiable from this mark type in future return years.

Chilliwack R – Recipient River

Fall-run population

CWT sampling between 1998–2021 indicated low, but consistent annual straying from Lower Fraser systems was observed in the Chilliwack R (Figure 7.68), however *pHOS*$_{\text{stray}}$ never exceeded a 0.01 in any year. Between 1998 and 2004, when CWTs were applied to Stave R Chinook, they were observed in Chilliwack R escapements. Harrison R Chinook were also sporadically observed between 2003 and 2019. Beginning in the 2013 brood year, Chilliwack R Chinook were transplanted into Capilano R, and since 2016, they have been observed as strays in Chilliwack R. This relationship could be expected, and is consistent with observation by other authors' of a low, but consistent affinity to the ancestral site if a population is reared in a location different than its release (Hard and Heard, 1999). Strays originating from distant SMUs included sporadic observations from Spius Cr, Cowichan R, Robertson Cr, and US hatcheries over the 24 year period (Table E55).

Thermal mark samples were available from 1998–2011 and indicated negligible strays in Chilliwack R escapements (average $pHOS_{stray}$ = 0.00, Figure 7.68). Strays from distant Robertson Cr were recovered in 2004 and 2006, but did not contribute significantly to escapements in those years (Table E54). No other stray thermal mark recoveries were observed in this period.

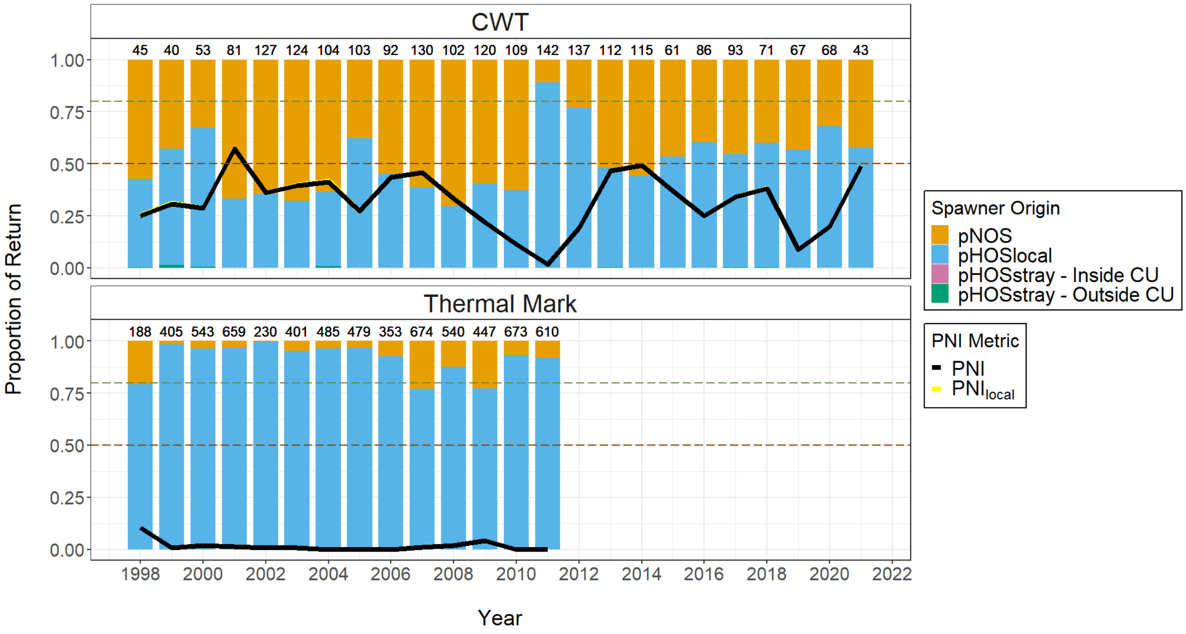

Figure 7.78. Origin of spawners returning to Chilliwack R between 1998 and 2021 estimated from CWT and thermal mark recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs or otoliths examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

7.7. STOCK MANAGEMENT UNIT: FRASER SPRING RUN 4_2 CHINOOK SALMON

7.7.1. Conservation Unit: CK-17 – Lower Thompson

The Thompson River, the largest basin of the Fraser R drainage, is divided into Lower, Southern and Northern sub-basins. In the Lower Thompson area (CK-17, Figure 7.69), three nearby and connected tributaries, Nicola R, Spius Cr and Coldwater R are all enhanced at Spius Creek Hatchery and represent approximately 69% of total average escapement to the CU. All three of these populations have historically been marked using CWTs. $pHOS_{stray}$ and $pHOS_{stray,OCU}$ for this CU both averaged 0.00, and average *PNI* values indicated all three sampled populations were designated as integrated-transition (*PNI* between 0.50 and 0.80). As per our definition of straying for Fraser R systems (Section 2), a Chinook Salmon has only strayed if it is recovered outside the sub-basin of origin. For this work, the CU, and sub-basin are essentially synonymous, i.e., recoveries are not considered strays if they are recovered within the same CU/sub-basin. Tributary-level straying is still described in appendices.

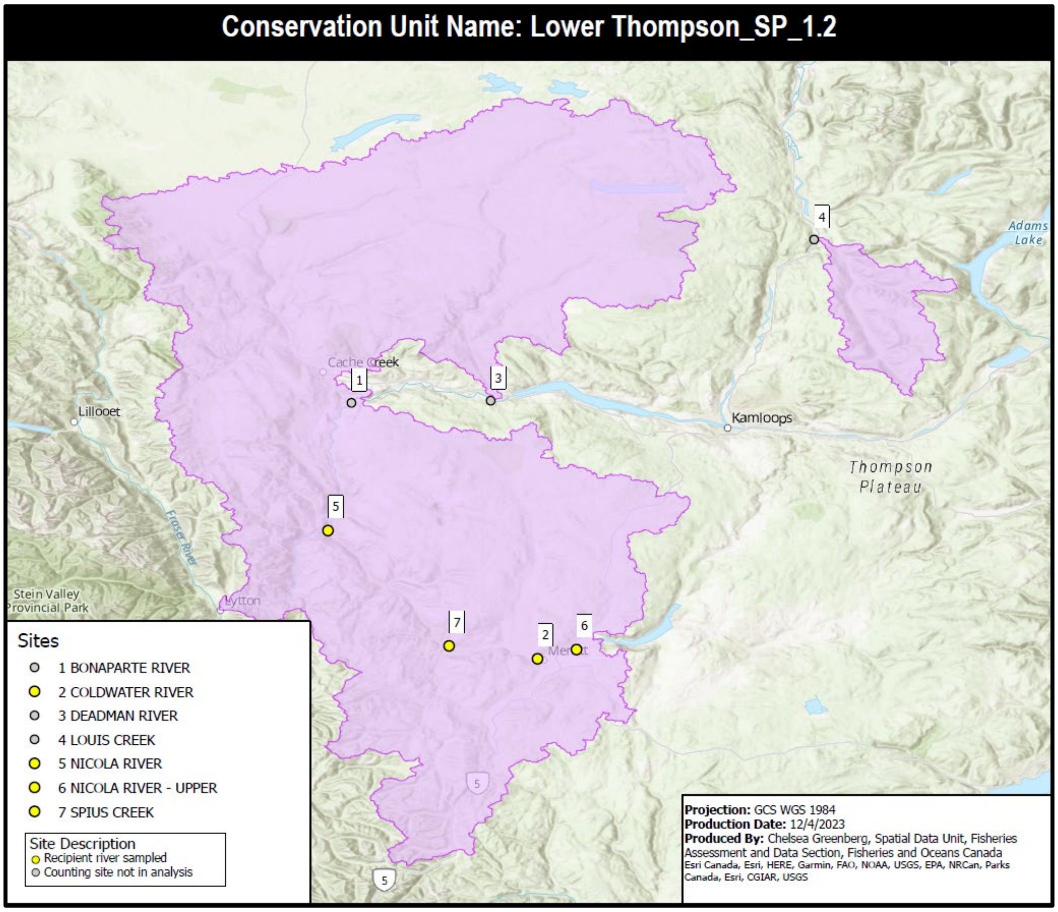

Figure 7.79. Boundary map of the CK-17 Conservation Unit (Lower Thompson) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

Spius Creek Hatchery – Nicola R donor stock

Nicola R Chinook, enhanced at Spius Cr Hatchery, are CWT-marked for the assessment of Lower Thompson, Spring 4_2 Chinook. From 1998–2003, expanded CWT recoveries from the Nicola R population were recovered in nearby Spius Cr and Coldwater R, all tributaries of the Lower Thompson R sub-basin (Table D28). Nicola R Chinook were not recovered in either of these tributaries after 2003.

Nicola R – Recipient River

All non-local recoveries in the Nicola R between 1998–2021 originated from tributaries of the Lower Thompson River (Table E56). Recoveries from Spius Cr were observed between 1999–2001, corresponding to the few years in which CWTs were applied to this population (brood years 1995–1997). Similarly, CWTs from nearby Coldwater R were observed in all but one year between 1998–2004, which corresponds to the sporadic application of CWTs between 1994 and 2000 brood years. Lastly, a single CWT recovery, representing an expanded four fish from Deadman R (another tributary of the Lower Thompson drainage) was observed straying into the Nicola R in 2001. No stray recoveries were observed in the Nicola R since 1998. *pHOS* values for Nicola R Chinook ranged from 0.05 to 0.74 between 1998–2021. *PNI* averaged 0.70, but fluctuated regularly between integrated-transition and integrated-wild designations between 1998–2021 (Figure 7.70).

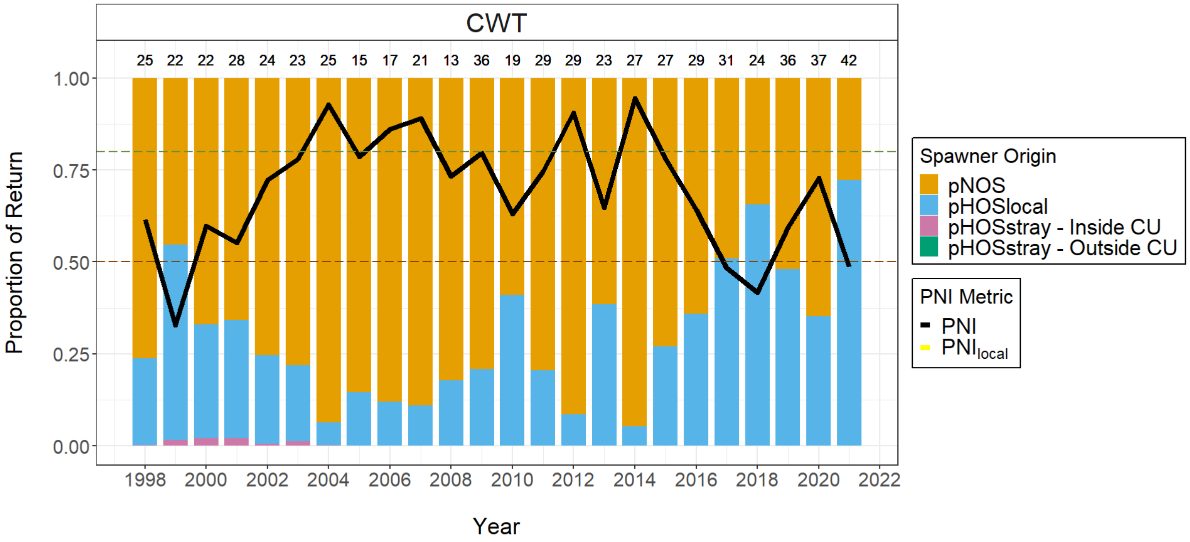

Figure 7.80. Origin of spawners returning to Nicola R between 1998 and 2021 estimated from CWT recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Spius Creek Hatchery – Spius Cr and Coldwater R donor stocks

Spius Cr Hatchery has historically enhanced two CK-17 populations under rebuilding objectives: Spius Cr and Coldwater R. CWT data for Spius Cr was analyzed from 1998–2002, where recoveries were regularly observed straying into nearby Coldwater R and Nicola R. Outside of the Lower Thompson sub-basin, a single Spius Cr Chinook was observed in Chilliwack R in 2000, representing an expanded 22 Chinook.

CWT data for Coldwater R from 1998–2004 shows regular straying into Spius Cr and Nicola R systems, but no strays were observed outside of the Lower Thompson.

Spius Cr and Coldwater R – Recipient Rivers

The Spius Cr Chinook population was supplemented since the mid-1980s, but CWT data were only available in EPAD between 1998 and 2004. During this time, both Coldwater and Nicola R Chinook were regularly observed (Table E57). In 2000, an expanded 61 recoveries of Shuswap R – Lower Chinook were observed, but this was the only instance of outside-CU strays being recovered. Because Spius Cr Chinook were not consistently marked during this period, *pHOS* and *PNI* could not be accurately calculated. Coldwater R was sampled for CWTs during this same period, and saw Nicola R and Spius Cr each contributing strays in one year of sampling. No outside-CU strays were observed.

7.8. STOCK MANAGEMENT UNIT: FRASER SUMMER RUN 4_1 CHINOOK SALMON

7.8.1. Conservation Unit: CK-15 – Shuswap River

CK-15 (Shuswap R) is located in the South Thompson area of the SBC Interior and encompasses the Shuswap River's Lower, Middle and Upper reaches (Figure 7.71). Hatchery enhancement is achieved on both 'Lower' and 'Middle' Chinook populations via Shuswap Falls Hatchery to fulfill Pacific Salmon Treaty obligations for assessment. Both of these populations are marked using CWTs. $pHOS_{stray}$ for this CU both averaged 0.01 and $pHOS_{stray,OCU}$ averaged 0.00 between 1998–2021. Average *PNI* values indicated one integrated-transition population (*PNI* between 0.50 and 0.80), and one integrated-wild population (*PNI* > 0.8) present in the CU.

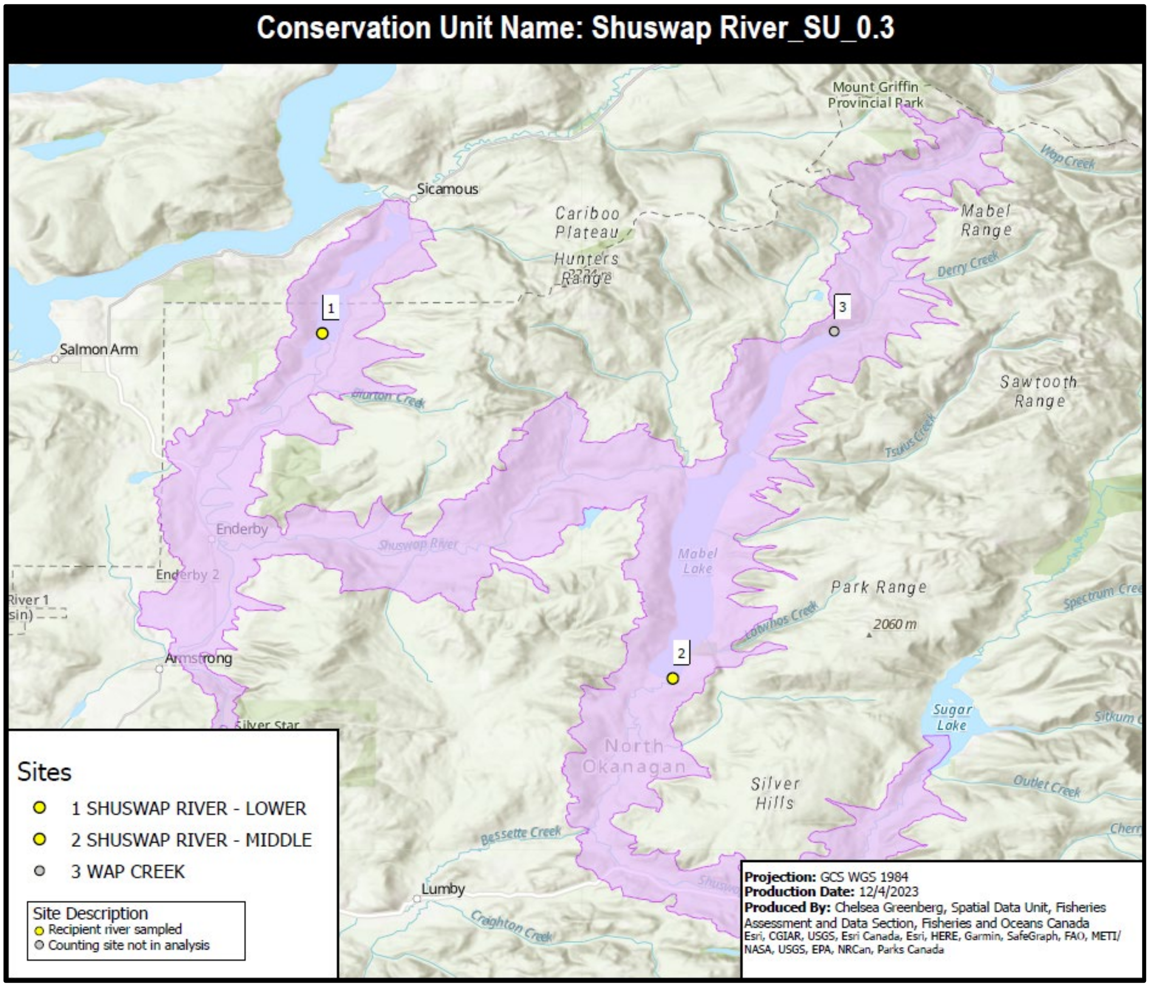

Figure 7.81. Boundary map of the CK-15 Conservation Unit (Shuswap R) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

Shuswap Falls Hatchery – Shuswap R Lower and Shuswap R Middle donor stocks

Shuswap Falls Hatchery enhances Lower and Middle Shuswap R Chinook. Each population is reared and marked separately, however recoveries from either population in either reach of the river were designated as homed. Expanded CWT recoveries from Lower Shuswap R were only observed returning to Lower and Middle Shuswap Rs between 1998–2021, except for two recoveries representing an expanded 61 Chinook straying into Spius Cr in 2000 (Table D29). Middle Shuswap R hatchery Chinook were recovered regularly in the Lower Shuswap R tributary (Table D30), however no strays were observed between 1998–2021. Like other populations in the Thompson R basin, the Shuswap R appears to be of low risk to donate strays to any SBC Chinook population.

Lower and Middle Shuswap Rivers – Recipient Rivers

The Lower Shuswap R received out-of-tributary strays primarily from nearby Middle Shuswap R, and $pHOS_{\text{stray}}$ was negligible over the time series (Figure 7.72). It is apparent from CWT recovery data that genetic exchange between the Lower and Middle Shuswap tributaries likely occurs regularly. CWT recoveries from this system were recovered in 1998, 2000, 2001, 2004 and in each year between 2012 and 2021 (Table E59).

CWTs from nearby (but not within-CU) Salmon R/TOMF were observed between 1998 and 2002, and in 2005 and 2010. CWT recoveries from Salmon R/TOMF in the Lower Shuswap R would only be expected up until 2012, as CWT marking for this population ceased in 2008. The only other outside-CU strays observed in Lower Shuswap R were recovered in 1999–2001, and in 2017 originating from Cowichan R. $pHOS_{local}$ in the Lower Shuswap R ranged between 0.03 and 0.19 between 1998 and 2021, with *PNI* values averaging 0.89 for the times series. Single-year values dipped only as low as 0.75, indicating that the system has maintained an integrated-wild designation in most years since 1998.

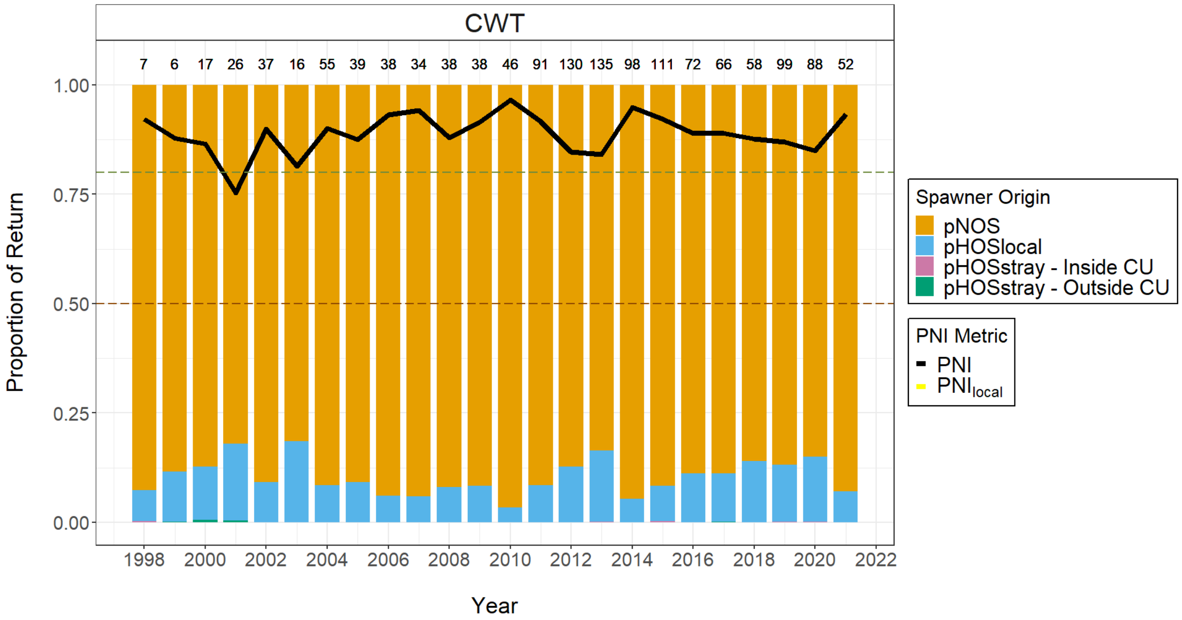

Figure 7.82. Origin of spawners returning to Shuswap R - Low between 1998 and 2021 estimated from CWT recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

Chinook escapements to the Middle Shuswap R are far lower than those observed in the Lower Shuswap R. The only strays recovered in this system between 1998 and 2021 originated from Lower Shuswap R, and occurred in 14/24 years (Table E60). $pHOS_{local}$ was consistently high in Middle Shuswap R, likely due to its proximity to the hatchery, and ranged from 0.05 to 0.91 over the time series (Figure 7.73). *PNI* fluctuated between 0.09 and 0.95, transitioning from an era of low *PNI* between 1998–2006, to a modern era where recent *PNI*s indicates an integrated-transition population.

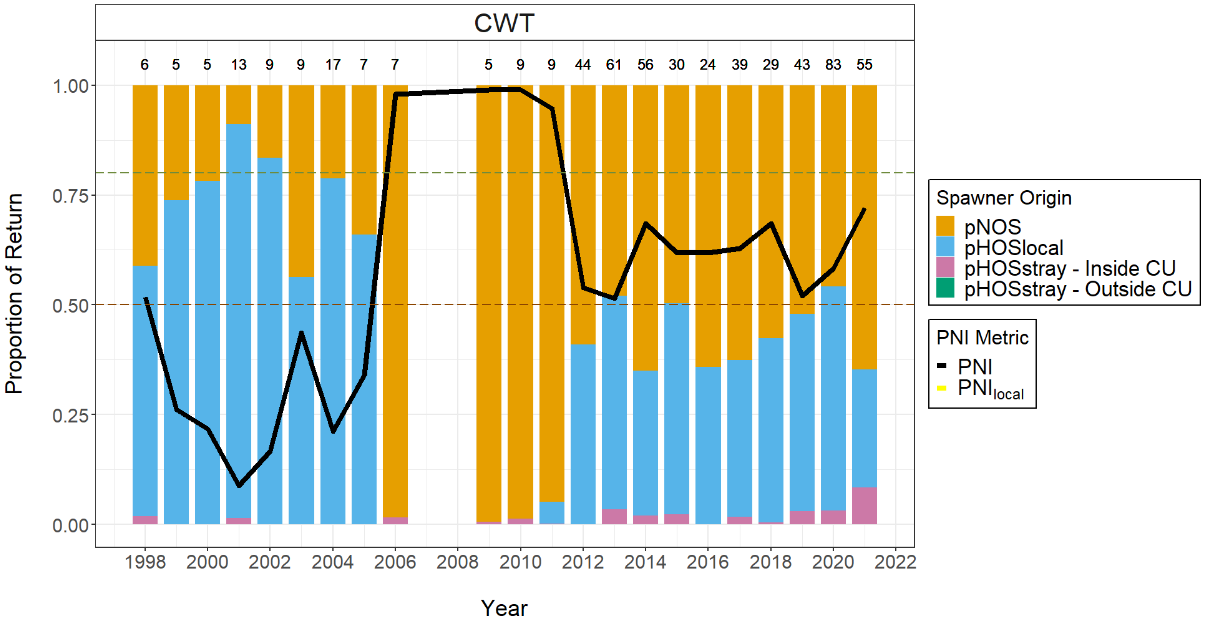

Figure 7.83. Origin of spawners returning to Shuswap R - Middle between 1998 and 2021 estimated from CWT recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners (pHOSlocal), strayed hatchery-origin spawners originating from inside the CU (pHOSstray – Inside CU), and strayed hatchery-origin spawners originating from outside the CU (pHOSstray – Outside CU) are described annually. The unexpanded, annual sample size of CWTs examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

7.8.2. Conservation Unit: CK-07 – Maria Slough

Maria Slough is a single site CU, located upstream of the Harrison R (Figure 7.74). It is the only Lower Fraser Chinook population with a summer-run, 4_1 life history. The population has been periodically enhanced since 1996 at Chehalis R Hatchery, but CWT sample data were only available between 2000–2003. No strays were observed in these years, and correctly homed, natural-origin Maria Slough Chinook returned in the majority in all years except for 2001 (Figure 7.75, Table E61). $pHOS_{local}$ ranged from 0.05 to 0.60, and *PNI* from 0.11 to 0.64, fluctuating between an integrated-hatchery and integrated-transition *PNI* designation. The stock is currently enhanced with an objective of conservation.

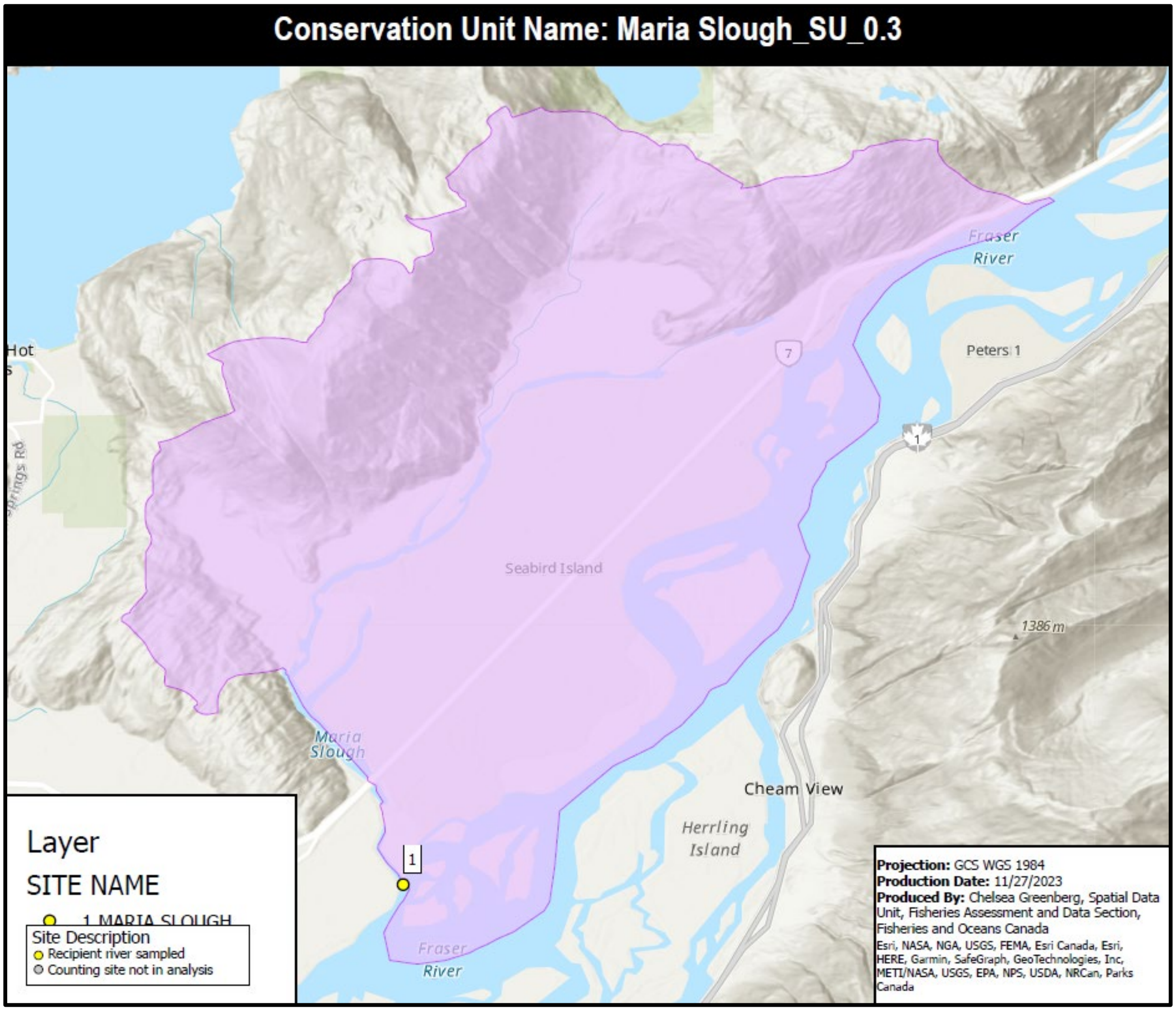

Figure 7.84. Boundary map of the CK-07 Conservation Unit (Maria Slough) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

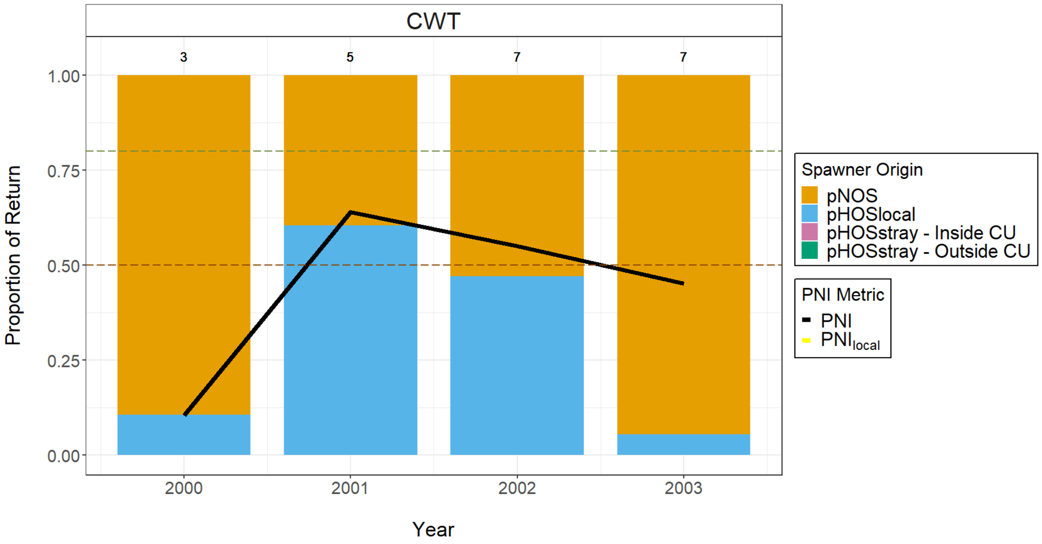

Figure 7.85. Origin of spawners returning to Maria Slough between 2000 and 2003 estimated from CWT recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners (pHOSlocal), strayed hatchery-origin spawners originating from inside the CU (pHOSstray – Inside CU), and strayed hatchery-origin spawners originating from outside the CU (pHOSstray – Outside CU) are described annually. The unexpanded, annual sample size of CWTs examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

7.9. STOCK MANAGEMENT UNIT: FRASER SUMMER RUN 5_2 CHINOOK SALMON

7.9.1. Conservation Unit: CK-14 – South Thompson-Summer Run (1.3)

In CK-14 (South Thompson-Summer Run (1.3)), Chinook occur mainly in Salmon R and Eagle R, with smaller populations present in Seymour River and Scotch Cr (Figure 7.76). In this analysis, we only present data for Salmon R/TOMF. This river joins Shuswap Lake south of the entrance to the Lower Shuswap R, near the town of Salmon Arm, BC. The population was historically enhanced by SEP at the Eagle River Hatchery, but is now supplemented by Spius Cr Hatchery. The population was marked with CWTs until brood year 2008. During this time, no stray recoveries were observed (Table E62). $pHOS_{local}$ was relatively low between 1998–2012, averaging 0.29 and peaking at 0.44 in 1999 and 2002 (Figure 7.77). *PNI* values averaged 0.72 during this time, and fluctuated between 0.56 and 0.94. Currently, this population is designated as integrated-transition (*PNI* between 0.50 and 0.80).

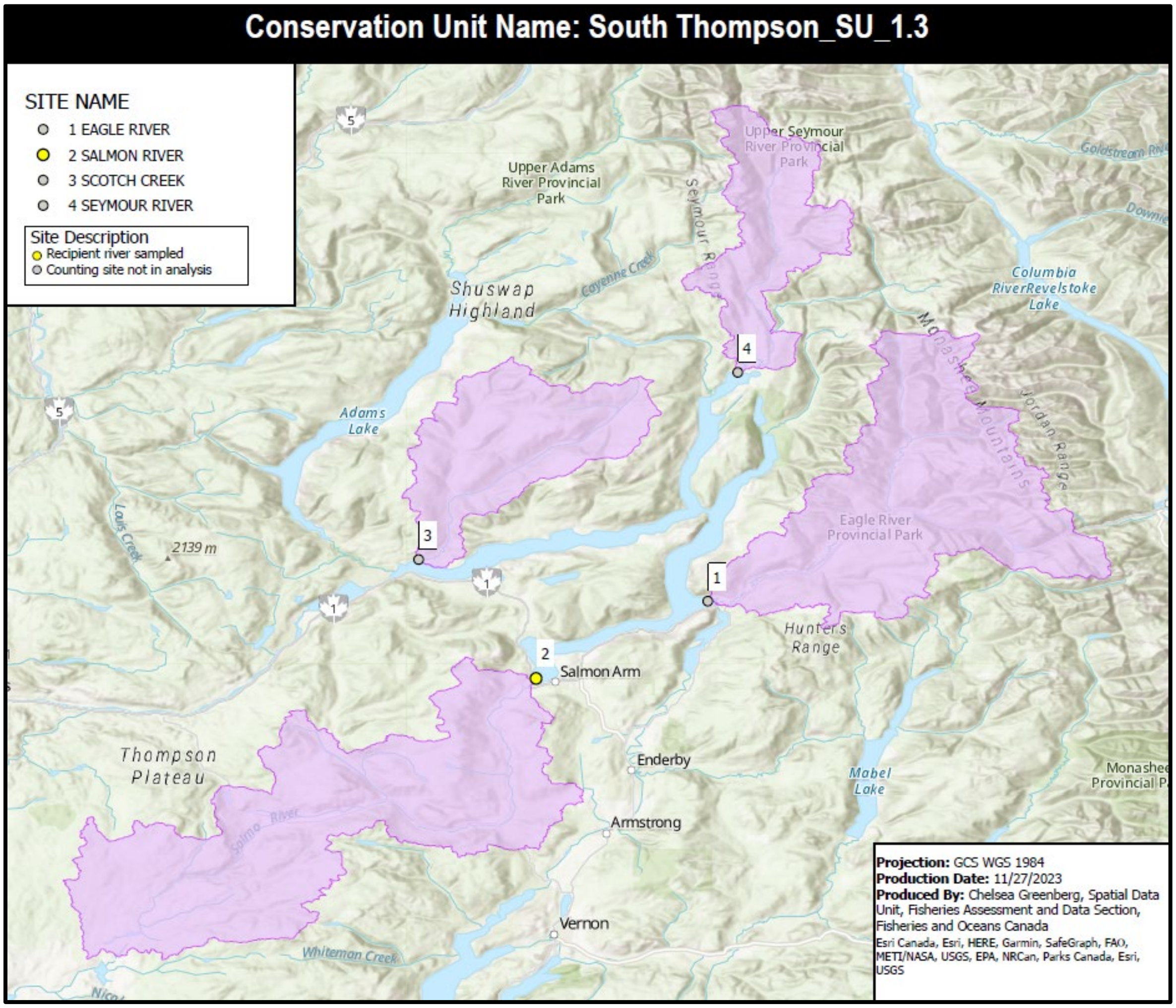

Figure 7.86. Boundary map of the CK-14 Conservation Unit (South Thompson-Summer Run (1.3)) including all recorded Chinook sampling sites in NuSEDS since 1953. Recipient rivers used in this analysis are described in yellow.

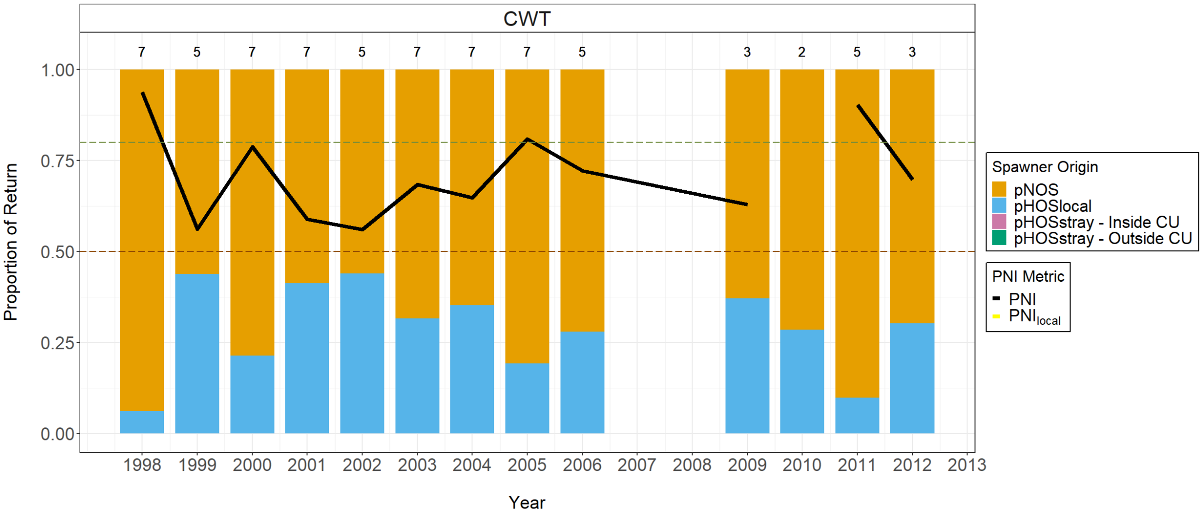

Figure 7.87. Origin of spawners returning to Salmon R/TOMF between 1998 and 2012 estimated from CWT recoveries. The proportion of local natural-origin spawners (pNOS), local hatchery-origin spawners ($pHOS_{local}$), strayed hatchery-origin spawners originating from inside the CU ($pHOS_{stray}$ – Inside CU), and strayed hatchery-origin spawners originating from outside the CU ($pHOS_{stray}$ – Outside CU) are described annually. The unexpanded, annual sample size of CWTs examined is described above each year. Estimates of the proportionate natural influence (PNI); and PNI from local-only spawners (PNI_{local}) are described by the black and yellow lines respectively. Benchmarks for PNI designations are provided based on Withler et al. (2018): Integrated Wild – PNI ≥ 0.80; Integrated Transition – PNI between 0.50 and 0.80; Integrated-Hatchery – PNI < 0.5.

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9. REFERENCES CITED

Anderson, J.H., Warheit, K.I., Craig, B.E., Seamons, T.R., and Haukenes, A.H. 2020. A review of hatchery reform science in Washington State. Final Report to the Washington Fish and Wildlife Commission. 168 pp.

Arkoosh, M.R., Strickland, S., VanGaest, A., Ylitalo, G.M., Johnson, L., Yanagida, G.K., Collier, T.K., Dietrich, J.P. 2011. Trends in organic pollutants and lipids in juvenile Snake River spring Chinook salmon with different outmigrating histories through the lower Snake and middle Columbia rivers. Sci. Total Environ. 409(23): 5086–5100.

Araki, H., Berejikian, B.A., Ford, M.J., and Blouin, M.S. 2008. Fitness of hatchery-reared salmonids in the wild. Evolut. App. 1(2): 342–355.

Beacham, T.D., Wallace, C., MacConnachie, C., Jonsen, K., McIntosh, B., Candy, J.R., and Withler, R.E. 2017. Population and individual identification of Chinook salmon in British Columbia through parentage-based tagging and genetic stock identification with single nucleotide polymorphisms. Can. J. Fish. Aquat. Sci. 75(7): 1096–1105.

Beacham, T.D., Wallace, C., Jonsen, K., McIntosh, B., Candy, J.R., Willis, D., Lynch, C., and Withler, R.E. 2019. Variation in migration pattern, broodstock origin, and family productivity of coho salmon hatchery populations in British Columbia, Canada, derived from parentage-based tagging. Ecol. Evolut. 9(17): 9891–9906.

Beacham, T.D., Wallace, C., Jonsen, K., Sutherland, B.J.G., Gummer, C., and Rondeau, E.B. 2021a. Estimation of conservation unit and population contribution to Chinook salmon mixed-stock fisheries in British Columbia, Canada, using direct DNA sequencing for single nucleotide polymorphisms. Can. J. Fish. Aquat. Sci. 78(10): 1422–1434.

Beacham, T.D., Wallace, C., Jonsen, K., McIntosh, B., Candy, J.R., Horst, K., Lynch, C., Willis, D., Luedke, W., Kearey, L., and Rondeau, E.B. 2021b. Parentage-based tagging combined with genetic stock identification is a cost-effective and viable replacement for coded-wire tagging in large-scale assessments of marine Chinook salmon fisheries in British Columbia, Canada. Evolut. App. 14(5): 1365–1389.

Beacham, T.D., Jonsen, K., Sutherland, B.J.G., Ramshaw, B., and Rondeau, E.B. 2022. Parentage-based tagging and genetic stock identification applied to assessment of mixed-stock fisheries and hatchery broodstocks for Chinook salmon in British Columbia, Canada. Fish. Res. 253: 1063–1069.

Bett, N.N., Hinch, S.G., Burnett, N.J., Donaldson, M.R., and Naman, S.M. 2017. Causes and Consequences of Straying into Small Populations of Pacific Salmon. Fisheries. 42(4): 220–230.

Brown, G.S., Baillie, S.J., Thiess, M.E., Bailey, R.E., Candy, J.R., Parken, C.K., and Willis, D.M. 2019. Pre-COSEWIC review of southern British Columbia Chinook Salmon (*Oncorhynchus tshawytscha*) conservation units, Part I: Background. DFO Can. Sci. Advis. Sec. Res. Doc. 2019/011. vii + 67 p.

Candy, J.R., and Beacham, T.D. 2000. Patterns of homing and straying in southern British Columbia coded-wire tagged chinook salmon (*Oncorhynchus tshawytscha*) populations. Fish. Res. 47(1): 41–56.

Candy, J.R., Bonnell, R.G., Beacham, T. D., Wallace, C. G., and Withler, R.E. 2009. Dividing population genetic distance data with the software Partitioning Optimization with Restricted Growth Strings (PORGS): an application for Chinook salmon (*Oncorhynchus tshawytscha*), Vancouver Island, British Columbia. Fish. Bull. 107: 45–56.

Chapman, D., Carlson, C., Weitkamp, D., Matthews, G., Stevenson, J., and Miller, M. 1997. Homing in sockeye and chinook salmon transported around part of the smolt migration route in the Columbia River. N. Am. J. Fish. Manag. 17: 101–113.

Dat, C.G., LeBlond, P.H., Thompson, K.A., and Ingraham, W.J. Jr. 1995. Computer simulations of homeward migrating Fraser River sockeye salmon: is compass orientation a sufficient direction-finding mechanism in the north-east Pacific Ocean? Fish. Oceanogr. 4: 209–219.

DFO. 2013. Review and update of southern BC Chinook conservation unit assignments. DFO Can. Sci. Advis. Sec. Sci. Resp. 2013/022.

Dittman, A.H., and Quinn, T.P. 1996. Homing in Pacific salmon: mechanisms and ecological basis. J. Experimental Biol. 199: 83–91.

English, K.K, Bailey, R.E., and Robichaud, D. 2007. Assessment of chinook salmon returns to the Fraser River watershed using run reconstruction techniques, 1982–2004. DFO Can. Sci. Advis. Sec. Res. Doc. 2007/020. vi + 76 p.

Ford, M.J. 2002. Selection in captivity during supportive breeding may reduce fitness in the wild. Conserv. Biol. 16: 815–825.

Ford, M.J., Murdoch, A., and Hughes, M. 2015. Using parentage analysis to estimate rates of straying and homing in Chinook salmon (*Oncorhynchus tshawytscha*). Mol. Ecol. 24(5): 1109–21.

Habicht, C., Sharr, S., Evans, D., and Seeb, J.E. 1998. Coded Wire Tag Placement Affects Homing Ability of Pink Salmon. Trans. Am. Fish. Soc. 127(4): 652–657.

Hard, J.J., and Heard, W.R. 1999. Analysis of straying variation in Alaskan hatchery chinook salmon (*Oncorhynchus tshawytscha*) following transplantation. Can. J. Fish. Aquat. Sci. 56: 578–589.

Hasler, A.D. 1971. Orientation and fish migration. pp. 429–510. *In*: W.S. Hoar and D.J. Randall (Eds.) Fish Physiology. Vol. 6. Academic Press, New York.

Hasler, A.D., and Scholz, A.T. 1983. Olfactory imprinting and homing in salmon: Investigations into the mechanism of the imprinting process. SpringerVerlag, Berlin, New York.

Hatchery Scientific Review Group (HSRG). 2009. Columbia River Hatchery Reform System Wide Report.

Hatchery Scientific Review Group (HSRG). 2014. On the Science of Hatcheries: An updated perspective on the role of hatcheries in salmon and steelhead management in the Pacific Northwest. A. Appleby, H.L. Blankenship, D. Campton, K. Currens, T. Evelyn, D. Fast, T. Flagg, J. Gislason, P. Kline, C. Mahnken, B. Missildine, L. Mobrand, G. Nandor, P. Paquet, S. Patterson, L. Seeb, S. Smith, and K. Warheit. June 2014; revised October 2014.

Hatchery Scientific Review Group (HSRG). 2017. Implementation of hatchery reform in the context of recovery planning using the AHA/ISIT tool.

Hatchery Scientific Review Group (HSRG). 2020. Developing recovery objectives and phase triggers for salmonid populations. Hatchery Scientific Review Group (HSRG) White Paper. 84 pp.

Healey, M.C. 1991. Life history of chinook salmon (*Oncorhynchus tshawytscha*). *In*: Groot C, Margolis, L. (Eds.) Pacific salmon life histories. University of British Columbia Press, Vancouver, pp 313–393.

Heard, W.R. 1996. Sequential imprinting in chinook salmon: Is it essential for homing fidelity? Bull. Nat. Res. Inst. Aquacult. Supp 2: 59–64.

Hendry, A.P., Castric, V., Kinnison, M.T., and Quinn, T.P. 2004. The evolution of philopatry and dispersal: homing versus straying in salmonids. *In*: Hendry, A.P., Stearns, S.C. (Ed.) Evolution Illuminated: Salmon and Their Relatives. Oxford University Press, New York, pp 52–91.

Hess, J.E., and Matala, A.P. 2014. Archival genetic analysis suggests recent immigration has altered a population of Chinook salmon in an unsupplemented wilderness area. Conserv. Genet. 15: 387–403.

Holtby, L.B. and Ciruna, K.A. 2007. Conservation Units for Pacific Salmon under the Wild Salmon Policy. DFO Can. Sci. Advis. Sec. Res. Doc. 2007/070. viii + 350 p.

Jefferts, K.B., Bergman, P.K., and Fiscus, H.F. 1963. A coded wire identification system for macroorganisms. Nature. 98: 460–462.

Johnson, J.K. 2004. Regional Overview of Coded Wire Tagging of Anadromous Salmon and Steelhead in Northwest America Paper updated from 1989 to current year 2004. Regional Mark Processing Center, Pacific States Marine Fisheries Commission.

Keefer, M.L., Peery, C.A., Firehammer, J., and Moser, M.L. 2005. Straying rates of known-origin adult Chinook salmon and steelhead within the Columbia River basin, 2000-2003. Technical Report 2005-5, Idaho Cooperative Fish and Wildlife Research, University of Idaho, Moscow.

Keefer, M.L., Caudill, C.C., Peery, C.A., and Boggs, C.T. 2008. Non-direct homing behaviours by adult Chinook salmon in a large, multi-stock river system. J. Fish. Biol. 72: 27–44.

Keefer, M.L., and Caudill, C.C. 2014. Homing and straying by anadromous salmonids: a review of mechanisms and rates. Rev. Fish Biol. Fish. 24: 333–368.

Labelle, M. 1992. Straying patterns of coho salmon (*Oncorhynchus kisutch*) stocks from southeastern Vancouver Island, British Columbia. Can. J. Fish. Aquat. Sci. 49: 1843–1855.

Leider, S.A. 1989. Increased straying by adult steelhead trout, Salmo gairdneri, following the 1980 eruption of Mount St. Helens. Env. Biol. Fish. 24: 219–229.

Le Luyer, J., Laporte, M., Beacham, T.D., Kaukinen, K.H., Withler, R.E., Leong, J.S., Rondeau, E.B., Koop, B.F., and Bernatchez, L. 2017. Parallel epigenetic modifications induced by hatchery rearing in a Pacific Salmon. Proceedings of the National Academy of Sciences U.S.A. 114: 12964–12969.

Masuda, M.M., and Celewycz, A.G. 2019. Coded-Wire Tag Sampling: The Case for Electronic-Field Detection. Northwest Sci. 93(2): 102–111.

McCormick, S.D., O'Dea, M.F., Moeckel, A.M., and Bjørnsson, B.T. 2003. Endocrine and physiological changes in Atlantic salmon smolts following hatchery release. Aquaculture. 222: 45–57.

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. U.S. Dept. Commer., NOAA Tech. Memo. NMFS-NWFSC-42,156 p.

Milner, A.M., and Bailey, R.G. 1989. Salmonid colonization of new streams in Glacier Bay National Park, Alaska. Aqua. Fish. Mgmt. 20: 179–192.

Moore, A., Lower, N., Mayer, I., and Greenwood, L. 2007. The impact of a pesticide on migratory activity and olfactory function in Atlantic salmon (*Salmo salar*) smolts. Aquaculture. 273: 350–359.

Mortensen, D.G., Wertheimer, A.C., Maselko, J.M., and Taylor, S.G. 2002. Survival and straying of Auke Creek, Alaska, pink salmon marked with coded wire tags and thermally induced otolith marks. Trans. Am. Fish. Soc. 131: 14–26.

Nandor, G.F., Longwill, J.R., and Webb, D.L. 2010. Overview of the coded wire tag program in the greater Pacific region of North America. PNAMP Special Publication: Tagging, Telemetry and Marking Measures for Monitoring Fish Populations—A compendium of new and recent science for use in informing technique and decision modalities: Pacific Northwest Aquatic Monitoring Partnership Special Publication. 2: 5–46.

Nevitt, G.A., Dittman, A.H., Quinn, T.P., Moody, W.J. Jr. 1994. Evidence for a peripheral olfactory memory in imprinted salmon. P. Nat. Acad. Sci. USA. 91: 4288–4292.

O’Brien, D.O., DiNovo, S., and Till, J. 2012. Estimates of the abundance of hatchery chinook in wild spawning populations and Canadian otolith thermal mark data summary (1997-2010). Report to the Southern Endowment Fund.

Pacific Salmon Commission (PSC). 2005. Expert Panel on the Future of the Coded Wire Tag Program for Pacific Salmon. Pacific Salmon Comm. Tech. Rep. No. 18 p.

Pacific Salmon Commission (PSC). 2008. Pacific Salmon Commission Coded Wire Tag Workgroup. An action plan in response to Coded Wire Tag (CWT) Expert Panel Recommendations. Pacific Salmon Comm. Tech. Rep. No. 25: 170 p.

Pascual, M.A., and Quinn, T.P. 1994. Geographical patterns of straying of fall chinook salmon, *Oncorhynchus tshawytscha* (Walbaum), from Columbia River (USA) hatcheries. Aquacult. Fish. Manag. 25(Supp. 2): 17–30.

Pearsons, T.N., and O'Connor, R.R. 2020. Stray Rates of Natural-Origin Chinook Salmon and Steelhead in the Upper Columbia River Watershed. Trans. Am. Fish. Soc. 149: 147–158.

Pearsons, T.N., and Miller, M.D. 2023. Stray compositions of hatchery-origin Chinook Salmon and steelhead in natural spawning populations of the upper Columbia watershed. Trans. Am. Fish. Soc. 152(5): 515–529.

Pess, G.R., 2009. Patterns and processes of salmon colonization. Dissertation. University of Washington.

Pollock, A.M.M., Kamran, M., Dittman, A.H., Johnson, M.A., and Noakes, D.L.G. 2020. Within-river straying: sex and size influence recovery location of hatchery Chinook salmon (*Oncorhynchus tshawytscha*). Can. J. Fish. Aquat. Sci. 77(2): 226–235.

Pritchard, J.K., Stephens, M., and Donnelly, P. 2000. Inference of population structure using multilocus genotype data. Genetics. 155: 945–959.

Putman, N.F., Lohmann, K.J., Putman, E.M., Quinn, T.P., Klimley, A.P., and Noakes, D.L.G. 2013. Evidence for geomagnetic imprinting as a homing mechanism in Pacific salmon. Curr Biol. 23: 312–316.

Quinn, T.P. 1984. Homing and straying in Chinook salmon (*Oncorhynchus tshawytscha*) from the Cowlitz River hatchery, Washington. Can. J. Fish. Aquat. Sci. 41: 1078–1082.

Quinn, T.P. 1993. A review of homing and straying of wild and hatchery-produced salmon. Fish. Res. 18: 29–44.

Quinn, T.P. 2005. The behavior and ecology of Pacific salmon and trout. Am. Fish. Soc. Bethesda.

Quinn, T.P., and Fresh, K. 1984. Homing and straying in chinook salmon (*Oncorhynchus tshawytscha*) from Cowlitz River Hatchery, Washington. Can. J. Fish. Aquat. Sci. 41: 1078–1082.

Quinn, T.P., Nemeth, R.S., and McIsaac, D.O. 1991. Homing and straying patterns of fall chinook salmon in the lower Columbia River. Trans. Am. Fish. Soc. 120: 150–156.

Ricker, W.E. 1972. Hereditary and environmental factors affecting certain salmonid populations. *In*: The stock concept of Pacific salmon. R.C. Simon and P. Larkin. (Eds.) 19–160. Univ. British Columbia Press, Vancouver, B.C.

Satterthwaite, W., Anderson, E., Campbell, M., Carlos Garza, J., Mohr, M., Narum, S., and Speir, C. 2015. Multidisciplinary evaluation of the feasibility of parentage-based tagging (PBT) for management of Pacific Salmon. Report to the Pacific Salmon Commission.

Schindler, D.E., Hilborn, R., Chasco, B., Boatright, C.P., Quinn, T.P., Rogers, L.A., and Webster, M.S. 2010. Population diversity and the portfolio effect in an exploited species. Nature. 465(7298): 609–612.

Schubert, N.D. 1993. Enumeration of the 1988-1992 Squamish River Chinook Salmon escapement. Can. Manuscr. Rep. Fish. Aquat. Sci. 2187: 96 p.

Sharp, D., Sharr, S., and Peckham, C. 1994. Homing and straying patterns of coded wired tagged pink salmon in Prince William Sound. In: Proceedings of the 16th Northeast Pacific pink and chum salmon workshop. Alaska Sea Grant College Program, Juneau, pp 77–82.

Stewart, I.J., Carlson, S.M., Boatright, C.P., Buck, G.B., and Quinn, T.P. 2004. Site fidelity of spawning sockeye salmon (*Oncorhynchus nerka*) in the presence and absence of olfactory cues. Ecol. Freshwater Fish. 13: 104–110.

Tallman, R.F., and Healey, M.C. 1994. Homing, straying, and gene flow among seasonally separated populations of chum salmon (*Oncorhynchus keta*). Can. J. Fish. Aquat. Sci. 51: 577–588.

Taylor, E.B. 1990. Environmental correlates of life-history variation in juvenile chinook salmon, *Oncorhynchus tshawytscha* (Walbaum). J. Fish. Biol. 37(1): 1–17.

Volk, E.C., Schroder, S.L., Grimm, J.J., and Sprague Ackley, H. 1994. Use of a Bar Code Symbology to Produce Multiple Thermally Induced Otolith Marks. Trans. Am. Fish. Soc. 123(5): 811–816.

Waples, R.S., Pess, G.R. and Beechie, T. 2008. Evolutionary history of Pacific salmon in dynamic environments. Evol. App. 1: 189–206.

Westley, P.A.H, Quinn, T.P., and Dittman, A.H. 2013. Rates of straying by hatchery-produced Pacific salmon (*Oncorhynchus* spp.) and steelhead (*Oncorhynchus mykiss*) differ among species, life history types, and populations. Can. J. Fish. Aquat. Sci. 70: 735–746.

Withler, R.E., Bradford, M.J., Willis, D.M., and Holt, C. 2018. Genetically Based Targets for Enhanced Contributions to Canadian Pacific Chinook Salmon Populations. DFO Can. Sci. Advis. Sec. Res. Doc. 2018/019. xii + 88 p. (Erratum: October 2023)

Zimmer-Faust, R.K., Finellli, C.M., Pentcheff, N.D., and Wethey, D.S. 1995. Odor plumes and animal navigation in turbulent water flow: a field study. Biol. Bull. 188: 111–116.

APPENDIX A. DEFINITION OF TERMS AND DATABASES

Basin (for non-Fraser R populations): For non-Fraser R systems, a basin is defined as a distinct river that empties into the ocean *i.e.* there is no mixing of freshwater prior to entering the ocean.

Basin (for Fraser R populations; adapted from Ford et al. (2015) and others): A large reach of a connected watershed or drainage basin that drain into a common outlet (e.g., the Lower Fraser, or Thompson R reaches).

BioData: All biological sampling data and measurements collected for SBC Chinook Salmon. Here, thermal mark records from Otomanager were appended along with any available age and release data.

Community and Economic Development (CEDP) facility: Hatchery facilities with the intended goal of conserving or rebuilding salmon populations, typically while providing an economic benefit to an Indigenous or other community group.

Conservation Unit: A geographic region representing an ecological zone, containing Pacific salmon populations that share a specific life history type and genetic distinctiveness at neutral genetic loci. A CU contains a group of wild salmon sufficiently isolated from other groups that, if lost, is very unlikely to recolonize naturally within an acceptable timeframe (e.g., a human lifetime).

CWT: Coded-wire tag; a small piece of magnetized wire (0.25 x 1.1 mm) implanted into the nasal cartilage of juvenile salmon that encodes hatchery-specific rearing and release group information.

Deadpitch: A sampling method of surveying carcasses on the spawning grounds of natural river systems.

Donor Straying: The loss of individuals from a source population or hatchery stock (Bett et al. 2017). The donor stray rate, or *stray rate* is defined for a given stock as the proportion of salmon returning to spawn at all non-natal sites out of the total number of spawners originating from that stock, both homed and strayed.

Escapement: The number of salmon returning to the spawning grounds. In the absence of other sources of mortality, the total run-size to a system is the total catch plus the total escapement.

Enhancement Planning and Assessment Database (EPAD): A database that stores all brood collection, marking, sampling and assessment records from SEP hatcheries; the source of all CWT data and associated hatchery information used in this study. Data from OPS hatcheries are entered directly by facilities, which are then populated in the EPAD database.

Gene flow: The movement of genes from one population to another, causing the populations to become more similar.

Hatchery-origin: A spawning adult salmon incubated and reared in the hatchery environment.

Homing: The biological process of salmon species to return to spawn in the river basin in which they were born.

Integrated Hatchery Program: Hatchery-origin and natural-origin fish are two components of a single population and spawn in both the hatchery and natural environments of the local watershed. The intent of an integrated program is for the natural environment to drive the adaptation of the combined hatchery-natural population.

Integrated-wild populations (Withler et al. 2018): Populations that have a *PNI* > 0.80, and are managed to achieve conservation and natural-origin genetic goals while contributing to hatchery production. Benchmarks for this category are set to ensure the majority (>50%) of salmon spawning in the river meet the criteria for Wild under the WSP, and nearly three-fourths of the spawning population are of natural origin. The resultant *PNI* is considered large enough (> 0.80) to ensure the population will be dominated by natural-origin spawners.

Integrated-transition populations (Withler et al. 2018): Populations that have a *PNI* value between 0.5 and 0.80, indicating that there is a net gene flow from the natural-origin component to the hatchery component. In these populations, we would expect 25–50% of spawners in the natural environment to be considered Wild under the WSP.

Integrated-hatchery populations (Withler et al. 2018): Populations that have a *PNI* < 0.5, in which hatchery produced salmon dominate both the broodstock and natural spawning components. In these instances, it is recognized that the magnitude of hatchery production, the small proportion of natural-origin and near absence of wild fish are likely to have impacts on the fitness and productivity of the integrated population.

Introgression: The incorporation of genetic material from one population into another through interbreeding, that can result in a loss of genetic distinctiveness among groups.

Mark recovery program (MRP): A database of marked Chinook and Coho Salmon recoveries in Canada and the USA.

Natural-origin (spawner): A spawning adult salmon born in the natural environment from parents born in either the natural or hatchery environment (compare to ‘wild’ salmon).

NuSEDS (New Salmon Escapement Database System): Annual salmon escapement reports, stream inspection logs (SILs) and estimates of annual returns collated by DFO. All escapement data used in this analysis were originally queried from NuSEDS, except in cases where data were missing. For such cases, annual data reports from DFO's Stock Assessment Branch were used, if available.

OPS (Major operations) hatcheries: Large-scale hatchery facilities that typically enhance salmon populations for harvest or assessment purposes (e.g., Robertson Cr Hatchery).

Otomanager: A database of otolith samples analyzed for thermal marks and associated hatchery IDs.

Out-of-basin stray: An adult Chinook Salmon that returns to spawn in a *river basin* other than that in which they were born.

Out-of-CU stray: An adult Chinook Salmon that returns to spawn in a *CU* other than that in which they were born.

Pacific Salmon Commission (PSC): A governmental body formed by the Canada and the United States in 1985 to implement the Pacific Salmon Treaty.

Parr-smolt transformation (PST): A critical salmon life stage in which juveniles transition from freshwater to the marine environment. Increased hormone release at this stage is theorized to be critical for correct imprinting.

***pHOS* (proportion of hatchery-origin spawners):** The proportion of Chinook on the spawning grounds that are of hatchery origin, first defined by the US Hatchery Scientific Review Group (2009). *pHOS* is typically estimated from natural spawners in the river. In this analysis, *pHOS* was calculated using natural spawners when available, and broodstock collection samples when unavailable.

$pHOS_{census}$: The census or count-based estimate of the proportion of hatchery-origin spawners**.** In this analysis, we use this value as our calculated *pHOS* metric.

$pHOS_{eff}$: An adjusted *pHOS* value that accounts for the decreased relative-reproductive success, and selection pressures acting against hatchery-origin spawners.

$pHOS_{local}$: The proportion of correctly homed, hatchery-origin Chinook Salmon (i.e., local hatchery spwaners).

$pHOS_{stray}$: The proportion of hatchery-origin Chinook Salmon, that originated from an out-of-basin river system (i.e., strayed hatchery spawners).

PIP facility (Public Involvement Program): Small-scale salmon enhancement activities that are typically run by small community groups with the goal of stewardship or education.

Proportionate Natural Influence (*PNI*): a metric that ranges between 0 and 1 to indicate the relative influences of the natural and hatchery environments on a salmon population. *PNI* values are approximated by *pNOB*/(*pNOB* + *pHOS*). Values > 0.5 indicate that the natural environment is the primary environment influencing adaptation.

PNI_{local}: A theoretical derivation of the PNI calculation that includes only local hatchery fish, indicating what relative influence of natural and hatchery environments would be, if no out-of-basin strays were observed.

***pNOB*:** The proportion of a hatchery broodstock that is composed of natural-origin adults.

***pNOS*:** The proportion of a natural spawning populations that is comprised of natural-origin adults.

Population: A group of interbreeding adults, typically confined to a geographic location that collectively interbreed and contain genetic material available for future adaptation; used synonymously with *stock* in this report.

Recipient population: Any river or system that receives strays from a donor population. This includes both hatchery enhanced systems that may produce and receive strays, as well as unenhanced populations that only receive strays alongside natural-origin salmon. In this work, we describe the proportion of strays in a recipient population as the contribution of strays to a river.

Relative reproductive success (RRS): The reproductive success of hatchery-origin adults as relative to natural-origin adults measured as the contribution of individuals to the next generation of spawners. Factors that may influence the RRS include environmental modification due to the hatchery environment, domestication and epigenetic alteration of hatchery fish.

Salmonid Enhancement Program (SEP): A group within DFO that manages, and administers hatchery enhancement in British Columbia.

Satellite-rearing: A hatchery rearing practice in which adults are taken as broodstock in the river, spawned either on or offsite; and have their brood incubated and reared at a facility, before being released back into the natal river as juveniles.

Southern BC (SBC): The study area used in this analysis demarcated by a latitudinal line drawn approximately from Cape Caution, BC (~51.17^{o}N) across the province.

Straying: The biological process of an adult salmon returning to and spawning in a non-natal river basin.

Stock Management Unit (SMU): A group of one or more conservation units (CU) that are managed together with shared objectives.

Sub-basin (for Fraser R populations; adapted from Ford et al. (2015) and others): A smaller subunit of a watershed within a larger drainage area that exists within and drains into other sub-basins that make up a larger basin (e.g., the Lower and South Thompson R).

Thermal Mark: A permanent modification of otolith microchemistry during juvenile rearing that is observable as a series of distinct bands on the otolith of an adult salmon; and corresponds to a specific hatchery.

Transplant: A hatchery practice in which juveniles from a non-local stock are released into a system with the goal of having those fish return to the river of their release (a transplanted Chinook is said to have homed correctly only if it returns to spawn at the location of its release).

Tributary (for Fraser R populations; adapted from Ford et al. (2015) and others): A small section of river that resides within a sub-basin and flows into other streams within a larger geographical unit. Chinook Salmon in this analysis were not said to have strayed if recovered in another tributary within the same sub-basin.

Wild (Salmon): As defined in the Wild Salmon Policy, a wild salmon is any salmon that spawns in the natural environment, and is itself the progeny of *two natural-origin parents*.

Wild-stray influenced populations (Withler et al. 2018): Populations lacking hatchery supplementation that receive strays from out-of-basin hatcheries at rates that exceed the limits specified for a Wild designation (3%) under the WSP. Although the majority of salmon may be Wild, one-way gene flow modelling suggests that over time the population will be dominated by hatchery influences.

WSP (Wild Salmon Policy): Canada’s national policy framework concerning the conservation, protection and management of wild Pacific Salmon.

APPENDIX B. CONSERVATION UNITS IN BRITISH COLUMBIA

Table B1. Conservation units of southern BC Chinook Salmon grouped by geographic region, not including Columbia River. From Brown et al. 2016.

Area	CU Index	CU Name	CU Acronym	Juvenile Life History	Adult Run Timing	Average Generation Time	Total Census Sites	Basis for CU
Fraser River-Lower	CK-03	Lower Fraser River_FA_0.3	LFR-fall	Ocean	Fall	4	1	Life history and run timing
	CK-04	Lower Fraser River_SP_1.3	LFR-spring	Stream	Spring	5	3	Life history and run timing
	CK-05	Lower Fraser River-Upper Pitt_SU_1.3	LFR-UPITT	Stream	Summer	5	1	Spawn (and run?) timing
	CK-06	Lower Fraser River_SU_1.3	LFR-summer	Stream	Summer	5	8	Life history and run timing
	CK-07	Maria Slough_SU_0.3	Maria	Ocean	Summer	4	1	Geography (otherwise similar to CK-13)
	CK-9008	Fraser-Harrison fall transplant_FA_0.3	Chil_trans_FA	Ocean	Fall	3	1	Enhancement bin
Fraser River-Upper	CK-08	Middle Fraser River-Fraser Canyon_SP_1.3	FRCanyon	Stream	Spring	5	2	Genetics (confirmed since original designation)
	CK-09	Middle Fraser River-Portage_FA_1.3	Portage	Stream	Fall	5	1	Life history and run timing
	CK-10	Middle Fraser River_SP_1.3	MFR-spring	Stream	Spring	5	24	Run timing
	CK-11	Middle Fraser River_SU_1.3	MFR-summer	Stream	Summer	5	18	Run timing
	CK-12	Upper Fraser River_SP_1.3	UFR-spring	Stream	Spring	5	41	Run timing
Fraser River-Thompson	CK-13	South Thompson_SU_0.3	STh-0.3	Ocean	Summer	4	5	Life history, age and spawning location (genetics similar to CK-07)
	CK-14	South Thompson_SU_1.3	STh-1.3	Stream	Summer	5	4	Life history, age and genetics
	CK-15	Shuswap River_SU_0.3	STh-SHUR	Ocean	Summer	4	3	Genetics (otherwise similar to CK-13)

Area	CU Index	CU Name	CU Acronym	Juvenile Life History	Adult Run Timing	Average Generation Time	Total Census Sites	Basis for CU
	CK-82	Upper Adams River_ SU_1.X	UADAMS	Ocean	Summer	5	1	Genetics and run timing, new CU. Does not fit with other South Thompson CUs.
	CK-16	South Thompson-Bessette Creek_SU_1.2	STh-BESS	Stream	Summer	4	4	Life history and age
	CK-17	Lower Thompson_SP_1.2	LTh	Stream	Spring	4	9	Genetics, run timing and age
	CK-18	North Thompson_SP_1.3	NTh-spr	Stream	Spring	5	7	Genetics, run timing and age
	CK-19	North Thompson_SU_1.3	NTh-sum	Stream	Summer	5	7	Run timing (otherwise similar to CK-18)
Strait of Georgia Basin	CK-02	Boundary Bay_FA_0.3	BB	Ocean	Fall	4	3	Life history and geography.
	CK-20	Southern Mainland-Georgia Strait_FA_0.X	SMn-GStr	Ocean	Fall	4	42	Geography and comparison to Coho and Chum population structure.
	CK-21	East Vancouver Island-Goldstream_FA_0.X	Goldstr	Ocean	Fall	3	2	Genetics
	CK-22	East Vancouver Island-Cowichan & Koksilah_FA_0.X	CWCH-KOK	Ocean	Fall	3	6	Genetics and run timing
	CK-23	East Vancouver Island-Nanaimo-SP	NanR-spr	Stream	Spring	4	1	Age, genetics, run timing
	CK-83	East Vancouver Island-Georgia Strait_SU_0.3	EVI-sum	Ocean	Summer	4	4	Genetics and run timing, CK-24 and CK-26 merged
	CK-25	East Vancouver Island-Nanaimo & Chemainus_FA_0.X	EVI-fall	Ocean	Fall	3	4	Genetics and run timing
	CK-27	East Vancouver Island-Qualicum & Puntledge_FA_0.X	QP-fall	Ocean	Fall	4	17	Genetics and run timing
WCVI NEVI	CK-28	Southern Mainland-Southern Fjords_ FA_0.X	SMn-SFj	Ocean	Fall	4	25	Run timing and habitat

Area	CU Index	CU Name	CU Acronym	Juvenile Life History	Adult Run Timing	Average Generation Time	Total Census Sites	Basis for CU
Upper South Coast	CK-29	East Vancouver Island-North_FA_0.X	NEVI	Ocean	Fall	4	18	Run timing and habitat
	CK-31	West Vancouver Island-South_FA_0.X	SWVI	Ocean	Fall	4	69	Run timing and habitat, CK-30 and CK-31 merged
	CK-32	West Vancouver Island-Nootka & Kyuquot_ FA_0.X	NoKy	Ocean	Fall	4	57	Run timing
	CK-33	West Vancouver Island-North_FA_0.X	NWVI	Ocean	Fall	4	17	Ecotype
	CK-34	Homathko_SU_X.X	HOMATH	Stream	Summer	5	2	Genetics
	CK-35	Klinaklini_SU_1.3	KLINA	Stream	Summer	5	2	Genetics

APPENDIX C. ESCAPEMENT SAMPLING, MARKING METHODS AND DATA QUALITY

C.1. DATA QUALITY OF SPAWNER ESTIMATES

Obtaining accurate estimates of annual escapement is not trivial. For example, annual variation in river conditions (e.g., years with low water, flooding, water clarity issues) can influence Chinook spawning behaviour and the ability to accurately enumerate them. In addition, due to operational needs (e.g., budget restrictions, personnel shortages, weather delays, equipment failure) enumeration effort can also vary from year to year and potentially bias annual estimates.

Note that locations with time series data for escapement estimates (identified by a unique *population ID* (called ‘POP_ID’ in NuSEDS) will be referred to in this document as river populations or spawning sites. This terminology was adopted to highlight that escapement enumeration can occur at different types of locations, not just at spawning ground locations. It also recognizes that data from a given census or survey site may or may not be representative of the escapement for an entire population.

Until 1992, Chinook Salmon escapement data collection was primarily the responsibility of DFO Fishery Officers who were stationed in field offices. Observational methods with varying degrees of scientific rigour were used to provide estimates of escapement in each river. These estimates were recorded on a standardized form known as the “BC-16”. DFO Science became responsible for escapement monitoring, guidance/coordination of partners, and analysis and estimation of escapement in 1993.

A summary of rivers which were sampled for strays in the period 1998–2021 are provided in Table C1.

Currently, in the WCVI, we use six estimate types to indicate estimate quality, here collapsed under the following three levels:

1. High Quality – Indicator Systems, providing True Abundance

These estimates are subject to quality control and peer review. Estimates of abundance are reliable and include an estimate of uncertainty.

Full quantitative escapement assessments of indicator streams or other complete escapement counts are classified as True Abundance; fish are counted as they move upstream past a fixed location at fishways or fences, using video recordings or sonar counting systems (e.g., DIDSON), mark-recapture, or other method with known accuracy and precision. Some indicator stocks are marked (e.g., using coded-wire tags or thermally-marked otoliths) and recovery of marks in fisheries and escapement allows survival, distribution, and exploitation rate parameters to be estimated.

NuSEDS Estimate Classifications: Type-1, True, high resolution; Type-2, True, medium resolution

2. Medium (or mixed high and medium) quality – Intensive Monitoring providing Relative Abundance

Estimates for most systems that are monitored for escapement are classified as relative abundance estimates, where a partial quantitative escapement assessment is conducted. The type of these survey assessments are periodic and include swim surveys, helicopter counts, bank or stream walks, tagging and index surveys. Methods are generally consistent from year to year, so relative change can be monitored. AUC estimates are calculated when the system was surveyed with good coverage of the population on a regular basis (from 4 to 10 surveys over the spawning season, covering the start, peak and end of the run) and PL+D estimates are used when the surveys are too far apart (longer than the expected survey life of the species for that system), or there are too few surveys to calculate an AUC.

Relative abundance estimates in hatchery systems are often monitored more closely than other systems, and may include a mixed survey type (e.g., True Abundance counts of fish entering the hatchery mixed with estimates for the river via swim surveys or overflights). Salmon returns to PSC escapement indicators as well as key systems such as Nitinat, Conuma, and San Juan are in this category.

These estimates have greater uncertainly and potential biases relative to Level 1, but are useful for informing fishery management decisions.

NuSEDS Estimate Classifications: Type-3, Relative, high resolution; Type-4, Relative, medium resolution

3. Lower quality – Extensive Monitoring providing Presence/Absence and distribution information

This category defines the estimate when only a partial count was available, and/or the count was not representative of the entire population or habitat. These are generally reliable as adults present (when one or more adults were observed), or absent (none observed during a survey).

These estimates generally fail to meet standards of scientific quality for informing fishery management decisions. However, the information is still used to monitor salmon spatial distribution, habitat usage, and response to habitat change.

NuSEDS Estimate Classification: Type-5, Consistent, Relative, low resolution; Type-6, Presence or Absence

Table C1. Summary of rivers which were sampled for strays in the period 1998–2021, termed recipient rivers. This table was adapted from Brown et al. (2019). Rivers are identified to region and WSP Conservation Unit (CU). Key information for each river is enhancement level, escapement (esc.) monitoring start date, data quality and average decadal escapement of both natural and hatchery origin spawners since 2000. Average escapement estimate quality is based on quality 'type' scores reported in NuSEDS for annual escapement estimates by river; where Type-3 or Type-4 scores reflect consistent inter-annual indices of abundance and Type-1 or Type-2 reflect true estimates of spawner abundance. Quality score 1 is the highest quality and quality score 4 is the lowest quality. Escapement estimates with mostly Type 5 and 6 estimates were not included in Brown et al (2019) assessment and not included in this review. Decadal average escapements were calculated from all non-zero escapement estimates reported in NuSEDS between the years described.

Recipient River	Region	CU	Enhancement Level	Escapement Sampling Start Year	Mean Data Quality of Escapement (from Brown et al. 2019)	Avg. Escapement (2000–2009)	Avg. Escapement (2010–2019)
Marble R	Quatsino Sd (WCVI)	CK-033	Mod	1996	3.94	2652	3260
Artlish R	Kyuquot Sd (WCVI)	CK-032	None	1995	3.33	269	382
Kaouk R		CK-032	None	1995	3.28	437	361
Kauwinch R		CK-032	None	--	--	--	154
Tahsish R		CK-032	None	1995	3.71	341	736
Conuma R	Nootka Sd (WCVI)	CK-032	High	1995	3.31	20248	25730
Burman R		CK-032	Mod	1995	3.12	817	4221
Gold R		CK-032	LowMod	--	--	627	1503
Leiner R		CK-032	LowMod	1995	3.35	444	876
Sucwoa R		CK-032	None	1995	3.00	84	80
Tahsis R		CK-032	LowMod	1995	3.83	576	641
Tlupana R		CK-032	None	1995	3.67	532	276
Zeballos R		CK-032	Low	1995	3.69	240	240
Bedwell R	Clayoquot Sd (WCVI)	CK-031	VeryLow	1995	2.06	119	311
Cypre R		CK-031	Low	1995	4.00	481	1274

Recipient River	Region	CU	Enhancement Level	Escapement Sampling Start Year	Mean Data Quality of Escapement (from Brown et al. 2019)	Avg. Escapement (2000–2009)	Avg. Escapement (2010–2019)
Megin R		CK-031	None	1995	3.86	57	42
Moyeha R		CK-031	None	1995	3.35	136	83
Tranquil Cr		CK-031	Low	1995	3.00	891	272
Robertson Cr	Barkley Sd (WCVI)	CK-031	VeryHigh	1995	1.11	45863	38014
Nahmint R		CK-031	Low	1995	3.50	443	441
Sarita R		CK-031	Mod	1995	3.40	2009	1956
Toquart R		CK-031	Low	--	--	450	243
Nitinat R	NIT-SKE (WCVI)	CK-031	High	1995	3.11	16062	22540
San Juan R		CK-031	Mod	1995	4.00	1890	1656
Sooke R		CK-031	Mod	1995	3.11	536	575
Cowichan R	ECVI	CK-022	Mod	1988	1.32	4787	11731
Chemainus R		CK-025	None	--	--	194	540
Nanaimo Fall		CK-025	Mod	1995	2.00	3114	3968
Nanaimo Summ		CK-083	Low	1995	4.00	555	761
Big Qualicum R		CK-027	High	1995	1.78	8904	6832
L Qualicum R		CK-027	Mod	1995	3.00	4690	4780
Puntledge Fall		CK-027	Mod	1995	2.44	9326	7911
Puntledge Sum		CK-083	Mod	1995	2.11	1536	875
Camp/Quins		CK-029	High	1995	2.00	9197	5778
Nimpkish R		CK-029	None	--	--	533	1632
Capilano R	Coastal Inlets	CK-9007	Mod	--	--	1198	2200
Lang Cr		CK-9007	Low	--	--	1430	1151
Salmon R/JNST		CK-029	Mod	1995	3.20	903	550
Phillips R		CK-028	Mod	2002	3.22	441	2067
Chilliwack R	Lower Fraser	CK-9008	High	1986	3.93	45245	40172
Chehalis R		CK-9006	Mod	--	--	377	369
Stave R		CK-9006	Mod	--	--	887	180
Maria Sl		CK-007	Low	1996	3.63	524	618
Birkenhead R		CK-004	Mod	1975	4.00	788	503
Harrison R		CK-003	Low	1984	2.00	99974	62431
Coldwater R	Lower Thompson	CK-017	Mod	1995	4.00	657	388
Nicola R		CK-017	Mod	1995	2.00	7026	3932

Recipient River	Region	CU	Enhancement Level	Escapement Sampling Start Year	Mean Data Quality of Escapement (from Brown et al. 2019)	Avg. Escapement (2000–2009)	Avg. Escapement (2010–2019)
Spius Cr		CK-017	Mod	1995	4.00	701	350
Shuswap R Low	South Thompson	CK-015	Mod	1983	2.77	31007	27463
Shuswap R Mid		CK-015	Mod	1983	2.77	3446	1968
Salmon R/ TOMF		CK-014	Mod	1999	2.79	865	582

C.2. ESCAPEMENT SAMPLING TYPES IN SBC

Dead pitch sampling (the examination of spawned out carcasses in the river), gives a direct estimate of the origin of spawner from CWT or otolith thermal mark. It is often more difficult to execute due to carcass decay, predation, and restricted river access under certain flow conditions. It is also subject to representation biases, often lacking temporal coverage of the run as samples are typically taken before water levels rise and wash away carcasses. Further, shore access during sampling may limit the ability to obtain representative coverage across sizes of returning Chinook. Dead pitch sampling is part of all Level 1 escapement monitoring and some Level 2 depending on funding, feasibility, and sampler capacity.

Brood stock samples are taken annually to supplement enhanced river systems, and so can provide a more consistent data time series. Brood stock can be taken from hatchery swim-ins or from rivers. Swim-ins have been shown to have a higher proportion hatchery compared to brood stock taken from the river. This is a potential source of bias. In key indicator systems, including SEP major facilities, this is taken into account in reconstructing the total return by hatchery and natural origin.

Brood stock is examined for sex and adipose fin clip status; heads are removed from clipped Chinook to check for the presence of a CWT. Broader systematic sampling of all Chinook is conducted to obtain general biological information (e.g., age, sex, length, DNA) and take heads for CWT and/or otolith removal. Sample data are entered and stored in the Enhancement Planning and Assessment (EPAD) database.

For each recipient river examined, we describe the escapement sample types and number of years where marked fish were recovered in Table C2. Sampling types were not necessarily consistent over time, and in some years multiple types were used to calculate stray rates and contribution to the escapement.

Table C2. Sample types used in the analysis of stray rate and contribution to SBC rivers. The total years sampled reflect how many years of data exist in Biodata and EPAD databases between 1998–2021, and the 'number (No.) of years w/recoveries' denote in how many sampling years coded-wire-tag (CWT), or thermally marked (TM) hatchery-Chinook were recovered.

Recipient River	Region	CU	Sample Types Analyzed	Total Years Sampled (1998–2021)	No. of Years w/Recoveries (1998–2021)	
					CWT	TM
Marble R	Quatsino Sd	CK-033	Broodstock, Deadpitch	9	2	9
Artlish R	Kyuquot Sd	CK-032	Deadpitch	2	--	2
Kaouk River		CK-032	Deadpitch	7	--	7
Kauwinch River		CK-032	Deadpitch	1	--	1

Recipient River	Region	CU	Sample Types Analyzed	Total Years Sampled (1998–2021)	No. of Years w/Recoveries (1998–2021)	
					CWT	TM
Tahsish River		CK-032	Deadpitch	5	--	5
Conuma R	Nootka Sd	CK-032	Broodstock, Swim-ins, Deadpitch	23	10	23
Burman R		CK-032	Broodstock, Deadpitch	18	1	18
Gold R		CK-032	Broodstock	16	2	16
Leiner R		CK-032	Broodstock	13	1	13
Sucwoa R		CK-032	Broodstock	5	--	5
Tahsis R		CK-032	Broodstock	15	--	15
Tlupana R		CK-032	Broodstock	9	3	9
Zeballos River		CK-032	Broodstock, Deadpitch	7	--	7
Bedwell R	Clayoquot Sd	CK-031	Broodstock, Deadpitch	8	5	8
Cypre R		CK-031	Deadpitch	7	1	7
Megin River		CK-031	Deadpitch	2	--	2
Moyeha River		CK-031	Deadpitch	3	1	3
Tranquil Cr		CK-031	Broodstock, Deadpitch	9	--	9
Robertson Cr	Barkley Sd	CK-031	Broodstock, Swim-ins, Deadpitch	24	24	24
Nahmint R		CK-031	Broodstock, Deadpitch	21	14	21
Sarita R		CK-031	Broodstock, Deadpitch	23	13	23
Toquart R		CK-031	Broodstock, Deadpitch	2	1	2
Nitinat R	NIT-SKE	CK-031	Broodstock, Swim-ins, Deadpitch	24	13	24
San Juan R		CK-031	Broodstock, Deadpitch, FSC Fisheries	11	--	11
Sooke R		CK-031	Broodstock	14	2	14
Cowichan R	ECVI	CK-022	Broodstock, Deadpitch, FSC Fisheries	24	24	18
Chemainus R		CK-025	Broodstock, Deadpitch	4	1	4
Nanaimo R - Fall		CK-025	Broodstock, Swim-ins, Deadpitch	15	--	15
Nanaimo R - Summer		CK-083	Broodstock, Swim-ins, Deadpitch	15	--	15
Big Qualicum R		CK-027	Broodstock, Swim-ins, Deadpitch	24	24	--
L Qualicum R		CK-027	Swim-ins (Spawning Channel Sampling)	12	12	--
Puntledge R - Fall		CK-027	Broodstock, Swim-Ins	24	24	1
Puntledge R - Summer		CK-083	Broodstock, Swim-Ins	24	24	3
Campbell/Quinsam		CK-029	Broodstock, Swim-ins, Deadpitch	24	24	4
Nimpkish R		CK-029	Broodstock	6	6	6
Capilano R	Coastal Inlets	CK-9007	Swim-Ins	14	14	--
Lang Cr		CK-9007	Deadpitch	0	--	--
Salmon R/JNST		CK-029	Broodstock	10	--	10
Phillips R		CK-028	Broodstock, Natural Spwaner Escapement	1	--	1
Chilliwack R	Lower Fraser	CK-9008	Broodstock, Swim-ins, Deadpitch	24	24	14
Chehalis R		CK-9006	Broodstock, Swim-Ins	6	1	6
Stave R		CK-9006	Deadpitch	6	6	--
Maria Sl		CK-007	Deadpitch	4	4	--

Recipient River	Region	CU	Sample Types Analyzed	Total Years Sampled (1998–2021)	No. of Years w/Recoveries (1998–2021)	
					CWT	TM
Birkenhead R		CK-004	Deadpitch	2	2	--
Harrison R		CK-003	Deadpitch	24	24	--
Coldwater R	Lower Thompson	CK-017	Deadpitch	6	6	--
Nicola R		CK-017	Broodstock, Deadpitch	24	24	--
Spius Cr		CK-017	Broodstock	7	7	5
Shuswap R Low	South Thompson	CK-015	Broodstock, Deadpitch	24	24	--
Shuswap R Middle		CK-015	Broodstock, Deadpitch	22	22	--
Salmon R/TOMF		CK-014	Broodstock	13	13	7

C.3. HATCHERY MARKING OF CHINOOK IN SOUTHERN BC

Table C3. Table of donor hatchery and stocks by region, hatchery facility, donor stock, and the period in which marks were applied (coded-wire tags, thermal marks, and parentage-based tags (PBT). Stocks indicated in bold had a continuous time-series in which they were marked and sufficient sample recoveries such that trends in stray rate could be described in this analysis. There 11 Canadian CWT indicator stocks distributed among 11 southern BC Chinook CUs. All are based in large-scale conventional hatchery facilities with five located in the Fraser River drainage and six distributed around Vancouver Island. Also included are non-indicator stocks enhanced for harvest or rebuilding objectives that were regularly marked between 1998–2021. Recent pilots of hatchery mass marking along the WCVI (Conuma, Burman, Gold, Sarita populations) started in 2019, were interrupted by COVID, and so visual assessment of hatchery contributions to subsequent spawning escapement were not available for this report.

Region	Hatchery Facility	Donor Stocks Reared at Facility	Available Marks	Years Marked*		
				CWT	TM	PBT
WCVI	Nitinat River	**Nitinat R, Sarita R**	PBT, TM, CWT	1980–Present	1992–Present	2013–Present
WCVI	Robertson Creek	**Somass-Sproat-GC System, Nahmint R**	PBT, TM, CWT	1980–Present	1992–Present	2013–Present
WCVI	Conuma River	**Conuma R, Burman R, Gold R**, Leiner R, Sucwoa R, Tahsis R, Tlupana R, Zeballos R	PBT, TM	1980–2002	1994–Present	2014–Present
ECVI	Big Qualicum River	**Big Qualicum R**	PBT, CWT	1980–Present	--	2013–Present
ECVI	Cowichan River H	**Cowichan R**	PBT, TM, CWT	1980–Present	2006–Present	2013–Present
ECVI	LQR Spawning Channel	Little Qualicum R, Big Qualicum R	PBT	1984–2002	--	2018–Present
ECVI	Nanaimo River	**Nanaimo R (Fall and Summer runs)**	PBT, TM	1980–2004	2005–Present	2018–Present
ECVI	Puntledge River	**Puntledge R (Fall and Summer runs)**	PBT, CWT	1980–Present	--	2013–Present
ECVI	Quinsam River	**Campbell R, Quinsam R**	PBT, TM, CWT	1980–Present	1996–Present	2013–Present
Coastal Inlets	Tenderfoot Creek	Ashlu Cr, Cheakamus R, Mamquam R, Shovelnose Cr	PBT, CWT	1982–Present	--	2016–Present

Region	Hatchery Facility	Donor Stocks Reared at Facility	Available Marks	Years Marked*		
				CWT	**TM**	**PBT**
Coastal Inlets	Capilano River	**Capilano R, Chilliwack R**	PBT, CWT	1992–Present	--	2013–Present
Lower Fraser	Chilliwack River	**Chilliwack R (Fall** and Summer runs)	PBT, CWT, TM	1984–Present**	1995–Present**	2013–Present**
Lower Fraser	Chehalis River	**Harrison R**, Chehalis R	PBT, CWT	1980–Present	--	2018–Present
Mid-Fraser (Lower Thompson)	Spius Creek	**Nicola R**, Spius Cr, Coldwater Cr, Salmon R/TOMF	PBT, CWT	1981–Present	--	2013–Present
Mid-Fraser (South Thompson)	Shuswap Falls	**Lower Shuswap R, Middle Shuswap R**	PBT, CWT	1984–Present	--	2013–Present

* ‘years marked’ may not include stocks satellite reared at the facility, but will always include the ‘home stock’ returning to the facility.

** Chilliwack R ‘years marked’ is described for the Fall run population. The summer run was not CWT marked until brood year 2022, and was not PBT marked until 2018.

C.4. PARENTAGE-BASED TAGGING

An alternative tag for the assessment of hatchery versus wild salmon stocks is the use of genetically based tags. There are diagnostic genetic differences among salmon stocks, CUs and individuals, and once this genetic variation is resolved, salmon collected in a mixed-stock sample can be identified by comparison to the known catalog of variation. For Chinook salmon, DFO has established a coast-wide baseline for genetic variation at 547 single-nucleotide polymorphisms (SNPs) covering over 369 collection sites (Beacham et al. 2021a). This baseline supports genetic-stock identification (GSI) to the CU level for the majority of BC Chinook stocks (Beacham et al. 2021a; Beacham et al. 2022). Moreover, essentially all Chinook hatchery broodstocks in BC are now genotyped at these same SNPs. Thus, mixed-stock hatchery individuals can also be assigned back to their specific parents as a result of the inheritance of diagnostic variation among brood fish, with assignment accuracy estimated to be >99.5% (Beacham et al. 2017). These parentage assignments, which are known as parentage-based tags (PBTs), dramatically improve the resolution of identifications possible for hatchery-origin Chinook salmon. For instance, PBTs allow straightforward assessment of hatchery of origin, age structure, proportion of hatchery-origin fish and effects of hatchery practices on returning salmon (e.g., Beacham et al. 2019).

The potential utility of a GSI-PBT approach for monitoring and managing the mixed-stock Chinook fishery was appreciated by the Pacific Salmon Commission as early as 2005 (PSC 2005). Three necessary requirements were set out that would need to be met before GSI-PBTs could potentially replace CWT assessments:

1. GSI-PBTs would need to generate equivalent information to CWTs;
2. GSI-PBTs could not increase overall costs associated with monitoring; and
3. any increase in costs associated with GSI-PBTs would need to generate information above and beyond that provided by CWTs.

Based on the recent large-scale coast-wide evaluation of GSI-PBT in Canadian Chinook Salmon, all three of these requirements have been met for Canadian stocks through application of the current DFO SNP panel (Beacham et al. 2021a).

PBT application began in 2013 and has steadily increased such that effectively all SBC Chinook broodstocks have been genotyped with the DFO SNP panel since 2020, which means comprehensive

PBT analyses for SBC Chinook are now ongoing. The increased resolution allows hatchery-origin SBC Chinook salmon to be definitively assigned back to the site and year of production. While PBTs were not used to assess hatchery stray rates in this report, the availability of PBTs moving forward will represent a substantial benefit for comprehensive monitoring of hatchery strays in SBC (see Table 5 in Beacham et al. 2022).

For the purposes of monitoring hatchery straying in SBC Chinook Salmon, PBTs offer two primary advantages in comparison to thermal marks and CWTs. First, the methods used to genotype PBTs are standard molecular techniques that can be applied by many laboratories without the specialized technical skills involved in otolith analysis, which requires intensive training. Second, as SBC Chinook broodstocks are already fully genotyped, the PBT tagging rate of hatchery-origin SBC Chinook Salmon can be as high as 100% (barring sample quality issues), which is much higher than CWT tagging rates (typically ~10% in BC; Satterthwaite et al. 2015). Given published hatchery stray rates are typically low in SBC (~5% or less; e.g., Candy and Beacham 2000), nearly complete tagging with PBT substantially improves the ability to accurately detect the rate of hatchery straying, and straying can be monitored comprehensively at an equivalent or lower expense (Beacham 2021b).

APPENDIX D. DONOR RIVER STRAYING TABLES

*Table D1. Total expanded recoveries for the **Conuma R** donor stock based **on CWT sampling** in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: CONUMA R												
Recipient CU	**Recipient River**	**1998**	**1999**	**2000**	**2001**	**2002**	**2004**	**2005**	**2006**	**2007**	**2008**	**AVG**
CK-32	**Conuma R**	20461	10366	5151	12369	19533	31715	35856	4656	17626	891	**–**
CK-31	**Sarita R**	–	–	–	–	–	–	3	–	–	–	–
CK-27	**Puntledge R - Fall**	–	15	–	–	–	–	–	–	–	–	–
S_{TOT}	–	0	15	0	0	0	0	3	0	0	0	**2**
S_{OCU}	–	0	15	0	0	0	0	3	0	0	0	**2**
H_{TOT}	–	20461	10381	5151	12369	19533	31715	35859	4656	17626	891	**15864**
SR	–	**0.0%**	**0.1%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**
SR_{OCU}	–	**0.0%**	**0.1%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**

Table D2. Total expanded recoveries for the ***Conuma R*** *donor stock based* ***on thermal mark sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: CONUMA R

Recipient CU	Recipient River	1998	1999	2000	2001	2002	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	AVG
CK-033	**Marble R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	6	–	–	–	–	–	–
CK-032	**Conuma R**	18612	15610	9188	17542	27266	29857	7248	23165	8747	12639	17162	16426	21627	6590	61167	21172	40865	37109	23984	11482	8924	9201	13442	–
	Artlish R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	602	59	–	–	–	–	–	–
	Burman R	–	–	–	–	–	201	91	71	22	–	541	287	–	8	837	712	2025	1277	140	1620	–	81	537	–
	Gold R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	85	–	–	6	–	–	–
	Kaouk R	–	–	–	–	–	–	–	–	–	–	86	–	–	–	–	94	–	–	–	–	–	–	–	–
	Kauwinch R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	254	–	–	–	–	–	–	–
	Leiner R	–	–	–	–	–	–	–	63	44	–	182	–	–	230	47	84	362	453	715	188	44	207	85	–
	Sucwoa R	–	–	–	–	40	–	25	–	–	–	–	16	–	40	–	–	–	–	–	–	–	–	–	–
	Tahsis R	–	–	–	–	–	51	–	9	–	31	61	18	–	–	–	–	90	51	88	13	–	–	–	–
	Tahsish R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	383	–	312	317	1156	–	–	–	–	–
	Tlupana R	–	–	–	359	1140	–	–	–	–	66	–	21	–	46	948	–	–	–	–	–	–	–	–	–
	Zeballos R	–	–	–	–	154	256	39	268	261	196	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-031	**Bedwell R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	16	–	–	–	–
	Megin R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	36	–	32	–	–	–	–	–
	Moyeha R	–	–	–	–	–	–	–	–	–	–	–	109	–	–	–	–	–	–	–	–	–	–	–	–
	Nahmint R	–	–	–	–	3	–	–	5	–	–	–	–	–	–	–	–	28	44	5	–	21	17	–	–
	San Juan R	–	–	–	–	–	–	–	91	–	–	–	–	–	–	–	–	25	–	–	–	–	–	–	–
	Sarita R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	5	–	30	–	–	–	–	–	–	–
	Toquart R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	26	9	–	–	–	–	–	–
S_{TOT}	–	**0**	**0**	**0**	**359**	**1337**	**508**	**154**	**506**	**327**	**294**	**870**	**451**	**0**	**324**	**2221**	**890**	**3790**	**2299**	**2134**	**1838**	**71**	**305**	**623**	**839**
S_{OCU}	–	**0**	**0**	**0**	**0**	**3**	**0**	**0**	**96**	**0**	**0**	**0**	**109**	**0**	**0**	**5**	**0**	**145**	**58**	**36**	**16**	**21**	**17**	**0**	**22**
H_{TOT}	–	**18612**	**15610**	**9188**	**17901**	**28603**	**30364**	**7402**	**23671**	**9074**	**12933**	**18032**	**16877**	**21627**	**6913**	**63388**	**22061**	**44655**	**39408**	**26118**	**13320**	**8995**	**9506**	**14065**	**20797**
SR	–	**0.0%**	**0.0%**	**0.0%**	**2.0%**	**4.7%**	**1.7%**	**2.1%**	**2.1%**	**3.6%**	**2.3%**	**4.8%**	**2.7%**	**0.0%**	**4.7%**	**3.5%**	**4.0%**	**8.5%**	**5.8%**	**8.2%**	**13.8%**	**0.8%**	**3.2%**	**4.4%**	**3.6%**
SR_{OCU}	–	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.4%**	**0.0%**	**0.0%**	**0.0%**	**0.6%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.3%**	**0.1%**	**0.1%**	**0.1%**	**0.2%**	**0.2%**	**0.0%**	**0.1%**

Table D3. Total expanded recoveries for the ***Burman R*** *donor stock based* ***on thermal mark sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: BURMAN R

Recipient CU	Recipient River	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	AVG
CK-032	**Conuma R**	–	–	–	–	–	698	–	–	–	–	129	–	–	55	29	–	–
	Burman R	234	237	419	1174	2549	1995	1297	7299	2124	2799	7342	857	1154	1939	2222	3146	–
	Gold R	–	–	–	–	–	14	–	–	–	–	57	–	–	75	246	–	–
	Kaouk R	–	–	–	–	–	–	–	–	–	14	–	–	–	–	–	–	–
	Leiner R	–	–	–	–	–	–	–	–	–	8	–	–	9	7	–	–	–
	Tahsis R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	21	–
	Tahsish R	–	–	–	–	–	–	–	–	–	62	26	26	–	–	–	–	–
	Zeballos R	27	–	12	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-031	**Robertson Cr**	–	–	–	–	–	–	–	–	–	56	–	–	–	–	–	–	–
CK-022	**Cowichan R**	–	–	–	–	8	–	–	–	–	–	–	–	–	–	–	–	–
S_{TOT}	–	**27**	**0**	**12**	**0**	**8**	**712**	**0**	**0**	**0**	**141**	**212**	**26**	**9**	**137**	**275**	**21**	**99**
S_{OCU}	–	**0**	**0**	**0**	**0**	**8**	**0**	**0**	**0**	**0**	**56**	**0**	**0**	**0**	**0**	**0**	**0**	**4**
H_{TOT}	–	**261**	**237**	**430**	**1174**	**2557**	**2706**	**1297**	**7299**	**2124**	**2939**	**7554**	**883**	**1163**	**2076**	**2497**	**3167**	**2398**
SR	–	**10.2%**	**0.0%**	**2.7%**	**0.0%**	**0.3%**	**26.3%**	**0.0%**	**0.0%**	**0.0%**	**4.8%**	**2.8%**	**3.0%**	**0.8%**	**6.6%**	**11.0%**	**0.7%**	**4.3%**
SR_{OCU}	–	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.3%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**1.9%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.1%**

*Table D4. Total expanded recoveries for the **Gold R** donor stock based **on thermal mark sampling** in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported. Years where < 20 thermally marked Chinook were sampled in the donor river system are listed in grey and marked with an asterisk (*). Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} (located in the right-hand column) were calculated using only those years in which ≥ 20 homed, thermally marked Chinook were recovered in the donor river.*

DONOR RIVER: GOLD R

Recipient CU	Recipient River	2005*	2006*	2009*	2011*	2012	2013	2015*	2016	2017*	2018*	2019	2020	AVG
CK-032	**Conuma R**	–	–	–	–	–	–	–	–	130	–	–	–	–
	Burman R	13	22	7	–	–	–	402	91	9	142	31	58	–
	Gold R	50	–	–	70	198	297	167	699	–	–	445	2733	–
	Leiner R	–	–	–	–	–	–	–	–	–	–	7	–	–
	Tahsis R	–	–	–	–	–	–	20	31	–	–	–	–	–
	Zeballos R	2	27	–	–	–	–	–	–	–	–	–	–	–
CK-031	**Robertson Cr**	–	–	–	–	34	–	–	117	62	–	–	–	–
	Bedwell R	–	–	–	–	–	–	120	171	51	–	14	–	–
	Nahmint R	–	–	–	–	–	–	14	15	–	–	–	–	–
S_{TOT}	–	15	49	7	0	**34**	**0**	556	**425**	252	142	**52**	**58**	**114**
S_{OCU}	–	0	0	0	0	**34**	**0**	134	**303**	113	0	**14**	**0**	**70**
H_{TOT}	–	65	49	7	70	**232**	**297**	723	**1123**	252	142	**497**	**2791**	**988**
SR	–	23.1%	–	–	0.0%	**14.8%**	**0.0%**	76.9%	**37.8%**	–	–	**10.5%**	**2.1%**	**13.0%**
SR_{OCU}	–	0.0%	–	–	0.0%	**14.8%**	**0.0%**	18.6%	**27.0%**	–	–	**2.8%**	**0.0%**	**8.9%**

Table D5. Total expanded recoveries for the ***Robertson Cr*** *donor stock based* ***on CWT sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: ROBERTSON CR

Recipient CU	Recipient River	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	AVG
CK-032	**Burman R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	931	–	–	–	–	–
	Gold R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	1377	–	–
CK-031	**Nahmint R**	–	–	–	–	–	–	6	–	–	–	–	–	–	–	–	–	7	–	–	–	–	–	–	–	–
	Robertson Cr	28304	11599	5782	29132	38333	50790	67660	25633	37634	17711	23217	16234	27067	16708	11788	13378	19589	25684	33567	34263	25268	23630	27262	40515	–
	Nitinat R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	332	71	11	–	–
CK-029	**Campbell/ Quinsam R**	74	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	17	–	–	–	–	–
CK-022	**Cowichan R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	114	–	–	–	–	–	–	–
CK-027	**Puntledge R - Fall**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	27	–	–	9	–	–	–	–
CK-9007	**Capilano R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	13	–	–	–	–	–	–	–
CK-9008	**Chilliwack R**	–	–	–	–	–	–	462	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-03	**Harrison R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	194	–	–	–	–	–
S_{TOT}	–	**74**	**0**	**0**	**0**	**0**	**0**	**468**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**7**	**153**	**0**	**1142**	**341**	**71**	**1388**	**0**	**152**
S_{OCU}	–	**74**	**0**	**0**	**0**	**0**	**0**	**462**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**153**	**0**	**1142**	**9**	**0**	**1377**	**0**	**134**
H_{TOT}	–	**28378**	**11599**	**5782**	**29132**	**38333**	**50790**	**68128**	**25633**	**37634**	**17711**	**23217**	**16234**	**27067**	**16708**	**11788**	**13378**	**19595**	**25837**	**33567**	**35405**	**25609**	**23701**	**28650**	**40515**	**27266**
SR	–	**0.3%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.7%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.6%**	**0.0%**	**3.2%**	**1.3%**	**0.3%**	**4.8%**	**0.0%**	**0.5%**
SR_{OCU}	–	**0.3%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.7%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.6%**	**0.0%**	**3.2%**	**0.0%**	**0.0%**	**4.8%**	**0.0%**	**0.4%**

*Table D6. Total expanded recoveries for the **Robertson Cr** donor stock based **on thermal mark sampling** in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: ROBERTSON CR

Recipient CU	Recipient River	‘98	‘99	‘00	‘01	‘02	‘03	‘04	‘05	‘06	‘07	‘08	‘09	‘10	‘11	‘12	‘13	‘14	‘15	‘16	‘17	‘18	‘19	‘20	‘21	AVG
CK-033	**Marble R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	6	–	–	–	–	–	–
CK-032	**Artlish R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	33	–	–	–	–	–	–	–
	Kaouk R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	262	–	–	–	–	–	–	–	–	–	–
	Conuma R	–	204	–	–	–	–	–	–	–	–	–	–	–	–	17	–	–	–	–	259	–	55	29	–	–
	Burman R	–	–	–	–	–	–	–	39	–	2	–	7	–	8	4	–	–	89	46	23	263	–	58	472	–
	Gold R	–	–	–	–	–	–	–	552	–	–	–	–	–	817	485	943	–	490	1095	–	1556	705	4115	–	–
	Leiner R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	39	–	9	–	–	17	–
	Sucwoa R	–	–	–	–	–	–	–	6	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Tahsis R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	10	13	49	–	–	–
	Tlupana R	–	–	–	15	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Zeballos R	–	–	–	–	–	–	–	1	–	60	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-031	**Bedwell R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	68	–	–	–
	Cypre R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	37	–	–	–
	Tranquil Cr	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	29	–	–	–
	Robertson Cr	52785	16011	8135	51867	50472	62465	77103	42016	61721	19826	23993	22037	31188	23056	14136	25928	20174	43265	42934	46478	40569	30999	30759	31634	–
	Nahmint R	–	11	–	69	337	224	18	11	25	–	–	–	19	–	–	–	30	–	15	2	–	11	–	16	–
	Sarita R	–	–	–	–	–	40	–	–	–	–	–	–	5	–	–	–	5	10	–	9	–	–	4	11	–
	Nitinat R	–	–	–	–	–	–	63	–	32	–	–	35	9	–	–	42	36	–	–	219	440	–	40	67	–
	San Juan R	–	–	–	–	–	–	–	12	–	–	–	–	–	–	–	–	32	–	–	–	–	–	–	–	–
	Sooke R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	6	–	–	–	4	7	–	42	–
CK-029	**Cam/Quins R**	–	–	–	–	–	–	–	–	56	–	–	–	–	–	–	–	–	24	–	–	25	–	–	–	–
	Salmon R/JNS	–	–	–	–	–	–	–	–	–	–	19	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-025	**Nanaimo R - F**	–	–	–	–	–	–	74	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-083	**Nanaimo R - S**	–	–	–	–	–	–	–	3	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	13	–
CK-022	**Cowichan R**	–	–	–	–	–	–	–	15	–	–	27	–	–	–	20	–	22	127	66	–	35	66	–	–	–
CK-9008	**Chilliwack R**	–	–	–	–	–	–	448	–	117	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
S_{TOT}	–	**0**	**215**	**0**	**84**	**337**	**265**	**604**	**640**	**230**	**63**	**46**	**42**	**34**	**825**	**788**	**984**	**132**	**774**	**1266**	**522**	**2346**	**1026**	**4246**	**637**	**322**
S_{OCU}	–	**0**	**204**	**0**	**15**	**0**	**0**	**523**	**617**	**173**	**63**	**46**	**7**	**0**	**825**	**788**	**943**	**22**	**764**	**1252**	**292**	**1902**	**874**	**4202**	**502**	**263**
H_{TOT}	–	**52785**	**16225**	**8135**	**51952**	**50809**	**62729**	**77707**	**42655**	**61950**	**19888**	**24039**	**22079**	**31221**	**23881**	**14924**	**26912**	**20306**	**44039**	**44200**	**47000**	**42914**	**32025**	**35005**	**32272**	**36743**
SR	–	**0.0%**	**1.3%**	**0.0%**	**0.2%**	**0.7%**	**0.4%**	**0.8%**	**1.5%**	**0.4%**	**0.3%**	**0.2%**	**0.2%**	**0.1%**	**3.5%**	**5.3%**	**3.7%**	**0.6%**	**1.8%**	**2.9%**	**1.1%**	**5.5%**	**3.2%**	**12.1%**	**2.0%**	**2.0%**
SR_{OCU}	–	**0.0%**	**1.3%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.7%**	**1.4%**	**0.3%**	**0.3%**	**0.2%**	**0.0%**	**0.0%**	**3.5%**	**5.3%**	**3.5%**	**0.1%**	**1.7%**	**2.8%**	**0.6%**	**4.4%**	**2.7%**	**12.0%**	**1.6%**	**1.8%**

Table D7. Total expanded recoveries for the ***Nahmint R*** *donor stock based* ***on CWT sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Years where < 3 CWT marked Chinook were sampled in the donor river system are listed in grey and marked with an asterisk (*). Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} (located in the right-hand column) were calculated using only those years in which ≥3 homed, CWT-marked Chinook were recovered in the donor river.*

DONOR RIVER: NAHMINT R

Recipient CU	Recipient River	2002	2004	2010*	2012*	2013	2014*	2015	2016	2017	2018	2019	2020	2021	AVG
CK-032	**Burman R**	–	–	–	–	–	–	–	–	13	–	–	–	–	–
CK-031	**Nahmint R**	186	968	111	39	39	4	202	145	85	121	332	346	127	–
	Robertson Cr	–	67	–	–	–	–	1	–	–	1	1	–	20	–
	Sarita R	–	–	–	–	–	–	–	–	–	8	–	–	–	–
CK-025	**Big Qualicum R**	–	–	–	–	–	–	2	–	–	–	–	–	–	–
S_{TOT}	–	**0**	**67**	0	0	**0**	0	**3**	**0**	**13**	**9**	**1**	**0**	**20**	**18**
S_{OCU}	–	**0**	**0**	0	0	**0**	0	**2**	**0**	**13**	**0**	**0**	**0**	**0**	**1**
H_{TOT}	–	**186**	**1034**	111	39	**39**	4	**205**	**145**	**98**	**130**	**333**	**346**	**147**	**211**
SR	–	**0.00%**	**6.50%**	**0.00%**	**0.00%**	**0.00%**	**0.00%**	**1.40%**	**0.00%**	**13.40%**	**6.70%**	**0.30%**	**0.00%**	**13.50%**	**4.20%**
SR_{OCU}	–	**0.00%**	**0.00%**	**0.00%**	**0.00%**	**0.00%**	**0.00%**	**0.90%**	**0.00%**	**13.40%**	**0.00%**	**0.00%**	**0.00%**	**0.00%**	**0.50%**

Table D8. Total expanded recoveries for the ***Nahmint R*** *donor stock based* ***on thermal mark sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Years where < 20 thermally marked Chinook were sampled in the donor river system are listed in grey and marked with an asterisk (*). Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} (located in the right-hand column) were calculated using only those years in which ≥ 20 homed, thermally marked Chinook were recovered in the donor river.*

DONOR RIVER: NAHMINT R

Recipient CU	Recipient River	2000*	2001	2002	2003	2004	2005*	2006	2007*	2008*	2009*	2010	2012	2013	2014*	2015	2016	2017	2018*	2019	AVG
CK-032	**Leiner R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	7	–
CK-031	**Robertson Cr**	–	140	62	71	–	–	–	25	–	145	43	–	–	–	–	–	62	–	–	–
	Nahmint R	48	139	79	255	814	88	394	–	71	22	174	49	41	10	21	250	87	49	296	–
	Sarita R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	10	–	–	–	–	–
S_{TOT}	–	0	140	62	71	0	0	0	25	0	145	43	0	0	0	10	0	62	0	7	32
S_{OCU}	–	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	7	1
H_{TOT}	–	48	279	141	325	814	88	394	25	71	167	217	49	41	10	31	250	149	49	303	232
SR	–	0.0%	**50.3%**	**44.0%**	**21.7%**	**0.0%**	0.0%	**0.0%**	–	0.0%	86.8%	**20.0%**	**0.0%**	**0.0%**	0.0%	**32.6%**	**0.0%**	**41.5%**	0.0%	**2.4%**	**17.7%**
SR_{OCU}	–	0.0%	**0.0%**	**0.0%**	**0.0%**	**0.0%**	0.0%	**0.0%**	–	0.0%	0.0%	**0.0%**	**0.0%**	**0.0%**	0.0%	**0.0%**	**0.0%**	**0.0%**	0.0%	**2.4%**	**0.2%**

Table D9. Total expanded recoveries for the ***Sarita R*** *donor stock based* ***on CWT sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Years where < 3 CWT marked Chinook were sampled in the donor river system are listed in grey and marked with an asterisk (*). Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} (located in the right-hand column) were calculated using only those years in which ≥3 homed, CWT-marked Chinook were recovered in the donor river.*

DONOR RIVER: SARITA R

Recipient CU	Recipient River	1998	1999	2002	2003	2004	2011*	2012	2013	2014	2018*	2019	2020	2021	AVG
CK-031	**Robertson Cr**	18	–	–	–		–	–	–	–	–	–	–	–	–
	Sarita R	272	108	605	217	73	5	79	358	36	16	37	673	590	–
	Nitinat R	–	–	22	–	11	–	–	–	–	–	–	15	–	–
S_{TOT}	–	**18**	**0**	**22**	**0**	**11**	0	**0**	**0**	**0**	0	**0**	**15**	**0**	**5**
S_{OCU}	–	**0**	**0**	**0**	**0**	**0**	0	**0**	**0**	**0**	0	**0**	**0**	**0**	**0**
H_{TOT}	–	**290**	**108**	**627**	**217**	**84**	5	**79**	**358**	**36**	16	**37**	**689**	**590**	**241**
SR	–	**6.10%**	**0.00%**	**3.60%**	**0.00%**	**13.40%**	0.00%	**0.00%**	**0.00%**	**0.00%**	0.00%	**0.00%**	**2.20%**	**0.00%**	**2.30%**
SR_{OCU}	–	**0.00%**	**0.00%**	**0.00%**	**0.00%**	**0.00%**	0.00%	**0.00%**	**0.00%**	**0.00%**	0.00%	**0.00%**	**0.00%**	**0.00%**	**0.00%**

Table D10. Total expanded recoveries for the ***Sarita R*** *donor stock based* ***on thermal mark sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Years where < 20 thermally marked Chinook were sampled in the donor river system are listed in grey and marked with an asterisk (*). Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} (located in the right-hand column) were calculated using only those years in which ≥ 20 homed, thermally marked Chinook were recovered in the donor river.*

DONOR RIVER: SARITA R

Recipient CU	Recipient River	'98*	'99*	'00	'01	'02	'03	'04	'05	'06	'07	'08	'09	'10	'11	'12	'13	'14	'15	'16	'17	'18*	'19	'20	'21	AVG
CK-032	Kaouk R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	24	–	–	–	–	–	–	–	–
	Conuma R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	40	–
	Tahsis R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	10	13	–	–	21	–
	Zeballos R	–	–	–	–	–	–	–	1	13	20	–	5	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-031	Nahmint R	–	–	–	–	6	5	–	–	15	–	–	–	19	–	21	–	–	7	44	2	–	42	17	16	–
	Sarita R	30	5	275	206	2950	3272	2043	1199	3076	1581	929	612	783	1398	1463	952	515	2178	2947	2411	–	1695	1833	3255	–
	Nitinat R	–	242	–	–	97	–	–	–	–	–	28	35	9	–	14	–	–	25	85	292	147	–	321	67	–
	San Juan R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	4	–
S_{TOT}	–	0	242	0	0	103	5	0	1	28	20	28	41	28	0	34	0	24	32	129	305	160	42	338	147	**71**
S_{OCU}	–	0	0	0	0	0	0	0	1	13	20	0	5	0	0	0	0	24	0	0	10	13	0	0	61	**6**
H_{TOT}	–	30	247	275	206	3053	3277	2043	1200	3104	1601	957	653	811	1398	1497	952	538	2211	3077	2715	160	1737	2171	3401	**1555**
SR	–	**0.0%**	**98.1%**	**0.0%**	**0.0%**	**3.4%**	**0.2%**	**0.0%**	**0.1%**	**0.9%**	**1.3%**	**2.9%**	**6.2%**	**3.5%**	**0.0%**	**2.3%**	**0.0%**	**4.4%**	**1.5%**	**4.2%**	**11.2%**	–	**2.4%**	**15.6%**	**4.3%**	**3.1%**
SR_{OCU}	–	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.1%**	**0.4%**	**1.3%**	**0.0%**	**0.8%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**4.4%**	**0.0%**	**0.0%**	**0.4%**	–	**0.0%**	**0.0%**	**1.8%**	**0.4%**

*Table D11. Total expanded recoveries for the **Nitinat R** donor stock based **on CWT sampling** in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: NITINAT R											
Recipient CU	**Recipient River**	**1998**	**1999**	**2000**	**2001**	**2002**	**2003**	**2004**	**2005**	**2006**	**AVG**
CK-031	**Robertson Cr**	–	27	–	–	–	–	–	–	–	–
	Sarita R	–	42	–	–	–	–	23	–	–	–
	Nitinat R	33946	20162	8749	13273	4278	25100	14793	16334	10447	–
CK-029	**Campbell/Quinsam R**	–	–	–	–	–	–	57	–	–	–
S_{TOT}	–	**0**	**69**	**0**	**0**	**0**	**0**	**80**	**0**	**0**	**17**
S_{OCU}	–	**0**	**0**	**0**	**0**	**0**	**0**	**57**	**0**	**0**	**6**
H_{TOT}	–	**33946**	**20231**	**8749**	**13273**	**4278**	**25100**	**14873**	**16334**	**10447**	**16359**
SR	–	**0.0%**	**0.3%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.5%**	**0.0%**	**0.0%**	**0.1%**
SR_{OCU}	–	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.4%**	**0.0%**	**0.0%**	**0.0%**

Table D12. Total expanded recoveries for the ***Nitinat R*** *donor stock based* ***on thermal mark sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: NITINAT R

Recipient CU	Recipient River	'98	'99	'00	'01	'02	'03	'04	'05	'06	'07	'08	'09	'10	'11	'12	'13	'14	'15	'16	'17	'18	'20	'21	AVG
CK-032	**Leiner R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	5	–	–	–	–	–	–	–	–
	Tahsis R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	10	–	–	–	–
	Zeballos R	–	–	–	–	–	–	–	2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-031	**Robertson**	–	–	–	–	–	71	–	–	–	–	–	29	–	–	–	–	–	–	–	62	–	–	–	–
	Clemens Cr	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	41	–	–	–	–	–	–
	Nahmint R	–	–	–	–	–	–	–	–	5	–	–	–	39	–	–	–	–	7	–	–	–	–	–	–
	Sarita R	30	9	10	4	81	323	186	–	68	–	–	18	27	8	33	194	16	61	–	26	–	27	89	–
	Nitinat R	4152	10739	2998	7086	19523	37724	15172	14002	13591	6868	9712	6543	6573	9796	6840	36620	33033	23554	19866	19270	28012	34120	27116	–
	San Juan R	–	–	–	–	–	–	–	12	23	–	20	–	–	–	55	–	193	–	–	–	–	6	4	–
	Sooke R	–	–	–	–	–	–	–	117	–	–	–	–	–	–	74	–	390	–	–	245	348	408	85	–
CK-029	**Campbell/ Quinsam R**	–	–	–	–	–	–	–	–	28	–	–	–	–	–	–	–	–	–	–	–	–	–	31	–
	Salmon R/JNST	–	–	–	–	–	–	–	–	–	–	–	59	–	–	–	–	–	–	–	–	–	–	–	–
CK-025	**Nanaimo R**	–	–	–	–	–	–	–	–	–	–	55	–	–	–	–	–	–	–	–	–	–	–	–	–
S_{TOT}	–	30	9	10	4	81	394	186	131	123	0	75	106	65	8	162	199	599	109	0	342	348	442	209	**158**
S_{OCU}	–	0	0	0	0	0	0	0	2	28	0	55	59	0	0	0	5	0	0	0	10	0	0	31	**8**
H_{TOT}	–	4181	10748	3009	7090	19604	38118	15357	14133	13714	6868	9787	6648	6638	9804	7002	36819	33632	23662	19866	19612	28360	34562	27325	**17241**
SR	–	0.7%	0.1%	0.3%	0.1%	0.4%	1.0%	1.2%	0.9%	0.9%	0.0%	0.8%	1.6%	1.0%	0.1%	2.3%	0.5%	1.8%	0.5%	0.0%	1.7%	1.2%	1.3%	0.8%	**0.9%**
SR_{OCU}	–	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.2%	0.0%	0.6%	0.9%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	**0.1%**

*Table D13. Total expanded recoveries for the **Cowichan R** donor stock based **on CWT sampling** in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: COWICHAN R

Recipient CU	Recipient River	'98	'99	'00	'01	'02	'03	'04	'05	'06	'07	'08	'09	'10	'11	'12	'13	'14	'15	'16	'17	'18	'19	'20	'21	AVG
CK-022	**Cowichan R**	4182	2253	1885	2775	3447	1577	1352	1207	750	1217	628	430	774	1631	2265	1711	1041	718	1812	1560	1103	586	4180	1803	–
CK-025	**Nanaimo R - Fall**	–	7	–	–	13	12	67	187	–	–	3	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-083	**Puntledge R - Summer**	17	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-027	**L Qualicum R**	36	–	16	19	26	40	29	38	–	–	–	–	–	–	–	–	–	–	–	6	–	–	2	–	–
	Big Qualicum R	205	52	53	91	83	73	26	232	93	35	73	79	28	48	80	45	32	40	13	17	6	6	21	11	–
	Puntledge R - Fall	23	52	20	130	64	–	22	41	44	–	–	3	–	12	2	18	18	8	5	4	–	2	2	–	–
CK-029	**Campbell/ Quinsam R**	26	–	10	–	–	–	17	–	–	–	9	–	–	–	3	–	3	1	1	–	–	–	–	–	–
CK-03	**Harrison R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	113	–	–	18	–	19	–	–	–	–
CK-9006	**Stave R**	–	76	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-9007	**Capilano R**	48	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	1	–	–	–	–	–	–
CK-9008	**Chilliwack R**	–	–	–	–	10	–	–	–	–	–	–	34	–	–	–	15	–	–	1	–	–	–	–	–	–
CK-015	**Shuswap R Low**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	2	–	–	–	–	–
S_{TOT}	–	354	187	99	240	196	125	162	497	137	35	84	116	28	60	86	191	53	49	40	29	26	8	25	11	**118**
S_{OCU}	–	354	187	99	240	196	125	162	497	137	35	84	116	28	60	86	191	53	49	40	29	26	8	25	11	**118**
H_{TOT}	–	4536	2440	1984	3015	3643	1702	1514	1704	887	1252	712	546	802	1692	2350	1902	1094	767	1852	1589	1129	594	4205	1814	**1822**
SR	–	**7.8%**	**7.7%**	**5.0%**	**7.9%**	**5.4%**	**7.3%**	**10.7%**	**29.2%**	**15.4%**	**2.8%**	**11.8%**	**21.2%**	**3.5%**	**3.6%**	**3.6%**	**10.1%**	**4.9%**	**6.4%**	**2.1%**	**1.8%**	**2.3%**	**1.3%**	**0.6%**	**0.6%**	**7.2%**
SR_{OCU}	–	**7.8%**	**7.7%**	**5.0%**	**7.9%**	**5.4%**	**7.3%**	**10.7%**	**29.2%**	**15.4%**	**2.8%**	**11.8%**	**21.2%**	**3.5%**	**3.6%**	**3.6%**	**10.1%**	**4.9%**	**6.4%**	**2.1%**	**1.8%**	**2.3%**	**1.3%**	**0.6%**	**0.6%**	**7.2%**

Table D14. Total expanded recoveries for the ***Cowichan R*** *donor stock based* ***on thermal mark sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: COWICHAN R

Recipient CU	Recipient River	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	AVG
CK-022	**Cowichan R**	287	966	1576	1537	2137	1802	1411	1160	2404	1932	1661	668	2820	–
CK-025	**Nanaimo R - Fall**	34	27	–	–	–	–	–	49	43	–	–	–	–	–
S_{TOT}	–	**34**	**27**	**0**	**0**	**0**	**0**	**0**	**49**	**43**	**0**	**0**	**0**	**0**	**12**
S_{OCU}	–	**34**	**27**	**0**	**0**	**0**	**0**	**0**	**49**	**43**	**0**	**0**	**0**	**0**	**12**
H_{TOT}	–	**321**	**993**	**1576**	**1537**	**2137**	**1802**	**1411**	**1209**	**2447**	**1932**	**1661**	**668**	**2820**	**1578**
SR	–	**10.5%**	**2.7%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**4.1%**	**1.8%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**1.5%**
SR_{OCU}	–	**10.5%**	**2.7%**	**0.0%**	**0.0%**	**0.00**	**0.0%**	**0.0%**	**4.1%**	**1.8%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**1.5%**

Table D15. Total expanded recoveries for the ***Nanaimo R - Fall*** *donor stock based* ***on CWT sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: NANAIMO R - FALL

Recipient CU	Recipient River	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	AVG
CK-022	**Cowichan R**	–	–	33	–	–	23	–	–	31	14	–	–
CK-025	**Nanaimo R - Fall**	733	851	214	426	1010	1319	1334	425	1628	774	272	–

DONOR RIVER: NANAIMO R - FALL

CK-027	**Big Qualicum R**	–	–	–	2	–	7	–	–	–	–	2	–
	L Qualicum R	–	–	–	–	–	2	1	–	–	–	–	–
	Puntledge R - Fall	30	20	–	1	5	11	111	7	5	3	3	–
CK-029	**Campbell/Quinsam**	–	–	–	–	–	–	5	–	–	–	–	–
CK-083	**Puntledge R - Sum**	19	9	–	–	6	–	–	–	–	–	–	–
CK-9007	**Capilano R**	–	–	–	1	–	–	–	–	–	–	–	–
S_{TOT}	–	49	29	33	3	11	43	116	7	37	16	5	**32**
S_{OCU}	–	49	29	33	4	11	43	116	7	37	16	5	**32**
H_{TOT}	–	783	880	247	430	1021	1362	1451	432	1665	791	278	**849**
SR	–	**6.3%**	**3.3%**	**13.4%**	**0.7%**	**1.1%**	**3.1%**	**8.0%**	**1.6%**	**2.2%**	**2.0%**	**1.9%**	**4.0%**
SR_{OCU}	–	**6.3%**	**3.3%**	**13.4%**	**1.0%**	**1.1%**	**3.1%**	**8.0%**	**1.6%**	**2.2%**	**2.0%**	**1.9%**	**4.0%**

*Table D16. Total expanded recoveries for the **Nanaimo R - Fall** donor stock based **on thermal mark sampling** in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Years where < 20 thermally marked Chinook were sampled in the donor river system are listed in grey and marked with an asterisk (*). Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} (located in the right-hand column) were calculated using only those years in which ≥ 20 homed, thermally marked Chinook were recovered in the donor river.*

DONOR RIVER: NANAIMO R - FALL

Recipient CU	Recipient River	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2020*	2021*	AVG
CK-029	**Campbell/Quinsam R**	–	–	–	–	14	–	–	–	12	–	–	–	–	–	–
CK-025	**Chemainus R**	–	–	–	–	–	–	–	–	–	–	–	–	5	–	–

DONOR RIVER: NANAIMO R - FALL

	Nanaimo R - Fall	2253	2635	2163	2609	4213	1194	3526	1709	3133	2900	2836	2370	–	–	–
CK-022	**Cowichan R**	6	14	–	48	29	51	–	–	12	–	–	–	–	223	–
S_{TOT}	–	6	14	0	48	43	51	0	0	23	0	0	0	5	223	**29**
S_{OCU}	–	6	14	0	48	43	51	0	0	23	0	0	0	0	223	**15**
H_{TOT}	–	2258	2649	2163	2657	4256	1245	3526	1709	3157	2900	2836	2370	5	223	**2644**
SR	–	**0.2%**	**0.5%**	**0.0%**	**1.8%**	**1.0%**	**4.1%**	**0.0%**	**0.0%**	**0.7%**	**0.0%**	**0.0%**	**0.0%**	–	–	**0.7%**
SR_{OCU}	–	**0.2%**	**0.5%**	**0.0%**	**1.8%**	**1.0%**	**4.1%**	**0.0%**	**0.0%**	**0.7%**	**0.0%**	**0.0%**	**0.0%**	–	–	**0.7%**

Table D17. Total expanded recoveries for the ***Capilano R*** *donor stock based* ***on CWT sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: CAPILANO R

Recipient CU	Recipient River	1998	1999	2000	2001	2002	2003	2004	2015	2016	2017	2018	2019	2020	2021	AVG
CK-9007	**Capilano R**	669	240	154	761	102	164	12	199	859	463	1254	1128	1412	473	–
CK-9008	**Chilliwack R**	–	8	–	–	–	–	–	–	3	23	45	6	2	–	–
CK-9006	**Stave R**	–	24	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-03	**Harrison R**	69	86	–	–	–	–	–	–	89	63	71	23	103	119	–
S_{TOT}	–	**69**	**118**	**0**	**0**	**0**	**0**	**0**	**0**	**93**	**86**	**115**	**30**	**105**	**119**	**52**

DONOR RIVER: CAPILANO R															
S_{OCU}	–	**69**	**118**	**0**	**0**	**0**	**0**	**0**	**0**	**93**	**86**	**115**	**30**	**105**	**119**	**52**
H_{TOT}	–	**738**	**358**	**154**	**761**	**102**	**164**	**12**	**199**	**951**	**549**	**1369**	**1157**	**1517**	**593**	**616**
SR	–	**9.3%**	**32.9%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**9.7%**	**15.7%**	**8.4%**	**2.6%**	**6.9%**	**20.2%**	**7.6%**
SR_{OCU}	–	**9.3%**	**32.9%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**9.7%**	**15.7%**	**8.4%**	**2.6%**	**6.9%**	**20.2%**	**7.6%**

Table D18. Total expanded recoveries for the ***Big Qualicum R*** *donor stock based* ***on CWT sampling*** *in 49 recipient rivers across SBC, 1998–2021. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: BIG QUALICUM R

Recipient CU	**Recipient River**	**'98**	**'99**	**'00**	**'01**	**'02**	**'03**	**'04**	**'05**	**'06**	**'07**	**'08**	**'09**	**'10**	**'11**	**'12**	**'13**	**'14**	**'15**	**'16**	**'17**	**'18**	**'19**	**'20**	**'21**	**AVG**
CK-022	**Cowichan R**	–	12	–	76	59	58	–	–	–	–	–	60	–	–	39	–	–	7	–	–	–	–	–	–	–
CK-025	**Nanaimo R - Fall**	54	–	–	–	–	9	–	–	–	–	33	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-027	**Big Qualicum R**	2512	4083	3122	5667	3051	2759	4113	5426	8470	5938	4034	5907	4648	4773	2897	4207	7147	6748	4002	7452	3615	6104	7896	7088	–
	L Qualicum R	16	70	–	118	14	22	154	92	57	70	–	–	–	–	–	–	–	–	–	53	–	–	227	–	–
	Puntledge R - Fall	–	–	–	–	32	–	–	–	–	–	–	85	24	11	–	16	39	20	–	6	–	–	–	–	–
CK-029	**Campbell/ Quinsam R**	–	–	–	–	58	–	6	20	–	–	–	–	32	2	–	–	–	8	–	–	5	–	95	–	–
CK-083	**Puntledge R - Summer**	–	–	–	–	–	–	–	–	–	–	–	35	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-9007	**Capilano R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	6	–	–	–	–	–	–	–

DONOR RIVER: BIG QUALICUM R

No CU	**Porteau Cv**	–	32	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
S_{TOT}		71	115	0	194	163	89	160	112	57	70	33	181	55	13	39	16	39	41	0	59	5	0	322	0	**76**
S_{OCU}		54	45	0	76	117	67	6	20	0	0	33	96	32	2	39	0	0	21	0	0	5	0	95	0	**30**
H_{TOT}		2583	4198	3122	5861	3214	2848	4272	5537	8527	6009	4067	6087	4704	4787	2936	4223	7187	6789	4002	7512	3621	6104	8218	7088	**5146**
SR		**2.7%**	**2.7%**	**0.0%**	**3.3%**	**5.1%**	**3.1%**	**3.7%**	**2.0%**	**0.7%**	**1.2%**	**0.8%**	**3.0%**	**1.2%**	**0.3%**	**1.3%**	**0.4%**	**0.5%**	**0.6%**	**0.0%**	**0.8%**	**0.2%**	**0.0%**	**3.9%**	**0.0%**	**1.6%**
SR_{OCU}		**2.1%**	**1.1%**	**0.0%**	**1.3%**	**3.6%**	**2.4%**	**0.1%**	**0.4%**	**0.0%**	**0.0%**	**0.8%**	**1.6%**	**0.7%**	**0.0%**	**1.3%**	**0.0%**	**0.0%**	**0.3%**	**0.0%**	**0.0%**	**0.2%**	**0.0%**	**1.2%**	**0.0%**	**0.7%**

*Table D19. Total expanded recoveries for the **Puntledge R - Fall** donor stock based **on CWT sampling** in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: PUNTLEDGE R - FALL

Recipient CU	Recipient River	'98	'99	'00	'01	'02	'03	'04	'05	'06	'07	'08	'09	'10	'11	'12	'13	'14	'15	'16	'17	'18	'19	'20	'21	AVG
CK-025	**Nanaimo R - Fall**	2	–	–	–	–	–	–	–	–	–	239	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-027	**Big Qualicum R**	–	–	–	–	–	19	–	–	–	31	–	–	–	–	–	–	–	12	20	–	–	–	–	–	–
	Puntledge R - Fall	43	122	525	3195	3862	6569	5419	4154	7787	5501	4326	5559	2821	2756	2960	5242	5081	5188	5023	6336	4361	8885	6296	2174	–
CK-028	**Phillips R**	–	–	–	–	–	–	–	–	–	–	–	–	316	–	–	–	–	104	–	–	–	–	–	–	–
CK-029	**Campbell/ Quinsam R**	–	–	–	5	12	–	–	–	–	241	–	–	–	60	41	–	–	–	–	–	–	–	–	–	–
CK-083	**Puntledge R - Sum**	24	1	17	167	198	122	–	–	123	575	134	249	257	69	–	–	32	–	23	–	–	–	–	–	–

DONOR RIVER: PUNTLEDGE R - FALL

S_{TOT}	2	0	0	5	12	19	0	0	0	272	239	0	316	60	41	0	0	116	20	0	0	0	0	48	**48**
S_{OCU}	2	0	0	5	12	0	0	0	0	241	239	0	316	60	41	0	0	104	0	0	0	0	0	44	**44**
H_{TOT}	69	123	542	3367	4072	6710	5419	4154	7910	6349	4699	5808	3394	2884	3001	5242	5113	5304	5066	6336	4361	8885	6296	4570	**4570**
SR	**2.5%**	**0.0%**	**0.0%**	**0.2%**	**0.3%**	**0.3%**	**0.0%**	**0.0%**	**0.0%**	**4.3%**	**5.1%**	**0.0%**	**9.3%**	**2.1%**	**1.4%**	**0.0%**	**0.0%**	**2.2%**	**0.4%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**1.2%**	**1.2%**
SR_{OCU}	**2.5%**	**0.0%**	**0.0%**	**0.2%**	**0.3%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**3.8%**	**5.1%**	**0.0%**	**9.3%**	**2.1%**	**1.4%**	**0.0%**	**0.0%**	**2.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**1.2%**	**1.2%**

Table D20. Total expanded recoveries for the ***Nanaimo R - Summer*** *donor stock based* ***on CWT sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Years where < 3 CWT marked Chinook were sampled in the donor river system are listed in grey and marked with an asterisk (*). Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} (located in the right-hand column) were calculated using only those years in which ≥3 homed, CWT-marked Chinook were recovered in the donor river.*

DONOR RIVER: NANAIMO R - SUMMER

Recipient CU	Recipient River	1998	1999	2000	2001	2002	2003	2004	2005*	AVG
CK-025	**Nanaimo R - Fall**	5	74	28	97	47	113	–	–	**–**
CK-083	**Nanaimo R - Summer**	16	179	217	81	400	367	80	31	**–**
	Puntledge R - Summer	–	7	14	10	–	–	–	–	**–**
CK-027	**Puntledge R - Fall**	–	6	–	–	24	–	–	–	**–**
S_{TOT}	–	0	13	14	10	24	0	0	0	**9**
S_{OCU}	–	0	6	0	0	24	0	0	0	**4**

DONOR RIVER: NANAIMO R - SUMMER

H_{TOT}	–	21	265	258	188	471	480	80	31	**252**
SR	–	**0.0%**	**4.9%**	**5.3%**	**5.3%**	**5.0%**	**0.0%**	**0.0%**	0.0%	**2.9%**
SR_{OCU}	–	**0.0%**	**2.4%**	**0.0%**	**0.0%**	**5.0%**	**0.0%**	**0.0%**	0.0%	**1.1%**

Table D21. Total expanded recoveries for the ***Nanaimo R - Summer*** *donor stock based* ***on thermal mark sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Years where < 20 thermally marked Chinook were sampled in the donor river system are listed in grey and marked with an asterisk (*). Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} (located in the right-hand column) were calculated using only those years in which ≥ 20 homed, thermally marked Chinook were recovered in the donor river.*

DONOR RIVER: NANAIMO R - SUMMER

Recipient CU	Recipient River	2007*	2008	2009*	2010	2011	2012	2013	2014	2015	2017*	2018	2021	AVG
CK-022	**Cowichan R**	–	–	–	40	7	51	17	–	–	–	–	–	**–**
CK-083	**Nanaimo R - Summer**	44	249	95	343	540	443	645	479	107	180	178	623	**–**
S_{TOT}	–	0	0	0	40	7	51	17	0	0	0	0	0	**13**
S_{OCU}	–	0	0	0	40	7	51	17	0	0	0	0	0	**13**
H_{TOT}	–	44	249	95	383	547	493	663	479	107	180	178	623	**414**
SR	–	0.0%	**0.0%**	0.0%	**10.4%**	**1.3%**	**10.2%**	**2.6%**	**0.0%**	**0.0%**	0.0%	**0.0%**	**0.0%**	**2.7%**
SR_{OCU}	–	0.0%	**0.0%**	0.0%	**10.4%**	**1.3%**	**10.2%**	**2.6%**	**0.0%**	**0.0%**	0.0%	**0.0%**	**0.0%**	**2.7%**

Table D22: Total expanded recoveries for the ***Puntledge R - Summer*** *donor stock based* ***on CWT sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: PUNTLEDGE R - SUMMER

Recipient CU	Recipient River	'98	'99	'00	'01	'02	'03	'04	'05	'06	'07	'08	'09	'10	'11	'12	'13	'14	'15	'16	'17	'18	'19	'20	'21	AVG
CK-025	**Nanaimo R - Fall**	–	–	–	–	–	47	–	–	–	–	9	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-027	**Puntledge R - Fall**	13	55	100	458	192	355	751	963	615	253	185	204	194	267	82	90	259	323	153	124	41	108	67	53	–
CK-083	**Puntledge R - Summer**	89	498	524	1371	711	882	528	694	1317	1012	445	1713	1153	782	497	423	593	310	384	177	483	475	385	376	–
CK-020	**Cheakamus R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	2	–	–	–	–	–
S_{TOT}	–	0	0	0	0	0	47	0	0	0	0	9	0	0	0	0	0	0	0	0	2	0	0	0	3	**3**
S_{OCU}	–	0	0	0	0	0	47	0	0	0	0	9	0	0	0	0	0	0	0	0	2	0	0	0	3	**3**
H_{TOT}	–	102	553	624	1829	904	1285	1279	1656	1932	1265	638	1917	1348	1050	579	513	852	634	537	301	524	583	453	929	**929**
SR	–	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**3.7%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**1.4%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.6%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.2%**
SR_{OCU}	–	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**3.7%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**1.4%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.6%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.2%**

*Table D23. Total expanded recoveries for the **Campbell/Quinsam R** donor stock based **on CWT sampling** in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: CAMPBELL/QUINSAM R

Recipient CU	Recipient River	'98	'99	'00	'01	'02	'03	'04	'05	'06	'07	'08	'09	'10	'11	'12	'13	'14	'15	'16	'17	'18	'19	'20	'21	AVG
CK-027	**Big Qualicum R**	65	11	7	–	75	33	36	–	45	–	9	88	32	–	12	83	81	74	3	27	–	11	17	40	–
	L Qualicum R	–	–	–	–	–	–	9	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	18	–	–
	Puntledge R - Fall	–	–	7	–	–	–	–	–	–	–	15	–	–	–	–	–	7	–	–	–	10	6	52	–	–
CK-083	**Puntledge R - Sum**	–	–	–	–	–	–	–	–	–	–	–	–	20	–	–	–	–	–	–	–	–	–	–	–	–
CK-028	**Phillips R**	–	–	–	–	–	–	–	–	–	–	–	–	–	128	–	–	–	–	–	–	–	–	–	–	–
CK-029	**Campbell / Quinsam R**	3338	5927	6152	10684	8575	4938	6674	5703	6319	4660	4183	3445	2276	3301	2879	2928	1769	2484	6310	7180	5305	5699	5942	5500	–
S_{TOT}	–	65	11	14	0	75	33	46	0	45	0	25	88	52	128	12	83	88	74	3	27	10	17	86	40	**43**
S_{OCU}	–	65	11	14	0	75	33	46	0	45	0	25	88	52	128	12	83	88	74	3	27	10	17	86	40	**43**
H_{TOT}	–	3403	5938	6166	10684	8650	4971	6720	5703	6364	4660	4208	3533	2327	3429	2892	3011	1857	2558	6313	7207	5315	5716	6028	5540	**5133**
SR	–	**1.9%**	**0.2%**	**0.2%**	**0.0%**	**0.9%**	**0.7%**	**0.7%**	**0.0%**	**0.7%**	**0.0%**	**0.6%**	**2.5%**	**2.2%**	**3.7%**	**0.4%**	**2.8%**	**4.7%**	**2.9%**	**0.0%**	**0.4%**	**0.2%**	**0.3%**	**1.4%**	**0.7%**	**1.2%**
SR_{OCU}	–	**1.9%**	**0.2%**	**0.2%**	**0.0%**	**0.9%**	**0.7%**	**0.7%**	**0.0%**	**0.7%**	**0.0%**	**0.6%**	**2.5%**	**2.2%**	**3.7%**	**0.4%**	**2.8%**	**4.7%**	**2.9%**	**0.0%**	**0.4%**	**0.2%**	**0.3%**	**1.4%**	**0.7%**	**1.2%**

Table D24: Total expanded recoveries for the ***Campbell/Quinsam R*** *donor stock based* ***on thermal mark sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Years where < 20 thermally marked Chinook were sampled in the donor river system are listed in grey and marked with an asterisk (*). Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: CAMPBELL/QUINSAM R

Recipient CU	Recipient River	'00	'01	'02	'03*	'04	'05	'06	'07	'08	'09	'10	'11	'12	'13	'14	'15	'16	'17	'18	'19	'20	'21	AVG
CK-029	**Campbell/ Quinsam R**	4947	11927	10709	–	7623	7615	6502	4724	3861	4752	3345	3838	3846	2890	1932	2444	5961	8443	6202	6405	8222	5441	–
	Salmon R/ JNST	–	–	–	–	–	–	–	31	57	119	33	–	–	–	10	–	–	–	–	–	–	–	–
CK-022	**Cowichan R**	–	–	–	1003	77	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
S_{TOT}	–	0	0	0	1003	77	0	0	31	57	119	33	0	0	0	10	0	0	0	0	0	0	0	**60**
S_{OCU}	–	0	0	0	1003	77	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**49**
H_{TOT}	–	4947	11927	10709	1003	7701	7615	6502	4755	3918	4871	3378	3838	3846	2890	1942	2444	5961	8443	6202	6405	8222	5441	**5589**
SR	–	**0.0%**	**0.0%**	**0.0%**	–	**1.0%**	**0.0%**	**0.0%**	**0.7%**	**1.5%**	**2.4%**	**1.0%**	**0.0%**	**0.0%**	**0.0%**	**0.5%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.3%**
SR_{OCU}	–	**0.0%**	**0.0%**	**0.0%**	-	**1.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**

Table D25. Total expanded recoveries for the ***Harrison R*** *donor stock based* ***on CWT sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: HARRISON R

Recipient CU	Recipient River	'98	'99	'00	'01	'02	'03	'04	'05	'06	'07	'08	'09	'10	'11	'12	'13	'14	'15	'16	'17	'18	'19	'20	'21	AVG
CK-03	**Harrison R**	17486	6674	2813	8518	3801	7509	7474	9388	5010	2718	358	1905	1573	2249	2002	2931	1581	1635	2194	1141	2783	1909	1963	2289	–
CK-9008	**Chilliwack R**	–	–	–	–	–	52	–	66	–	–	–	1	–	–	1	49	–	–	25	4	24	19	–	–	–
CK-9006	**Stave R**	55	66	–	31	16	42	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-029	**Campbell/ Quinsam R**	–	–	–	–	–	–	–	–	–	–	–	–	1	–	–	0	–	–	–	–	–	–	–	–	–
S_{TOT}	**–**	**55**	**66**	**0**	**31**	**16**	**94**	**0**	**66**	**0**	**0**	**0**	**1**	**1**	**0**	**1**	**49**	**0**	**0**	**25**	**4**	**24**	**19**	**0**	**0**	**19**
S_{OCU}	**–**	**55**	**66**	**0**	**31**	**16**	**94**	**0**	**66**	**0**	**0**	**0**	**1**	**1**	**0**	**1**	**49**	**0**	**0**	**25**	**4**	**24**	**19**	**0**	**0**	**19**
H_{TOT}	**–**	**17542**	**6740**	**2813**	**8549**	**3817**	**7603**	**7474**	**9453**	**5010**	**2718**	**358**	**1906**	**1574**	**2249**	**2003**	**2980**	**1581**	**1635**	**2220**	**1145**	**2807**	**1927**	**1963**	**2289**	**4098**
SR	**–**	**0.3%**	**1.0%**	**0.0%**	**0.4%**	**0.4%**	**1.2%**	**0.0%**	**0.7%**	**0.0%**	**0.0%**	**0.0%**	**0.1%**	**0.1%**	**0.0%**	**0.0%**	**1.7%**	**0.0%**	**0.0%**	**1.1%**	**0.4%**	**0.8%**	**1.0%**	**0.0%**	**0.0%**	**0.4%**
SR_{OCU}	**–**	**0.3%**	**1.0%**	**0.0%**	**0.4%**	**0.4%**	**1.2%**	**0.0%**	**0.7%**	**0.0%**	**0.0%**	**0.0%**	**0.1%**	**0.1%**	**0.0%**	**0.0%**	**1.7%**	**0.0%**	**0.0%**	**1.1%**	**0.4%**	**0.8%**	**1.0%**	**0.0%**	**0.0%**	**0.4%**

Table D26. Total expanded recoveries for the ***Chilliwack R*** *donor stock based* ***on CWT sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: CHILLIWACK R - FALL

Recipient CU	Recipient River	'98	'99	'00	'01	'02	'03	'04	'05	'06	'07	'08	'09	'10	'11	'12	'13	'14	'15	'16	'17	'18	'19	'20	'21	AVG
CK-9008	**Chilliwack R**	41659	45463	61792	21269	24050	17092	17249	53617	25439	37199	29026	24658	70504	52637	23860	30017	29706	19769	27759	17178	23740	45164	30067	40234	–
CK-9006	**Stave R**	593	362	136	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-03	**Harrison R**	469	504	91	9	–	904	–	–	196	–	105	248	198	–	–	114	138	282	109	261	–	65	168	138	–
CK-029	**Campbell/ Quinsam R**	–	–	–	–	–	–	–	–	–	4	8	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-027	**Puntledge R - Fall**	–	–	–	–	–	–	–	–	–	13	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
S_{TOT}	–	**1061**	**867**	**227**	**9**	**0**	**904**	**0**	**0**	**196**	**17**	**113**	**248**	**198**	**0**	**0**	**114**	**138**	**282**	**109**	**261**	**0**	**65**	**168**	**138**	**213**
S_{OCU}	–	**1061**	**867**	**227**	**9**	**0**	**904**	**0**	**0**	**196**	**17**	**113**	**248**	**198**	**0**	**0**	**114**	**138**	**282**	**109**	**261**	**0**	**65**	**168**	**138**	**213**
H_{TOT}	–	**42720**	**46330**	**62019**	**21278**	**24050**	**17996**	**17249**	**53617**	**25635**	**37216**	**29138**	**24906**	**70702**	**52637**	**23860**	**30131**	**29844**	**20051**	**27868**	**17440**	**23740**	**45228**	**30235**	**40372**	**33928**
SR	–	**2.5%**	**1.9%**	**0.4%**	**0.0%**	**0.0%**	**5.0%**	**0.0%**	**0.0%**	**0.8%**	**0.0%**	**0.4%**	**1.0%**	**0.3%**	**0.0%**	**0.0%**	**0.4%**	**0.5%**	**1.4%**	**0.4%**	**1.5%**	**0.0%**	**0.1%**	**0.6%**	**0.3%**	**0.7%**
SR_{OCU}	–	**2.5%**	**1.9%**	**0.4%**	**0.0%**	**0.0%**	**5.0%**	**0.0%**	**0.0%**	**0.8%**	**0.0%**	**0.4%**	**1.0%**	**0.3%**	**0.0%**	**0.0%**	**0.4%**	**0.5%**	**1.4%**	**0.4%**	**1.5%**	**0.0%**	**0.1%**	**0.6%**	**0.3%**	**0.7%**

*Table D27: Total expanded recoveries for the **Chilliwack R** donor stock based **on thermal mark sampling** in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Years where < 20 thermally marked Chinook were sampled in the donor river system are listed in grey and marked with an asterisk (*). Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} (located in the right-hand column) were calculated using only those years in which ≥ 20 homed, thermally marked Chinook were recovered in the donor river.*

DONOR RIVER: CHILLIWACK R - FALL																	
Recipient CU	**Recipient River**	**1998**	**1999**	**2000**	**2001**	**2002**	**2003**	**2004**	**2005**	**2006**	**2007**	**2008**	**2009**	**2010**	**2011**	**2013***	**AVG**
CK-031	Nitinat R	–	–	–	–	–	–	–	–	–	–	–	–	–	13	42	–
CK-029	Campbell/ Quinsam R	–	–	–	–	–	–	–	–	–	21	–	–	–	–	–	–
CK-9008	Chilliwack R	61137	73465	68369	65969	56037	50073	51122	30060	38152	18106	31299	10926	69824	44131		–
***S*TOT**	–	0	0	0	0	0	0	0	0	0	21	0	0	0	13	42	**5**
***S*OCU**	–	0	0	0	0	0	0	0	0	0	21	0	0	0	13	42	**5**
***H*TOT**	–	61137	73465	68369	65969	56037	50073	51122	30060	38152	18127	31299	10926	69824	44144	42	**44583**
SR	–	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.1%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	–	**0.0%**
***SR*OCU**	–	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.1%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	–	**0.0%**

Table D28: Total expanded recoveries for the ***Nicola R*** *donor stock based* ***on CWT sampling*** *in 49 recipient rivers across SBC. *Note that the Nicola R is the only stream-type population in our study, and that under our definition of straying, recoveries in Coldwater R and Spius Cr would not be considered as strays, as they are tributaries off the mainstem of the Lower Thompson River. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: NICOLA R

Recipient CU	Recipient River	‘98	‘99	‘00	‘01	‘02	‘03	‘04	‘05	‘06	‘07	‘08	‘09	‘10	‘11	‘12	‘13	‘14	‘15	‘16	‘17	‘18	‘19	‘20	‘21	AVG
CK-017	**Coldwater R**	4	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Nicola R	406	4397	2570	2926	3136	3029	638	489	626	123	806	144	2216	590	504	1392	384	1323	760	945	1164	2173	1467	3039	–
	Spius Cr	27	–	125	246	–	27	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
S_{TOT}	–	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
S_{OCU}	–	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**	**0**
H_{TOT}	–	**437**	**4397**	**2695**	**3172**	**3136**	**3056**	**638**	**489**	**626**	**123**	**806**	**144**	**2216**	**590**	**504**	**1392**	**384**	**1323**	**760**	**945**	**1164**	**2173**	**1467**	**3039**	**1487**
SR	–	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**
SR_{OCU}	–	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**

Table D29. Total expanded recoveries for the ***Shuswap R Lower*** *donor stock based* ***on CWT sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: SHUSWAP R - LOWER

Recipient CU	Recipient River	‘98	‘99	‘00	‘01	‘02	‘03	‘04	‘05	‘06	‘07	‘08	‘09	‘10	‘11	‘12	‘13	‘14	‘15	‘16	‘17	‘18	‘19	‘20	‘21	AVG
CK-015	**Shuswap R Low**	2123	5317	4783	6996	5397	7320	2495	1799	3796	1192	3042	2308	2484	1716	1372	5568	2579	3466	1404	1784	3555	5655	5047	4055	–
	Shuswap R Middle	116	–	–	58	–	–	–	–	83	–	–	10	65	2	–	83	46	74	–	16	11	63	79	170	–
CK-017	**Spius Cr**	–	–	61	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
S_{TOT}	–	0	0	61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**3**
S_{OCU}	–	0	0	61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**3**
H_{TOT}	–	2239	5317	4844	7054	5397	7320	2495	1799	3879	1192	3042	2318	2549	1718	1372	5651	2625	3540	1404	1800	3566	5717	5126	4224	**3591**
SR	–	**0.0%**	**0.0%**	**1.3%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.1%**
SR_{OCU}	–	**0.0%**	**0.0%**	**1.3%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.1%**

Table D30. Total expanded recoveries for the ***Shuswap R Middle*** *donor stock based* ***on CWT sampling*** *in 49 recipient rivers across SBC. Total expanded stray recoveries (S_{TOT}), total expanded strays recovered outside the CU (S_{OCU}), total expanded hatchery recoveries (H_{TOT}), stray rate (SR) and stray rate-outside the CU (SR_{OCU}) are reported annually. Averages of S_{TOT}, S_{OCU}, H_{TOT}, SR, and SR_{OCU} are reported in the right-hand column.*

DONOR RIVER: SHUSWAP R - MIDDLE

Recipient CU	**Recipient River**	**'98**	**'99**	**'00**	**'01**	**'02**	**'03**	**'04**	**'05**	**'11**	**'12**	**'13**	**'14**	**'15**	**'16**	**'17**	**'18**	**'19**	**'20**	**'21**	**AVG**
CK-015	**Shuswap R Low**	79	–	16	9	–	–	8	–	–	4	25	7	118	2	9	14	57	33	12	–
	Shuswap R Middle	3474	2513	2837	3555	6534	3677	1615	1746	53	159	1162	751	1515	232	320	985	951	1297	546	–
S_{TOT}	–	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**0**
S_{OCU}	–	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	**0**
H_{TOT}	–	3553	2513	2853	3564	6534	3677	1623	1746	53	163	1187	758	1633	234	329	999	1008	1330	558	**1806**
SR	–	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**
SR_{OCU}	–	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**	**0.0%**

APPENDIX E. ANNUAL RECIPIENT RIVER HATCHERY AND STRAY CONTRIBUTION

*Table E1. Total expanded recoveries of southern BC Chinook returning to **Marble R** for return years 2005 to 2019, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners (pHOS$_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers (pHOS$_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU (pHOS$_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: MARBLE R

Donor CU	Donor River	Origin	2005	2006	2008	2009	2012	2013	2015	2016	2019	AVG
CK-033	**Marble R**	HO	–	–	29	637	214	–	–	404	24	–
		NO	2342	3100	2673	2833	2154	2089	6519	1205	4947	–
CK-032	**Conuma R**	–	–	–	–	–	–	–	–	6	–	–
CK-031	**Robertson Cr**	–	–	–	–	–	–	–	–	6	–	–
pNOS	–	–	1.00	1.00	0.99	0.82	0.91	1.00	1.00	0.74	1.00	**0.94**
***pHOS*$_{local}$**	–	–	0.00	0.00	0.01	0.18	0.09	0.00	0.00	0.25	0.00	**0.06**
***pHOS*$_{stray}$**	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	**0.00**
***pHOS*$_{stray,OCU}$**	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	**0.00**

Table E2. Total expanded recoveries of southern BC Chinook returning to ***Tahsish R*** *for return years 2013–2017, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*). Note: The Tahsish R stock has not been thermally marked historically, thus no homed HO individuals were observed.*

RECIPIENT RIVER: TAHSISH R								
Donor CU	**Donor River**	**Origin**	2013*	2014*	**2015**	**2016**	**2017**	**AVG**
CK-032	**Burman R**	–	–	–	62	26	26	–
	Conuma R	–	383	–	312	317	1156	–
	Leiner R	–	–	–	–	–	26	–
	Tahsish River	**NO**	–	796	457	422	499	–
pNOS	–	–	0.00	1.00	0.55	0.55	0.29	**0.60**
$pHOS_{local}$	–	–	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray}$	–	–	1.00	0.00	0.45	0.45	0.71	**0.40**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	0.00	0.00	**0.00**

*Table E3. Total expanded recoveries of southern BC Chinook returning to **Kaouk R** for return years 2009–2017, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*). Note: The Kaouk R stock has not been thermally marked historically, thus no homed HO individuals were observed.*

RECIPIENT RIVER: KAOUK R

Donor CU	Donor River	Origin	2009*	2010*	2012*	2014*	2015	2016*	2017*	AVG
CK-032	**Burman R**	–	–	–	–	–	14	–	–	–
	Conuma R	–	86	–	–	94	–	–	–	–
	Kaouk River	NO	514	235		118	391	423	671	–
CK-031	**Robertson Cr**	–	–	–	262	–	–	–	–	–
	Sarita R	–	–	–	–	24	–	–	–	–
pNOS	–	–	0.86	1.00	0.00	0.50	0.96	1.00	1.00	**0.96**
$pHOS_{local}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray}$	–	–	0.14	0.00	1.00	0.50	0.04	0.00	0.00	**0.04**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	1.00	0.10	0.00	0.00	0.00	**0.00**

*Table E4. Total expanded recoveries of southern BC Chinook returning to **Artlish R** for return years 2015 and 2016, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*). Note: The Artlish R stock has not been thermally marked historically, thus no homed HO individuals were observed.*

RECIPIENT RIVER: ARTLISH R

Donor CU	Donor River	Origin	2015	2016*	AVG
CK-032	**Artlish R**	NO	569	176	–
	Conuma R	–	602	59	–
CK-031	**Robertson Cr**	–	33	–	–
pNOS	–	–	0.47	0.75	**0.61**
$pHOS_{local}$	–	–	0.00	0.00	**0.00**
$pHOS_{stray}$	–	–	0.53	0.25	**0.39**
$pHOS_{stray,OCU}$	–	–	0.03	0.00	**0.01**

Table E5. Total expanded recoveries of southern BC Chinook returning to ***Kauwinch R*** *for return year 2015 (the only year sampled between 1998 and 2021), based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*). Note: The Kauwinch R stock has not been thermally marked historically, thus no homed HO individuals were observed.*

RECIPIENT RIVER: KAUWINCH R				
Donor CU	**Donor River**	**Origin**	**2015***	**AVG**
CK-032	**Conuma R**	–	254	–
	Kauwinch River	NO	170	–
pNOS	–	–	0.40	**0.40**
$pHOS_{local}$	–	–	0.00	**0.00**
$pHOS_{stray}$	–	–	0.60	**0.60**
$pHOS_{stray,OCU}$	–	–	0.00	**0.00**

*Table E6. Total expanded recoveries of southern BC Chinook returning to **Conuma R** for return years 1998–2021, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: CONUMA R

Donor CU	Donor River	Origin	'98	'99	'00	'01	'02	'04	'05	'06	'07	'08	'09	'10	'11	'12	'13	'14	'15	'16	'17	'18	'19	'20	'21	AVG
CK-031	**Robertson Cr**	–	–	204	–	–	–	–	–	–	–	–	–	–	–	17	–	–	–	–	259	–	55	29	–	–
	Sarita R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	40	–
CK-032	**Burman R**	–	–	–	–	–	–	–	–	–	–	–	–	–	698	–	–	–	–	129	–	–	55	29	–	–
	Conuma R	HO	18612	15610	10494	17542	27332	41053	7248	23165	8834	12780	17162	16426	21627	6590	61167	21172	40865	37109	23984	11482	8924	9201	13442	–
		NO	7735	1018	210	48	264	0	73	0	175	562	303	345	698	240	578	146	562	905	583	395	164	88	119	–
	Gold R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	130	–	–	–	–	–
	Sucwoa R	–	–	–	–	–	–	–	–	–	–	421	–	230	233	103	578	364	140	259	–	–	–	–	–	–
	Tlupana R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	65	–	27	–	–	–
No CU	**Unknown thermal mark**	–	–	68	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
pNOS		–	0.29	0.06	0.02	0.00	0.01	0.00	0.01	0.00	0.02	0.04	0.02	0.02	0.03	0.03	0.01	0.01	0.01	0.02	0.02	0.03	0.02	0.01	0.01	**0.03**
$pHOS_{local}$		–	0.71	0.92	0.98	1.00	0.99	1.00	0.99	1.00	0.98	0.93	0.98	0.97	0.93	0.95	0.98	0.98	0.98	0.97	0.96	0.97	0.97	0.98	0.99	**0.96**
$pHOS_{stray}$		–	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.03	0.00	0.01	0.04	0.02	0.01	0.02	0.00	0.01	0.02	0.00	0.01	0.01	0.00	**0.01**
$pHOS_{stray,OCU}$		–	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.01	0.00	0.00	**0.00**

Table E7. Total expanded recoveries of southern BC Chinook returning to ***Conuma R*** *for return years 1998–2007, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: CONUMA R

Donor CU	Donor River	Origin	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	AVG
CK-32	**Burman R**	–	–	–	–	–	–	–	–	–	–	9	–
	Conuma R	HO	20461	10366	5151	12369	19533	31715	35856	4656	17626	891	–
		NO	8185	5777	3828	5645	8354	10023	5375	2699	8498	6549	–
pNOS	–	–	0.29	0.36	0.43	0.31	0.30	0.24	0.13	0.37	0.33	0.88	**0.36**
$pHOS_{local}$	–	–	0.71	0.64	0.57	0.69	0.70	0.76	0.87	0.63	0.67	0.12	**0.64**
$pHOS_{stray}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

*Table E8. Total expanded recoveries of southern BC Chinook returning to **Burman R** for return years 2004 to 2021, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: BURMAN R

Donor CU	Donor River	Origin	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	AVG
CK-032	Burman R	HO	–	–	234	237	419	1174	2549	1995	1297	7299	2124	2799	7342	857	1154	1939	2222	3146	–
		NO	2458	507	191	94	125	132	174	46	55	397	259	968	2006	334	365	125	127	367	–
	Conuma R	–	201	91	71	22	–	541	287	–	8	837	712	2025	1277	140	1620	–	81	537	–
	Gold R	–	–	13	22	–	–	7	–	–	–	–	–	402	91	9	142	31	58	13	–
	Leiner R	–	–	–	–	–	–	–	–	–	–	–	–	15	–	5	–	–	–	–	–
	Sucwoa R	–	–	–	–	–	–	–	17	–	–	15	11	15	–	–	–	–	–	–	–
	Tahsis R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	13	–
	Tlupana R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	41	–	–	–	–
CK-031	Robertson Cr	–	–	39	–	2	–	7	–	8	4	–	–	89	46	23	263	–	58	472	–
pNOS		–	0.92	0.78	0.37	0.26	0.23	0.07	0.06	0.02	0.04	0.05	0.08	0.15	0.19	0.24	0.10	0.06	0.05	0.08	**0.21**
$pHOS_{local}$		–	0.00	0.00	0.45	0.67	0.77	0.63	0.84	0.97	0.95	0.85	0.68	0.44	0.68	0.63	0.32	0.93	0.87	0.69	**0.63**
$pHOS_{stray}$		–	0.08	0.22	0.18	0.07	0.00	0.30	0.10	0.00	0.01	0.10	0.23	0.40	0.13	0.13	0.58	0.01	0.08	0.23	**0.16**
$pHOS_{stray,OCU}$		–	0.00	0.06	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.02	0.07	0.00	0.02	0.10	**0.02**

Table E9. Total expanded recoveries of southern BC Chinook returning to ***Gold R*** *for return years 2005 to 2020, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*).*

RECIPIENT RIVER: GOLD R												
Donor CU	**Donor River**	**Origin**	**2005**	**2011**	**2012**	**2013**	**2015**	**2016**	**2018***	**2019**	**2020**	**AVG**
CK-032	**Burman R**	–	–	14	–	–	–	57	–	75	246	–
	Conuma R	–	–	–	–	–	–	85	–	6	–	–
	Gold R	HO	50	70	198	297	167	701	–	445	2733	–
		NO	402	99	287	543	235	569	–	549	983	–
CK-031	**Nitinat R**	–	–	–	13	–	–	9	–	–	–	–
	Robertson Cr	–	552	817	485	943	490	1099	1556	705	4115	–
	Sarita R	–	–	–	–	10	–	–	–	–	–	–
pNOS	–	–	0.40	0.10	0.29	0.30	0.26	0.23	0.00	0.31	0.12	**0.25**
$pHOS_{local}$	–	–	0.05	0.07	0.20	0.17	0.19	0.28	0.00	0.25	0.34	**0.19**
$pHOS_{stray}$	–	–	0.55	0.83	0.51	0.53	0.55	0.50	1.00	0.44	0.54	**0.56**
$pHOS_{stray,OCU}$	–	–	0.55	0.82	0.51	0.53	0.55	0.44	1.00	0.40	0.51	**0.54**

*Table E10. Total expanded recoveries of southern BC Chinook returning to **Leiner R** for return years 2006–2021, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: LEINER R																
Donor CU	**Donor River**	**Origin**	**2006**	**2007**	**2009**	**2012**	**2013**	**2014**	**2015**	**2016**	**2017**	**2018**	**2019**	**2020**	**2021**	**AVG**
CK-032	**Burman R**	–	–	–	–	–	–	–	8	–	–	9	7	–	–	–
	Conuma R	–	63	44	182	230	47	84	362	453	715	188	44	207	85	–
	Gold R	–	–	–	–	–	–	–	–	–	–	–	7	–	–	–
	Leiner R	HO	–	–	–	281	147	7	244	926	734	331	573	547	460	–
		NO	116	133	470	128	247	309	362	335	516	313	51	304	221	–
	Sucwoa R	–	–	–	15	13	5	–	8	20	–	–	–	–	–	–
	Tahsis R	–	–	4	121	38	42	–	–	–	–	9	73	85	238	–
CK-031	**Nahmint R**	–	–	–	–	–	–	–	–	–	–	–	7	–	–	–
	Nitinat R	–	–	–	–	–	5	–	–	–	–	–	–	–	–	–
	Robertson Cr	–	–	–	–	–	–	–	–	39	–	9	–	–	17	–
pNOS	–	–	0.65	0.73	0.60	0.19	0.50	0.77	0.37	0.19	0.26	0.36	0.07	0.27	0.22	**0.40**
***pHOS**local*	–	–	0.00	0.00	0.00	0.41	0.30	0.02	0.25	0.52	0.37	0.39	0.75	0.48	0.45	**0.30**
***pHOS**stray*	–	–	0.35	0.27	0.40	0.41	0.20	0.21	0.38	0.29	0.36	0.25	0.18	0.26	0.33	**0.30**
***pHOS**stray,OCU*	–	–	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.02	0.00	0.01	0.01	0.00	0.02	**0.01**

*Table E11. Total expanded recoveries of southern BC Chinook returning to **Tahsis R** for return years 2004–2021, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($\text{pHOS}_{\text{local}}$), proportion of strayed hatchery-origin spawners from all donor rivers ($\text{pHOS}_{\text{stray}}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($\text{pHOS}_{\text{stray,OCU}}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*).*

RECIPIENT RIVER: TAHSIS R

Donor CU	Donor River	Origin	2004	2005*	2006*	2008	2009	2010*	2013*	2014*	2015	2016	2017	2018	2019	2020	2021	AVG
CK-032	**Burman R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	21	–
	Conuma R	–	51	–	9	31	61	18	–	–	90	51	88	13	–	–	–	–
	Gold R	–	–	–	–	–	–	–	–	–	20	31	–	–	–	–	–	–
	Leiner R	–	–	–	–	–	–	–	139	–	160	214	253	658	681	243	609	–
	Sucwoa R	–	–	–	–	–	–	18	–	–	–	–	–	–	–	–	–	–
	Tahsis R	HO	–	–	18	197	656	18	277	–	–	–	68	497	1070	619	1427	–
		NO	868	197	127	62	153	326	139	111	180	112	321	309	49	55	231	–
CK-031	**Nitinat R**	–	–	–	–	–	–	–	–	–	–	–	10	–	–	–	–	–
	Robertson Cr	–	–	–	–	–	–	–	–	–	–	–	10	13	49	–	–	–
	Sarita R	–	–	–	–	–	–	–	–	–	–	–	10	13	–	–	21	–
pNOS	–	–	0.94	1.00	0.82	0.21	0.18	0.86	0.25	1.00	0.40	0.28	0.42	0.21	0.03	0.06	0.10	**0.45**
$\text{pHOS}_{\text{local}}$	–	–	0.00	0.00	0.12	0.68	0.75	0.05	0.50	0.00	0.00	0.00	0.09	0.33	0.58	0.67	0.62	**0.29**
$\text{pHOS}_{\text{stray}}$	–	–	0.06	0.00	0.06	0.11	0.07	0.10	0.25	0.00	0.60	0.73	0.49	0.46	0.39	0.27	0.28	**0.26**
$\text{pHOS}_{\text{stray,OCU}}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.02	0.03	0.00	0.01	**0.01**

Table E12. Total expanded recoveries of southern BC Chinook returning to ***Sucwoa R*** *for return years 2002–2012, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners (pHOS$_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers (pHOS$_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU (pHOS$_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*).*

RECIPIENT RIVER: SUCWOA R							
Donor CU	**Donor River**	**Origin**	**2002***	**2005***	**2010***	**2012***	**AVG**
CK-032	**Conuma R**	–	40	25	16	40	–
	Sucwoa R	HO	–	–	1	–	–
		NO	–	12	1	8	–
CK-031	**Robertson Cr**	–	–	–6	–	–	–
pNOS	–	–	0.00	0.29	0.06	0.17	**0.13**
pHOS$_{local}$	–	–	0.00	0.00	0.06	0.00	**0.01**
pHOS$_{stray}$	–	–	1.00	0.71	0.89	0.83	**0.86**
pHOS$_{stray,OCU}$	–	–	0.00	0.14	0.00	0.00	**0.04**

*Table E13. Total expanded recoveries of southern BC Chinook returning to **Tlupana R** for return years 2001–2013, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*).*

RECIPIENT RIVER: TLUPANA R

Donor CU	Donor River	Origin	2001	2002	2003	2008*	2010	2012	2013	AVG
CK-032	**Conuma R**	–	359	1140	325	66	21	46	948	–
	Tlupana R	HO	–	–	–	77	11	21	33	–
		NO	–	30	10	33	4	4	–	–
CK-031	**Robertson Cr**	–	15	–	–	–	–	–	–	–
pNOS	–	–	0.00	0.03	0.03	0.19	0.12	0.05	0.00	**0.06**
$pHOS_{local}$	–	–	0.00	0.00	0.00	0.44	0.30	0.30	0.03	**0.15**
$pHOS_{stray}$	–	–	1.00	0.97	0.97	0.38	0.58	0.65	0.97	**0.79**
$pHOS_{stray,OCU}$	–	–	0.04	0.00	0.00	0.00	0.00	0.00	0.00	**0.01**

Table E14. Total expanded recoveries of southern BC Chinook returning to ***Zeballos R*** *for return years 2004–2009, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: ZEBALLOS R

Donor CU	Donor River	Origin	2004	2005	2006	2007	2008	2009	AVG
CK-032	**Burman R**	–	–	–	27	–	12	–	–
	Conuma R	–	–	–	27	–	–	–	–
	Gold R	–	–	2	27	–	–	–	–
	Zeballos River	HO	256	39	241	261	219	–	–
		NO	183	2	120	100	242	117	–
CK-031	**Nitinat R**	–	–	2	–	–	–	–	–
	Robertson Cr	–	–	1	–	60	–	–	–
	Sarita R	–	–	1	13	20	–	5	–
pNOS	–	–	0.42	0.04	0.26	0.23	0.51	0.96	**0.40**
$pHOS_{local}$	–	–	0.58	0.82	0.53	0.59	0.46	0.00	**0.50**
$pHOS_{stray}$	–	–	0.00	0.13	0.21	0.18	0.02	0.04	**0.10**
$pHOS_{stray,OCU}$	–	–	0.00	0.09	0.03	0.18	0.00	0.04	**0.06**

Table E15. Total expanded recoveries of southern BC Chinook returning to ***Megin R*** *for return years 2015 to 2017, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*). Note: The Megin R stock has not historically been thermally marked, thus no homed HO individuals were observed.*

RECIPIENT RIVER: MEGIN R

Donor CU	Donor River	Origin	2015*	2017*	AVG
CK-032	**Conuma R**	–	36	32	–
CK-031	**Megin River**	NO	18	32	–
pNOS	–	–	0.33	0.50	**0.42**
$pHOS_{local}$	–	–	0.00	0.00	**0.00**
$pHOS_{stray}$	–	–	0.67	0.50	**0.58**
$pHOS_{stray,OCU}$	–	–	0.67	0.50	**0.58**

Table E16. Total expanded recoveries of southern BC Chinook returning to ***Moyeha R*** *for return years 2010–2017, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*). Note: The Moyeha R stock has not historically been thermally marked, thus no homed HO individuals were observed.*

RECIPIENT RIVER: MOYEHA R						
Donor CU	**Donor River**	**Origin**	**2010***	**2011***	**2017***	**AVG**
CK-032	**Conuma R**	–	109	–	–	–
CK-031	**Moyeha River**	NO	91	73	142	–
pNOS	–	–	0.45	1.00	1.00	**0.82**
$pHOS_{local}$	–	–	0.00	0.00	0.00	**0.00**
$pHOS_{stray}$	–	–	0.55	0.00	0.00	**0.18**
$pHOS_{stray,OCU}$	–	–	0.55	0.00	0.00	**0.18**

*Table E17. Total expanded recoveries of southern BC Chinook returning to **Bedwell R** for return years 2014–2021, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*). Note: The Bedwell R stock has not historically been thermally marked, thus no homed HO individuals were identified for this mark type.*

RECIPIENT RIVER: BEDWELL R

Donor CU	Donor River	Origin	2014*	2015*	2016*	2017*	2018	2019	2020*	2021*	AVG
CK-032	**Conuma R**	–	–	–	–	–	16	–	–	–	–
	Gold R	–	–	120	117	51	–	14	–	–	–
	Leiner R	–	–	–	–	–	–	14	–	–	–
CK-031	**Bedwell R**	NO	189	481	233	510	471	205	302	232	–
	Robertson Cr	–	–	–	–	–	–	68	–	–	–
No CU	**Unknown hatchery (ad-clipped)**	–	63	–	–	–	–	–	–	–	–
pNOS	–	–	0.75	0.80	0.67	0.91	0.97	0.68	1.00	1.00	**0.82**
$pHOS_{local}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray}$	–	–	0.25	0.20	0.33	0.09	0.03	0.32	0.00	0.00	**0.18**
$pHOS_{stray,OCU}$	–	–	0.00	0.20	0.33	0.09	0.03	0.09	0.00	0.00	**0.06**

Table E18. Total expanded recoveries of southern BC Chinook returning to ***Bedwell R*** *for return years 2015–2019, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: BEDWELL R								
Donor CU	**Donor River**	**Origin**	**2015**	**2016**	**2017**	**2018**	**2019**	**AVG**
CK-31	**Bedwell R**	HO	171	163	218	259	247	–
	Bedwell R	NO	261	187	344	465	148	–
pNOS	–	–	0.60	0.53	0.61	0.64	0.37	**0.55**
$pHOS_{local}$	–	–	0.40	0.47	0.39	0.36	0.63	**0.45**
$pHOS_{stray}$	–	–	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	0.00	0.00	**0.00**

*Table E19. Total expanded recoveries of southern BC Chinook returning to **Cypre R** for return years 2011–2020, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*). Note: The Cypre R stock has not historically been thermally marked, thus no homed HO individuals were observed.*

RECIPIENT RIVER: CYPRE R

Donor CU	Donor River	Origin	2011*	2014	2015	2016*	2017*	2019*	2020*	AVG
CK-031	Cypre R	NO	1564	1406	2674	1143	230	300	60	–
	Robertson Cr	–	–	–	–	–	–	37	–	–
No CU	unknown hatchery (ad-clipped)	–	–	–	–	114	–	–	–	–
pNOS	–	–	1.00	1.00	1.00	0.91	1.00	0.89	1.00	**0.97**
$pHOS_{local}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray}$	–	–	0.00	0.00	0.00	0.09	0.00	0.11	0.00	**0.03**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	0.09	0.00	0.11	0.00	**0.03**

Table E20. Total expanded recoveries of southern BC Chinook returning to ***Tranquil Cr*** *for return years 2011–2021, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*). Note: The Tranquil Cr stock has not historically been thermally marked, thus no homed HO individuals were observed.*

RECIPIENT RIVER: TRANQUIL CR												
Donor CU	**Donor River**	**Origin**	**2011***	**2014***	**2015***	**2016***	**2017**	**2018**	**2019***	**2020***	**2021***	**AVG**
CK-031	**Robertson Cr**	–	–	–	–	–	–	–	29	–	–	–
	Tranquil Cr	NO	361	244	224	321	149	116	57	173	425	–
pNOS	–	–	1.00	1.00	1.00	1.00	1.00	1.00	0.67	1.00	1.00	**0.96**
$pHOS_{local}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.33	0.00	0.00	**0.04**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

Table E21. Total expanded recoveries of southern BC Chinook returning to ***Kennedy R - Lower*** *for return years 2004–2018, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*). Note: The Tranquil Cr stock has not historically been thermally marked, thus no homed HO individuals were observed. As escapement estimates were unavailable for this system, unexpanded values are presented.*

RECIPIENT RIVER: KENNEDY R - LOWER								
Donor CU	**Donor River**	**Origin**	**2004**	**2015**	**2016**	**2017***	**2018**	**AVG**
CK-031	**Robertson Cr**	–	1	–	–	–	–	–
	Kennedy R - Lower	NO	48	113	95	12	47	–
pNOS	–	–	0.98	1.00	1.00	1.00	1.00	**1.00**
$pHOS_{local}$	–	–	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray}$	–	–	0.02	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	0.00	0.00	**0.00**

Table E22. Total expanded recoveries of southern BC Chinook returning to the ***Somass System/Robertson Cr*** *for return years 1998–2021, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: SOMASS SYSTEM / ROBERTSON CR																											
Donor CU	**Donor River**	**Origin**	**'98**	**'99**	**'00**	**'01**	**'02**	**'03**	**'04**	**'05**	**'06**	**'07**	**'08**	**'09**	**'10**	**'11**	**'12**	**'13**	**'14**	**'15**	**'16**	**'17**	**'18**	**'19**	**'20**	**'21**	**AVG**
CK-032	**Burman R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	64	–	–	–	–	–	–	–
	Gold R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	38	–	–	–	134	62	–	–	–	–	–
CK-031	**Nahmint R**	–	–	–	–	141	62	71	–	–	–	25	–	164	50	–	–	–	–	–	–	62	–	–	380	–	–
	Nitinat R	–	–	–	–	–	–	71	–	–	–	–	–	33	–	–	–	–	–	–	–	62	–	–	–	–	–
	Robertson	HO	52785	18662	8631	52005	50472	62465	86806	42257	62330	19826	27268	24938	35727	25927	15443	25986	23204	49391	48936	46535	40569	30999	30759	31634	–
		NO	5055	1378	754	1406	2294	3882	4498	1714	1982	1204	2548	788	1545	1050	1597	3248	1349	7658	4084	4152	5517	6569	9240	18035	–
No CU	**Unknown hatchery (ad-clipped)**	–	97	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	128	–	62	–	–	–	–	–
pNOS		–	0.09	0.07	0.08	0.03	0.04	0.06	0.05	0.04	0.03	0.06	0.09	0.03	0.04	0.04	0.09	0.11	0.05	0.13	0.08	0.08	0.12	0.17	0.23	0.36	**0.09**
$pHOS_{local}$		–	0.91	0.93	0.92	0.97	0.96	0.94	0.95	0.96	0.97	0.94	0.91	0.96	0.96	0.96	0.90	0.89	0.95	0.86	0.92	0.91	0.88	0.83	0.76	0.64	**0.91**
$pHOS_{stray}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	**0.00**
$pHOS_{stray,OCU}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

Table E23. Total expanded recoveries of southern BC Chinook returning to the ***Somass System/Robertson Cr*** *for return years 1998–2021, based on* ***CWT*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: SOMASS SYSTEM / ROBERTSON CR

Donor CU	Donor River	Origin	‘98	‘99	‘00	‘01	‘02	‘03	‘04	‘05	‘06	‘07	‘08	‘09	‘10	‘11	‘12	‘13	‘14	‘15	‘16	‘17	‘18	‘19	‘20	‘21	AVG
CK-031	**Marble R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	37	–	–	–	–	–	–	–	–	–
	Nahmint R	–	–	–	–	134	–	–	67	–	–	–	–	–	–	–	–	–	–	1	–	–	1	1	–	20	–
	Nitinat R	–	–	27	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Robertson	HO	28304	11599	5782	29132	38333	50790	67660	25633	37634	17711	23217	16234	27067	16708	11788	13378	19589	25684	33567	34263	25268	23630	27262	40515	–
		NO	12920	6221	3646	16013	10489	15397	24258	18316	26678	3343	6599	9688	13354	10269	9407	15856	4963	31575	19586	16641	20818	13938	13180	24923	–
	Sarita R	–	18	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
pNOS		–	0.31	0.35	0.39	0.35	0.21	0.23	0.26	0.42	0.41	0.16	0.22	0.37	0.33	0.38	0.44	0.54	0.20	0.55	0.37	0.33	0.45	0.37	0.33	0.38	**0.35**
$pHOS_{local}$		–	0.69	0.65	0.61	0.64	0.79	0.77	0.74	0.58	0.59	0.84	0.78	0.63	0.67	0.62	0.56	0.46	0.80	0.45	0.63	0.67	0.55	0.63	0.67	0.62	**0.65**
$pHOS_{stray}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray,OCU}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

*Table E24. Total expanded recoveries of southern BC Chinook returning to **Nahmint R** for return years 1999–2021, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners (pHOS$_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers (pHOS$_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU (pHOS$_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*).*

RECIPIENT RIVER: NAHMINT R

Donor CU	Donor River	Origin	1999	2000*	2001	2002	2003	2004	2005*	2006	2008*	2009*	2010	2012	2013	2014*	2015	2016	2017	201*8	2019	2020	2021	AVG
CK-032	**Conuma R**	–	–	–	–	3	–	–	–	5	–	–	–	–	–	–	48	44	5	–	21	17	–	–
	Gold R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	24	15	–	–	–	–	–	–
CK-031	**Nahmint R**	HO	–	48	164	79	255	902	88	394	71	22	174	49	41	14	36	250	90	49	296	35	–	–
		NO	926	95	164	198	255	362	98	105	99	88	232	209	188	101	406	676	137	148	190	933	372	–
	Nitinat R	–	–	–	–	–	–	–	–	5	–	–	39	–	–	–	12	–	–	–	21	–	–	–
	Robertson	–	11	–	82	337	224	20	11	25	–	–	19	–	–	43	–	15	2	–	11	–	16	–
	Sarita R	–	–	–	–	6	5	–	–	15	–	–	19	21	–	–	12	44	2	–	42	17	16	–
No CU	**Unknown hatchery (ad-clipped)**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	2	–	–	–	–	–
pNOS		–	0.99	0.67	0.40	0.32	0.34	0.28	0.50	0.19	0.58	0.80	0.48	0.75	0.82	0.64	0.76	0.65	0.57	0.75	0.33	0.93	0.92	**0.60**
pHOS$_{local}$		–	0.00	0.33	0.40	0.13	0.34	0.70	0.44	0.72	0.42	0.20	0.36	0.18	0.18	0.09	0.07	0.24	0.38	0.25	0.51	0.03	0.00	**0.28**
pHOS$_{stray}$		–	0.01	0.00	0.20	0.56	0.31	0.02	0.06	0.09	0.00	0.00	0.16	0.08	0.00	0.27	0.18	0.11	0.05	0.00	0.16	0.03	0.08	**0.11**
pHOS$_{stray,OCU}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.13	0.06	0.02	0.00	0.04	0.02	0.00	**0.01**

Table E25. Total expanded recoveries of southern BC Chinook returning to ***Nahmint R*** *for return years 2002–2021, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: NAHMINT R															
Donor CU	**Donor River**	**Origin**	**2002**	**2004**	**2010**	**2012**	**2013**	**2014**	**2015**	**2016**	**2017**	**2018**	**2019**	**2020**	**2021**	**AVG**
CK-31	**Nahmint R**	**HO**	186	968	111	39	39	4	202	145	85	121	332	346	127	–
		NO	40	345	359	179	182	80	325	533	153	73	230	603	253	–
	Robertson Cr	–	–	6	–	–	–	7	–	–	–	–	–	–	–	–
pNOS	–	–	0.18	0.26	0.76	0.82	0.82	0.88	0.62	0.79	0.64	0.38	0.41	0.64	0.67	**0.60**
$pHOS_{local}$	–	–	0.82	0.73	0.24	0.18	0.18	0.05	0.38	0.21	0.36	0.62	0.59	0.36	0.33	**0.39**
$pHOS_{stray}$	–	–	0.00	0.00	0.00	0.00	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.01**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

*Table E26. Total expanded recoveries of southern BC Chinook returning to **Sarita R** for return years 1998–2021, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: SARITA R

Donor CU	Donor River	Origin	‘98	‘99	‘00	‘01	‘02	‘03	‘04	‘05	‘06	‘07	‘08	‘09	‘10	‘11	‘12	‘13	‘14	‘15	‘16	‘17	‘19	‘20	‘21	AVG
CK-032	**Conuma R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	5	–	30	–	–	–	–	–	–
	Leiner R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	5	–	–	–
	Tlupana R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	9	–	–	–	–
CK-031	**Nahmint R**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	10	–	–	–	–	–	–
	Nitinat R	–	30	9	10	4	82	323	259	–	68	–	–	18	27	8	33	194	16	61	–	26	61	27	89	–
	Robertson	–	–	–	–	–	–	40	–	–	–	–	–	–	5	–	–	–	5	10	–	9	–	4	11	–
	Sarita R	HO	30	5	275	206	2960	3272	2847	1199	3076	1589	929	612	783	1398	1463	952	515	2178	2958	2411	1695	1833	3255	–
		NO	445	166	108	35	420	364	555	129	220	41	124	179	80	130	335	323	102	567	549	434	107	118	312	–
	Unknown hatchery (likely Nitinat) Thermal Mark	–	1930	629	87	35	12	–	–	–	–	–	–	11	5	–	–	–	–	–	–	–	–	–	–	–
pNOS		–	0.18	0.20	0.22	0.13	0.12	0.09	0.15	0.10	0.07	0.03	0.12	0.22	0.09	0.08	0.18	0.22	0.16	0.20	0.16	0.15	0.06	0.06	0.09	**0.13**
$pHOS_{local}$		–	0.01	0.01	0.57	0.73	0.85	0.82	0.78	0.90	0.91	0.97	0.88	0.75	0.87	0.91	0.80	0.65	0.81	0.76	0.84	0.83	0.91	0.92	0.89	**0.76**
$pHOS_{stray}$		–	0.80	0.79	0.20	0.14	0.03	0.09	0.07	0.00	0.02	0.00	0.00	0.02	0.04	0.00	0.02	0.14	0.03	0.04	0.00	0.01	0.03	0.02	0.03	**0.11**
$pHOS_{stray,OCU}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	**0.00**

Table E27. Total expanded recoveries of southern BC Chinook returning to ***Sarita R*** *for return years 1998–2021, based on* ***CWT*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners (pHOS$_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers (pHOS$_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU (pHOS$_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: SARITA R

Donor CU	Donor River	Origin	1998	1999	2002	2003	2004	2011	2012	2013	2014	2018	2019	2020	2021	AVG
CK-32	**Conuma R**	–	–	–	–	–	3	–	–	–	–	–	–	–	–	–
CK-31	**Nahmint R**	–	–	–	–	–	–	–	–	–	–	8	–	–	–	–
	Nitinat R	–	–	42	–	–	23	–	–	–	–	1	–	–	–	–
	Sarita R	**HO**	272	108	605	217	73	5	79	358	36	16	37	673	590	–
		NO	124	89	95	130	195	38	1696	1075	458	1873	1291	911	192	–
pNOS	–	–	0.31	0.37	0.14	0.37	0.66	0.87	0.96	0.75	0.93	0.99	0.97	0.57	0.25	**0.63**
pHOS$_{local}$	–	–	0.69	0.45	0.86	0.63	0.25	0.13	0.04	0.25	0.07	0.01	0.03	0.43	0.75	**0.35**
pHOS$_{stray}$	–	–	0.00	0.18	0.00	0.00	0.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.02**
pHOS$_{stray,OCU}$	–	–	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

Table E28. Total expanded recoveries of southern BC Chinook returning to ***Toquart R*** *for return years 1998–2021, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: TOQUART R					
Donor CU	**Donor River**	**Origin**	**2015**	**2016**	**AVG**
CK-032	**Conuma R**	–	26	9	–
CK-031	**Toquart R**	NO	352	174	–
pNOS	–	–	0.93	0.95	**0.94**
$pHOS_{local}$	–	–	0.00	0.00	**0.00**
$pHOS_{stray}$	–	–	0.07	0.05	**0.06**
$pHOS_{stray,OCU}$	–	–	0.07	0.05	**0.06**

Table E29. Total expanded recoveries of southern BC Chinook returning to ***Nitinat R*** *for return years 1998–2021, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: NITINAT R																										
Donor CU	**Donor River**	**Origin**	**‘98**	**‘99**	**‘00**	**‘01**	**‘02**	**‘03**	**‘04**	**‘05**	**‘06**	**‘07**	**‘08**	**‘09**	**‘10**	**‘11**	**‘12**	**‘13**	**‘14**	**‘15**	**‘16**	**‘17**	**‘18**	**‘20**	**‘21**	**AVG**
CK-031	**Nitinat R**	HO	4152	10739	2998	7086	19523	37724	15172	14048	13621	6892	9723	6543	6573	9796	6840	36620	33136	23554	19866	19295	28012	34120	27116	–
		NO	1510	727	1651	382	614	–	3555	2252	889	544	2271	887	931	191	1018	2122	2828	2079	1504	3752	3373	1323	2037	–
	Robertson	–	–	–	–	–	–	–	63	–	32	–	–	35	9	–	–	42	36	–	–	219	440	40	67	–
	Sarita R	–	–	242	–	–	97	–	–	–	–	–	28	35	9	–	14	–	–	25	85	292	147	321	67	–
CK-9008	**Chilliwack**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	13	–	42	–	–	–	–	–	–	–	–
No CU	**Unknown hatchery (thermal mark)**	–	–	–	–	–	–	–	–	–	–	–	14	–	–	–	–	–	–	–	–	–	–	–	–	–
pNOS		–	0.27	0.06	0.36	0.05	0.03	0.00	0.19	0.14	0.06	0.07	0.19	0.12	0.12	0.02	0.13	0.05	0.08	0.08	0.07	0.16	0.11	0.04	0.07	**0.11**
$pHOS_{local}$		–	0.73	0.92	0.64	0.95	0.96	1.00	0.81	0.86	0.94	0.93	0.81	0.87	0.87	0.98	0.87	0.94	0.92	0.92	0.93	0.82	0.88	0.95	0.93	**0.89**
$pHOS_{stray}$		–	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.02	0.01	0.00	**0.00**
$pHOS_{stray,OCU}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

*Table E30. Total expanded recoveries of southern BC Chinook returning to **Nitinat R** for return years 1998–2007, based on **CWT sampling**. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: NITINAT R													
Donor CU	**Donor River**	**Origin**	**1998**	**1999**	**2000**	**2001**	**2002**	**2003**	**2004**	**2005**	**2006**	**2007**	**AVG**
CK-31	**Nitinat R**	**HO**	33946	20162	8749	13273	4278	25100	14793	16334	10447	130	–
		NO	13173	2037	1041	2045	2949	12136	15558	617	3909	8219	–
	Sarita R	–	–	–	–	–	22	–	11	–	–	–	–
pNOS	–	–	0.28	0.09	0.11	0.13	0.41	0.33	0.51	0.04	0.27	0.98	**0.31**
$pHOS_{local}$	–	–	0.72	0.91	0.89	0.87	0.59	0.67	0.49	0.96	0.73	0.02	**0.68**
$pHOS_{stray}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

*Table E31. Total expanded recoveries of southern BC Chinook returning to **San Juan R** for return years 2005–2021, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. *This observation is likely the result of an incorrect application or reading of a thermal mark.*

RECIPIENT RIVER: SAN JUAN R													
Donor CU	**Donor River**	**Origin**	**2005**	**2006**	**2008**	**2012**	**2014**	**2015**	**2017**	**2019**	**2020**	**2021**	**AVG**
CK-032	**Conuma R**	–	–	91	–	–	–	25	–	–	–	–	–
	Tlupana R	–	–	–	–	–	–	–	–	–	3	58	–
CK-031	**Nitinat R**	–	12	23	20	55	193	–	–	26	6	4	–
	Robertson Cr	–	12	–	–	–	32	–	–	–	–	–	–
	San Juan R	**HO**	780	1414	–	–	3579	1863	888	–	–	–	–
		NO	446	2987	1680	1767	355	417	581	1006	861	1038	–
	Sarita R	–	–	–	–	–	–	–	–	–	–	4	–
CK-003	**Chehalis R**	–	–	–	–	–	–	–	–	9	–	–	–
CK-017	**Spius Cr**	–	–	–	–	–	–	–	–	344*	–	–	–
pNOS	–	–	0.36	0.66	0.99	0.97	0.09	0.18	0.40	0.73	0.99	0.94	**0.63**
$pHOS_{local}$	–	–	0.62	0.31	0.00	0.00	0.86	0.81	0.60	0.00	0.00	0.00	**0.32**
$pHOS_{stray}$	–	–	0.02	0.03	0.01	0.03	0.05	0.01	0.00	0.27	0.01	0.06	**0.05**
$pHOS_{stray,OCU}$	–	–	0.00	0.02	0.00	0.00	0.00	0.01	0.00	0.25	0.00	0.05	**0.03**

Table E32. Total expanded recoveries of southern BC Chinook returning to ***Sooke R*** *for return years 2005–2021, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: SOOKE R											
Donor CU	**Donor River**	**Origin**	**2005**	**2012**	**2014**	**2017**	**2018**	**2019**	**2020**	**2021**	**AVG**
CK-031	**Nitinat R**	–	33	–	–	7	32	7	86	106	–
	Robertson Cr	–	–	–	6	–	4	7	–	42	–
	Sooke R	**HO**	83	74	312	126	334	381	902	530	–
		NO	333	294	52	84	294	515	580	276	–
pNOS	–	–	0.74	0.80	0.14	0.39	0.44	0.57	0.37	0.29	**0.47**
$pHOS_{local}$	–	–	0.19	0.20	0.84	0.58	0.50	0.42	0.58	0.56	**0.48**
$pHOS_{stray}$	–	–	0.07	0.00	0.02	0.03	0.05	0.01	0.05	0.16	**0.05**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

*Table E33. Total expanded recoveries of southern BC Chinook returning to **Cowichan R** for return years 2001–2021, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners (pHOS$_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers (pHOS$_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU (pHOS$_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*).*

RECIPIENT RIVER: COWICHAN R

Donor CU	Donor River	Origin	‘01	‘03*	‘04	‘05	‘07	‘08	‘09	‘10	‘11	‘12	‘13	‘14	‘15	‘16	‘17	‘18	‘19	‘20	‘21	AVG
CK-022	**Cowichan R**	HO	–		–	–	–	–	287	1039	1582	1537	2137	1802	1411	1160	2404	1932	1661	668	2820	–
		NO	7678	5014	4487	4294	3774	2620	1098	3726	4109	4550	4929	3995	5622	9519	22602	20515	19864	24058	20703	–
CK-025	**Nanaimo R - Fall**	–	–		–	–	6	14	–	52	29	51	–	–	12	–	–	–	–	–	223	–
CK-083	**Nanaimo R - Sum**	–	–		–	–	–	–	–	43	7	51	17	–	–	–	–	–	–	–	–	–
CK-029	**Campbell/ Quinsam**	–	–	1003	77	–	–	–	–	–	–	–	–	–	–	22	–	–	–	–	–	–
CK-031	**Robertson Cr**	–	–		–	15	–	27	–	–	–	20	–	22	127	66	–	35	66	–	–	–
CK-032	**Burman R**	–	–		–	–	–	–	–	9	–	–	–	–	–	–	–	–	–	–	–	–
No CU	**unknown hatchery (thermal mark)**	–	–		–	–	11	–	–	17	7	20	–	–	–	–	–	–	–	–	–	–
pNOS		–	1.00	0.83	0.98	1.00	1.00	0.98	0.79	0.76	0.72	0.73	0.70	0.69	0.78	0.88	0.90	0.91	0.92	0.97	0.87	**0.86**
pHOS$_{local}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.21	0.21	0.28	0.25	0.30	0.31	0.20	0.11	0.10	0.09	0.08	0.03	0.12	**0.12**
pHOS$_{stray}$		–	0.00	0.17	0.02	0.00	0.00	0.02	0.00	0.02	0.01	0.02	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.01	**0.02**
pHOS$_{stray,OCU}$		–	0.00	0.17	0.02	0.00	0.00	0.02	0.00	0.02	0.01	0.02	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.01	**0.02**

Table E34. Total expanded recoveries of southern BC Chinook returning to ***Cowichan R*** *for return years 1998–2021, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: COWICHAN R

Donor CU	Donor River	Origin	‘98	‘99	‘00	‘01	‘02	‘03	‘04	‘05	‘06	‘07	‘08	‘09	‘10	‘11	‘12	‘13	‘14	‘15	‘16	‘17	‘18	‘19	‘20	‘21	AVG
CK-22	Cowichan R	HO	4182	2253	1885	2775	3447	1577	1352	1207	750	1217	628	430	774	1631	2265	1711	1041	718	1812	1560	1103	586	4180	1803	–
		NO	6015	5572	6764	4903	3851	4440	3216	3310	2300	2646	2159	1145	4108	4094	3926	5629	4041	6400	8413	21047	21922	20826	20547	19311	–
CK-25	Chemainus R	–	–	14	35	–	24	–	–	19	16	8	–	4	–	–	6	–	–	–	–	–	–	–	–	–	–
	Nanaimo R	–	–	–	33	–	–	23	–	–	31	14	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-27	Big Qualicum	–	–	12	–	76	59	58	–	–	–	–	–	60	–	–	39	–	–	7	–	–	–	–	–	–	–
CK-31	Robertson Cr	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	114	–	–	–	–	–	–	–
No CU	US Hatcheries	–	–	–	–	4	–	–	3	–	–	–	2	3	–	–	–	–	–	–	–	37	3	–	–	–	–
pNOS		–	0.59	0.71	0.78	0.63	0.52	0.73	0.70	0.73	0.74	0.68	0.77	0.70	0.84	0.72	0.63	0.77	0.80	0.88	0.82	0.93	0.95	0.97	0.83	0.91	**0.76**
$pHOS_{local}$		–	0.41	0.29	0.22	0.36	0.47	0.26	0.30	0.27	0.24	0.31	0.23	0.26	0.16	0.28	0.36	0.23	0.20	0.10	0.18	0.07	0.05	0.03	0.17	0.09	**0.23**
$pHOS_{stray}$		–	0.00	0.00	0.01	0.01	0.01	0.01	0.00	0.00	0.02	0.01	0.00	0.04	0.00	0.00	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	**0.01**
$pHOS_{stray,OCU}$		–	0.00	0.00	0.01	0.01	0.01	0.01	0.00	0.00	0.02	0.01	0.00	0.04	0.00	0.00	0.01	0.00	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.00	**0.01**

Table E35. Total expanded recoveries of southern BC Chinook returning to ***Nanaimo R – Fall Run*** *for return years 2004–2018, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners (pHOS$_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers (pHOS$_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU (pHOS$_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: NANAIMO R - FALL																		
Donor CU	**Donor River**	**Origin**	**2004**	**2005**	**2006**	**2007**	**2008**	**2009**	**2010**	**2011**	**2012**	**2013**	**2014**	**2015**	**2016**	**2017**	**2018**	**AVG**
CK-022	**Cowichan R**	–	–	–	–	–	–	34	27	–	–	–	–	–	50	43	–	–
CK-025	**Chemainus R**	–	–	–	–	–	–	–	9	–	–	–	–	–	–	–	–	–
	Nanaimo R - Fall	HO	–	–	–	2278	2644	2163	2609	4213	1194	3526	1709	3133	2929	2836	2370	–
		NO	2376	2920	5305	2227	1384	352	597	777	520	622	460	1890	1986	1332	1663	–
CK-031	**Nitinat R**	–	–	–	–	–	55	–	–	–	–	–	–	–	–	–	–	–
	Robertson Cr	–	74	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
No CU	**Unknown hatchery (thermal mark)**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	42	–
pNOS	–	–	0.97	1.00	1.00	0.49	0.34	0.14	0.18	0.16	0.30	0.15	0.21	0.38	0.40	0.32	0.41	**0.43**
pHOS$_{local}$	–	–	0.00	0.00	0.00	0.51	0.65	0.85	0.80	0.84	0.70	0.85	0.79	0.62	0.59	0.67	0.58	**0.56**
pHOS$_{stray}$	–	–	0.03	0.00	0.00	0.00	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	**0.01**
pHOS$_{stray,OCU}$	–	–	0.03	0.00	0.00	0.00	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	**0.01**

*Table E36. Total expanded recoveries of southern BC Chinook returning to **Nanaimo R – Fall Run** for return years 1998–2008, based on **CWT sampling**. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: NANAIMO R - FALL

Donor CU	**Donor River**	**Origin**	**1998**	**1999**	**2000**	**2001**	**2002**	**2003**	**2004**	**2005**	**2006**	**2007**	**2008**	**AVG**
CK-22	**Cowichan R**	–	–	7	–	–	13	12	67	187	–	–	3	–
CK-25	**Chemainus R**	–	–	–	10	–	31	–	1	210	415	35	11	–
	Nanaimo R - Fall	HO	733	851	214	426	1010	1319	1334	425	1628	774	272	–
		NO	630	1308	732	1947	846	899	772	2495	3922	3268	3006	–
CK-83	**Nanaimo R - Summer**	–	5	74	28	97	47	113	–	–	–	–	–	–
	Puntledge R - Summer	–	–	–	–	–		47	–	–	–	–	9	–
CK-27	**Big Qualicum R**	–	54	–	–	–		9	–	–	–	–	33	–
	Puntledge R - Fall	–	2	–	–	–		–	–	–	–	–	239	–
CK-31	**Sooke R**	–	–	30	–	–		–	–	–	–	–	–	–
pNOS	–	–	0.44	0.58	0.74	0.79	0.43	0.37	0.35	0.75	0.66	0.80	0.84	**0.62**
$pHOS_{local}$	–	–	0.52	0.37	0.22	0.17	0.52	0.55	0.61	0.13	0.27	0.19	0.08	**0.33**
$pHOS_{stray}$	–	–	0.04	0.05	0.04	0.04	0.05	0.08	0.03	0.12	0.07	0.01	0.08	**0.05**
$pHOS_{stray,OCU}$	–	–	0.04	0.05	0.03	0.04	0.03	0.08	0.03	0.06	0.00	0.00	0.08	**0.04**

Table E37. Total expanded recoveries of southern BC Chinook returning to ***Chemainus R*** *for return years 2019–2021, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*). Notes: The Chemainus R stock has not historically been thermally marked, thus no homed HO individuals were observed; no escapement estimates were available between 2019 and 2021, thus unexpanded recoveries are used.*

RECIPIENT RIVER: CHEMAINUS R

Donor CU	Donor River	Origin	2019*	2020*	2021	AVG
CK-025	Nanaimo R	–	2	1	3	–
	Chemainus R	NO	7	8	19	–
pNOS	–	–	0.78	0.89	0.86	**0.84**
$pHOS_{local}$	–	–	0.00	0.00	0.00	**0.00**
$pHOS_{stray}$	–	–	0.22	0.11	0.14	**0.16**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	**0.00**

Table E38. Total expanded recoveries of southern BC Chinook returning to ***Capilano R*** *for return years 1998–2021, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: CAPILANO R

Donor CU	Donor River	Origin	1998	1999	2000	2001	2002	2003	2004	2015	2016	2017	2018	2019	2020	2021	AVG
CK-20	Cheakamus R	–	–	–	–	–	–	–	–	–	–	–	–	–	2	–	–
	Porteau Cv	–	–	–	–	22	–	–	–	–	–	–	–	–	–	–	–
CK-22	Cowichan R	–	48	–	–	–	–	–	–	–	1	–	–	–	–	–	–
CK-25	Nanaimo R - Fall	–	–	–	–	1	–	–	–	–	–	–	–	–	–	–	–
CK-27	Big Qualicum R	–	–	–	–	–	–	–	–	6	–	–	–	–	–	–	–
CK-31	Robertson Cr	–	–	–	–	–	–	–	–	13	–	–	–	–	–	–	–
CK-9007	Capilano R	HO	669	240	154	761	102	164	12	199	859	463	1316	1404	1653	770	–
		NO	193	5	23	391	183	523	1724	196	360	49	4	150	391	648	–
pNOS		–	0.21	0.02	0.13	0.33	0.64	0.76	0.99	0.47	0.30	0.10	0.00	0.10	0.19	0.46	**0.34**
$pHOS_{local}$		–	0.74	0.98	0.87	0.65	0.36	0.24	0.01	0.48	0.70	0.90	1.00	0.90	0.81	0.54	**0.66**
$pHOS_{stray}$		–	0.05	0.00	0.00	0.02	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00	**0.01**
$pHOS_{stray,OCU}$		–	0.05	0.00	0.00	0.02	0.00	0.00	0.00	0.05	0.00	0.00	0.00	0.00	0.00	0.00	**0.01**

*Table E39. Total expanded recoveries of southern BC Chinook returning to **Big Qualicum R** for return years 1998–2021, based on **CWT sampling**. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners (pHOS$_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers (pHOS$_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU (pHOS$_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: BIG QUALICUM R

Donor CU	Donor River	Origin	‘98	‘99	‘00	‘01	‘02	‘03	‘04	‘05	‘06	‘07	‘08	‘09	‘10	‘11	‘12	‘13	‘14	‘15	‘16	‘17	‘18	‘19	‘20	‘21	AVG
CK-22	**Cowichan R**	–	205	52	53	91	83	73	26	232	93	35	73	79	28	48	80	45	32	40	13	17	6	6	21	11	–
CK-25	**Chemainus R**	–	–	1	–	–	–	7	2	11	20	–	2	8	–	–	–	–	–	–	–	–	–	–	–	–	–
	Nanaimo R - Fall	–	–	–	–	2	–	7	–	–	–	–	2	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-27	**Big Qual + L Qualicm**	–	–	–	113	334	239	64	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Big Qualicum R	**HO**	2512	4083	3122	5667	3051	2759	4113	5426	8470	5938	4034	5907	4648	4773	2897	4207	7147	6748	4002	7452	3615	6104	7896	7088	–
		NO	3385	1744	3822	4948	4515	4018	2958	3920	4082	3991	2637	3449	3280	2558	2356	740	1360	137	1063	50	1404	3076	3953	3617	–
	L Qualicum R	–	1108	380	538	275	520	771	212	1093	276	41	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Puntledge R - Fall	–	–	–	–	–	–	19	–	–	–	31	–	–	–	–	–	–	–	12	20	–	–	–	–	–	–
CK-29	**Campbell/ Quinsam R**	–	65	11	7	–	75	33	36	–	45	–	9	88	32	–	12	83	81	74	3	27	–	11	17	40	–
CK-31	**Nahmint R**	–	–	–	–	–	–		–	–	–	–	–	–	–	–	–	–	–	2	–	–	–	–	–	–	–
CK-9007	**Lang Cr**	–	–	10	–	–	–		–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
No CU	**US Hatcheries**	–	2	–	4	11	4		27	7	4	3	–	1	13	8	4	5	4	9	7	5	2	4	4	8	–
pNOS		–	0.47	0.28	0.50	0.44	0.53	0.52	0.40	0.37	0.31	0.40	0.39	0.36	0.41	0.35	0.44	0.15	0.16	0.02	0.21	0.01	0.28	0.33	0.33	0.34	**0.33**
pHOS$_{local}$		–	0.36	0.65	0.42	0.53	0.39	0.36	0.56	0.51	0.65	0.59	0.60	0.62	0.58	0.65	0.54	0.83	0.83	0.96	0.78	0.99	0.72	0.66	0.66	0.66	**0.63**
pHOS$_{stray}$		–	0.19	0.07	0.08	0.03	0.08	0.12	0.04	0.13	0.03	0.01	0.01	0.02	0.01	0.01	0.02	0.03	0.01	0.02	0.01	0.01	0.00	0.00	0.00	0.01	**0.04**
pHOS$_{stray,OCU}$		–	0.04	0.01	0.01	0.01	0.02	0.02	0.01	0.02	0.01	0.00	0.01	0.02	0.01	0.01	0.02	0.03	0.01	0.02	0.00	0.01	0.00	0.00	0.00	0.01	**0.01**

Table E40. Total expanded recoveries of southern BC Chinook returning to ***Little Qualicum R*** *for return years 1998–2020, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series. Years where < 20 thermally marked Chinook were sampled in the recipient river are shown in grey and marked with an asterisk (*).*

RECIPIENT RIVER: LITTLE QUALICUM R

Donor CU	Donor River	Origin	1998	1999	2000*	2001	2002	2003	2004	2005	2006*	2007*	2017*	2020*	AVG
CK-22	**Cowichan R**	–	36	–	16	19	26	40	29	38	–	–	6	2	–
CK-25	**Chemainus R**	–	–	–	–	1	–	–	–	–	–	–	–	–	–
	Nanaimo R - Fall	–	–	–	–	–	–	2	1	–	–	–	–	–	–
CK-27	**Big Qual+L Qualicum**	–	–	–	376	1176	932	105	–	–	–	–	–	–	–
	Big Qualicum R	–	16	70	–	118	14	22	154	92	57	70	53	227	–
	L Qualicum R	**HO**	2532	2498	1455	2346	2931	3302	3189	3056	1136	–	–	–	–
		NO	167	1154	1302	2034	652	1370	325	3748	3727	2683	7222	10410	–
CK-29	**Campbell/ Quinsam R**	–	–	–	–	–	–	–	9	–	–	–	–	18	–
CK-31	**San Juan R**	–	–	–	–	–	10	–	–	–	–	–	–	–	–
No CU	**US Hatcheries**	–	–	–	–	1	1	–	–	–	–	–	–	–	–
pNOS		–	0.06	0.31	0.41	0.36	0.14	0.28	0.09	0.54	0.76	0.97	0.99	0.98	**0.49**
$pHOS_{local}$		–	0.92	0.67	0.58	0.62	0.85	0.70	0.86	0.44	0.23	0.00	0.00	0.00	**0.49**
$pHOS_{stray}$		–	0.02	0.02	0.01	0.02	0.01	0.01	0.05	0.02	0.01	0.03	0.01	0.02	**0.02**
$pHOS_{stray,OCU}$		–	0.01	0.00	0.01	0.00	0.01	0.01	0.01	0.01	0.00	0.00	0.00	0.00	**0.00**

*Table E41. Total expanded recoveries of southern BC Chinook returning to **Puntledge R – Fall Run** for return years 1998–2021, based on **CWT sampling**. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners (pHOS$_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers (pHOS$_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU (pHOS$_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: PUNTLEDGE R - FALL

Donor CU	Donor River	Origin	'98	'99	'00	'01	'02	'03	'04	'05	'06	'07	'08	'09	'10	'11	'12	'13	'14	'15	'16	'17	'18	'19	'20	'21	AVG
CK-22	**Cowichan R**	–	23	52	20	130	64	–	22	41	44	–	–	3	–	12	2	18	18	8	5	4	–	2	2	–	–
CK-25	**Chemainus R**	–	–	6	5	4	22	12	7	8	–	10	6	20	3	–	–	2	2	–	–	–	–	–	–	–	–
	Nanaimo R - Fall	–	30	20	–	1	5	11	111	7	5	3	3	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-83	**Nanaimo R - Sum**	–	–	6	–	–	24	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Puntledge R - Sum	–	13	55	100	458	192	355	751	963	615	253	185	204	194	267	82	90	259	323	153	124	41	108	67	53	–
CK-27	**Big Qualicum R**	–	–	–	–	–	32	–	–	–	–	–	–	85	24	11	–	16	39	20	–	6	–	–	–	–	–
	L Qualicum R	–	–	46	–	82	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Puntledge R - Fall	**HO**	165	1495	2213	8439	5267	6582	5419	4154	7787	5501	4326	5559	2821	2756	2960	5242	5081	5188	5023	6336	4361	8885	6296	2174	–
		NO	269	324	554	4044	4238	6509	4730	2407	7208	2385	171	308	1590	2483	1419	485	579	2095	2582	5292	2782	8030	3488	4377	–
CK-29	**Campbell/ Quinsam**	–	–	–	7	–	–	–	–	–	–	–	15	–	–	–	–	–	7	–	–	–	10	6	52	–	–
CK-31	**Robertson Cr**	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	27	–	–	9	–	–	–	–
CK-32	**Conuma R**	–	–	15	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-42	**Kitimat R Low**	–	–	27	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Kitimat R Up	–	–	15	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-9008	**Chilliwack R**	–	–	–	–	–	–	–	–	–	–	13	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
No CU	**US Hatcheries**	–	–	–	–	–	3	–	3	–	2	–	–	–	2	–	2	–	3	2	–	–	–	–	–	–	–
pNOS		–	0.54	0.16	0.19	0.31	0.43	0.48	0.43	0.32	0.46	0.29	0.04	0.05	0.34	0.45	0.32	0.08	0.10	0.27	0.33	0.45	0.39	0.47	0.35	0.66	**0.33**
pHOS$_{local}$		–	0.36	0.75	0.80	0.68	0.55	0.52	0.56	0.68	0.54	0.70	0.96	0.93	0.65	0.55	0.68	0.91	0.89	0.72	0.67	0.55	0.61	0.53	0.64	0.34	**0.66**
pHOS$_{stray}$		–	0.11	0.09	0.01	0.02	0.02	0.00	0.01	0.01	0.00	0.00	0.01	0.02	0.01	0.00	0.00	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.01	0.00	**0.01**
pHOS$_{stray,OCU}$		–	0.11	0.07	0.01	0.01	0.01	0.00	0.01	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	**0.01**

*Table E42. Total expanded recoveries of southern BC Chinook returning to **Nanaimo R - Summer Run** for return years 2004–2018, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: NANAIMO R - SUMMER

Donor CU	Donor River	Origin	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2017	2018	2021	AVG
CK-083	**Nanaimo R - Sum**	HO	–	–	–	44	249	95	343	540	443	645	479	107	180	178	623	–
		NO	323	427	1001	326	584	254	441	585	377	194	518	486	780	283	356	–
CK-031	**Robertson Cr**	–	–	3	–	–	–	–	–	–	–	–	–	–	–	–	13	–
pNOS		–	1.00	0.99	1.00	0.88	0.70	0.73	0.56	0.52	0.46	0.23	0.52	0.82	0.81	0.61	0.36	**0.68**
$pHOS_{local}$		–	0.00	0.00	0.00	0.12	0.30	0.27	0.44	0.48	0.54	0.77	0.48	0.18	0.19	0.39	0.63	**0.32**
$pHOS_{stray}$		–	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	**0.00**
$pHOS_{stray,OCU}$		–	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	**0.00**

Table E43. Total expanded recoveries of southern BC Chinook returning to **Nanaimo R - Summer Run** for return years 1998–2005, based on **CWT sampling**. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.

RECIPIENT RIVER: NANAIMO R - SUMMER											
Donor CU	**Donor River**	**Origin**	**1998**	**1999**	**2000**	**2001**	**2002**	**2003**	**2004**	**2005**	**AVG**
CK-083	**Nanaimo R - Sum**	**HO**	**733**	**851**	**214**	**426**	**1010**	**1319**	**1334**	**425**	–
		NO	**630**	**1308**	**732**	**1947**	**846**	**899**	**772**	**2495**	–
pNOS	–	–	0.46	0.61	0.77	0.82	0.46	0.41	0.37	0.85	**0.59**
$pHOS_{local}$	–	–	0.54	0.39	0.23	0.18	0.54	0.59	0.63	0.15	**0.41**
$pHOS_{stray}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

Table E44. Total expanded recoveries of southern BC Chinook returning to ***Puntledge R - Summer Run*** *for return years 1998–2021, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: PUNTLEDGE R - SUMMER																											
Donor CU	**Donor River**	**Origin**	**‘98**	**‘99**	**‘00**	**‘01**	**‘02**	**‘03**	**‘04**	**‘05**	**‘06**	**‘07**	**‘08**	**‘09**	**‘10**	**‘11**	**‘12**	**‘13**	**‘14**	**‘15**	**‘16**	**‘17**	**‘18**	**‘19**	**‘20**	**‘21**	**AVG**
CK-22	**Cowichan R**	–	17	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-25	**Chemainus R**	–	–	–	–	–	4	–	–	–	–	–	–	–	–	–	2	–	–	–	–	–	–	–	–	–	–
	Nanaimo R - Fall	–	19	9	–	–	6	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-83	**Nanaimo R - Sum**	–	–	7	14	10	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Puntledge R - Sum	**HO**	183	537	590	2140	1008	1004	528	694	1440	1587	579	1962	1410	851	497	423	625	310	407	177	483	475	385	376	–
		NO	109	97	139	99	265	346	396	103	2	0	0	72	20	306	47	80	437	285	165	516	337	200	49	123	–
CK-27	**Big Qualicum R**	–	–	–	–	–	–	–	–	–	–	–	–	35	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-29	**Campbell/ Quinsam**	–	–	–	–	–	–	–	–	–	–	–	–	–	20	–	–	–	–	–	–	–	–	–	–	–	–
No CU	**US Hatcheries**	–	–	–	–	–	–	–	–	1	2	–	–	2	–	–	–	–	4	–	–	–	–	–	–	–	–
pNOS		–	0.33	0.15	0.19	0.04	0.21	0.26	0.43	0.13	0.00	0.00	0.00	0.03	0.01	0.26	0.09	0.16	0.41	0.48	0.29	0.74	0.41	0.30	0.11	0.25	**0.22**
$pHOS_{local}$		–	0.56	0.83	0.80	0.95	0.79	0.74	0.57	0.87	1.00	1.00	1.00	0.95	0.97	0.74	0.91	0.84	0.59	0.52	0.71	0.26	0.59	0.70	0.89	0.75	**0.77**
$pHOS_{stray}$		–	0.11	0.02	0.02	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.01**
$pHOS_{stray,OCU}$		–	0.11	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.01**

Table E45. Total expanded recoveries of southern BC Chinook returning to ***Phillips R*** *for return years 2009–2021, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: PHILLIPS R																
Donor CU	**Donor River**	**Origin**	**2009**	**2010**	**2011**	**2012**	**2013**	**2014**	**2015**	**2016**	**2017**	**2018**	**2019**	**2020**	**2021**	**AVG**
CK-27	**Puntledge R - Fall**	–	–	316	–	–	–	–	104	–	–	–	–	–	–	–
CK-28	**Phillips R**	**HO**	162	457	467	416	1045	1877	1402	1282	1561	638	1245	1297	599	–
		NO	85	399	444	1778	1635	721	807	898	917	618	1286	2033	1606	–
CK-29	**Campbell/ Quinsam R**	–	–	–	128	–	–	–	–	–	–	–	–	–	–	–
No CU	**US Hatcheries**	–	–	–	–	11	–	–	–	–	–	–	–	–	–	–
pNOS		–	0.34	0.34	0.43	0.81	0.61	0.28	0.35	0.41	0.37	0.49	0.51	0.61	0.73	**0.48**
$pHOS_{local}$		–	0.66	0.39	0.45	0.19	0.39	0.72	0.61	0.59	0.63	0.51	0.49	0.39	0.27	**0.48**
$pHOS_{stray}$		–	0.00	0.27	0.12	0.01	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	**0.03**
$pHOS_{stray,OCU}$		–	0.00	0.27	0.12	0.01	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.00	**0.03**

Table E46. Total expanded recoveries of southern BC Chinook returning to ***Campbell and Quinsam Rs*** *for return years 1999–2021, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners (pHOS$_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers (pHOS$_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU (pHOS$_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: CAMPBELL/QUINSAM R

Donor CU	Donor River	Origin	‘99	‘00	‘01	‘02	‘04	‘05	‘06	‘07	‘08	‘09	‘10	‘11	‘12	‘13	‘14	‘15	‘16	‘17	‘18	‘19	‘20	‘21	AVG
CK-025	**Nanaimo R**	–	–	–	–	–	–	–	–	–	–	–	–	15	–	–	–	13	–	–	–	–	–	–	–
CK-027	**Puntledge R - Fall**	–	–	–	–	42	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-029	**Campbell/ Quinsam**	HO	–	6150	11927	10709	8444	7615	7412	4857	3986	4907	3471	3872	3846	2890	1963	2789	6376	8443	6202	6405	8222	5441	–
		NO	8447	2203	2684	2319	1774	956	2077	1879	2395	1472	824	957	1342	1590	756	1193	1281	1344	1013	1111	1818	2114	–
CK-9008	**Chilliwack R**	–	–	–	–	–	–	–	–	21	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-031	**Nitinat R**	–	–	–	–	–	–	–	32	–	–	–	–	–	–	–	–	–	–	–	–	–	–	31	–
CK-031	**Robertson Cr**	–	–	–	–	–	–	–	64	–	–	–	–	–	–	–	–	27	–	–	25	–	–	–	–
No CU	**Friday Cr (US)**	–	–	–	–	–	–	–	–	–	–	–	–	–	14	–	–	–	–	–	–	–	–	–	–
	Unknown hatchery (thermally marked)	–	–	–	–	–	–	–	–	–	–	–	14	–	–	–	–	–	–	–	–	–	–	–	–
pNOS		–	1.00	0.26	0.18	0.18	0.17	0.11	0.22	0.28	0.38	0.23	0.19	0.20	0.26	0.36	0.28	0.30	0.17	0.14	0.14	0.15	0.18	0.28	**0.26**
pHOS$_{\text{local}}$		–	0.00	0.74	0.82	0.82	0.83	0.89	0.77	0.72	0.62	0.77	0.81	0.80	0.74	0.65	0.72	0.69	0.83	0.86	0.86	0.85	0.82	0.72	**0.74**
pHOS$_{\text{stray}}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
pHOS$_{\text{stray,OCU}}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

Table E47. *Total expanded recoveries of southern BC Chinook returning to* ***Campbell and Quinsam Rs*** *for return years 1998–2021, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: CAMPBELL/QUINSAM R

Donor CU	Donor River	Origin	‘98	‘99	‘00	‘01	‘02	‘03	‘04	‘05	‘06	‘07	‘08	‘09	‘10	‘11	‘12	‘13	‘14	‘15	‘16	‘17	‘18	‘19	‘20	‘21	AVG
CK-20	**Porteau Cv**	–	–	–	–	14	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-22	**Cowichan R**	–	26	–	10	–	–	–	17	–	–	–	9	–	–	–	3	–	3	1	1	–	–	–	–	–	–
CK-25	**Nanaimo R - Fall**	–	–	–	–	–	–	–	5	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-83	**Puntledge R - Sum**	–	–	–	–	–	–	–	–	–	–	15	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-27	**Big Qual+L Qualicm**	–	–	57	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Big Qualicum R	–	–	–	–	–	58	–	6	20	–	–	–	–	32	2	–	–	–	8	–	–	5	–	95	–	–
	L Qualicum R	–	–	–	13	–	–	–	–	79	27	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Puntledge R - Fall	–	–	–	–	5	12	–	–	–	–	241	–	–	–	60	41	–	–	–	–	–	–	–	–	–	–
CK-29	**Campbell/ Quinsam**	**HO**	3338	5927	6152	10684	8575	4938	6674	5703	6319	4660	4183	3445	2276	3301	2879	2928	1769	2484	6310	7180	5305	5699	5942	5500	–
		NO	1498	2572	2183	3986	4487	2379	3438	2892	3253	2115	2310	2743	1528	1445	2322	1525	945	1500	1324	2582	1906	1785	3569	1945	–
CK-03	**Harrison R**	–	–	–	–	–	–	–	–	–	–	–	–	–	1	–	–	0	–	–	–	–	–	–	–	–	–
CK-31	**Nitinat R**	–	–	–	–	–	–	–	57	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Robertson Cr	–	74	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	17	–	–	–	–	–
	San Juan R	–	15	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-9008	**Chilliwack R**	–	–	–	–	–	–	–	–	–	–	4	8	–	–	–	–	–	–	–	–	–	–	–	–	–	–
No CU	**US Hatcheries**	–	–	–	2	–	–	–	27	–	–	–	–	–	–	–	1	–	–	4	1	1	3	18	10	–	–
pNOS		–	0.30	0.30	0.26	0.27	0.34	0.33	0.34	0.33	0.34	0.30	0.35	0.44	0.40	0.30	0.44	0.34	0.35	0.38	0.17	0.26	0.26	0.24	0.37	0.26	**0.32**
$pHOS_{local}$		–	0.67	0.69	0.74	0.73	0.65	0.67	0.65	0.66	0.66	0.66	0.64	0.56	0.59	0.69	0.55	0.66	0.65	0.62	0.83	0.73	0.73	0.76	0.62	0.74	**0.67**
$pHOS_{stray}$		–	0.02	0.01	0.00	0.00	0.01	0.00	0.01	0.01	0.00	0.04	0.00	0.00	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	**0.01**
$pHOS_{stray,OCU}$		–	0.02	0.01	0.00	0.00	0.01	0.00	0.01	0.01	0.00	0.04	0.00	0.00	0.01	0.01	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	**0.01**

*Table E48. Total expanded recoveries of southern BC Chinook returning to **Salmon R/JNST** for return years 2006–2021, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: SALMON R/JNST													
Donor CU	**Donor River**	**Origin**	**2006**	**2007**	**2008**	**2009**	**2010**	**2012**	**2014**	**2017**	**2020**	**2021**	**AVG**
CK-029	**Campbell/Quinsam R**	–	–	31	57	119	33	–	10	–	–	–	–
	Salmon R/JNST	**HO**	–	15	38	119	232	259	108	338	176	130	–
		NO	2900	713	725	1782	595	492	372	794	2048	1273	–
CK-031	**Nitinat R**	–	–	–	–	59	–	–	–	–	–	–	–
	Robertson Cr	–	–	–	19	–	–	–	–	–	–	–	–
pNOS	–	–	1.00	0.94	0.86	0.86	0.69	0.66	0.76	0.70	0.92	0.91	**0.83**
$pHOS_{local}$	–	–	0.00	0.02	0.05	0.06	0.27	0.34	0.22	0.30	0.08	0.09	**0.14**
$pHOS_{stray}$	–	–	0.00	0.04	0.09	0.09	0.04	0.00	0.02	0.00	0.00	0.00	**0.03**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.02	0.03	0.00	0.00	0.00	0.00	0.00	0.00	**0.01**

*Table E49. Total expanded recoveries of southern BC Chinook returning to **Nimpkish R** for return years 2014–2020, based on **thermal mark** sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: NIMPKISH R									
Donor CU	**Donor River**	**Origin**	**2014**	**2015**	**2016**	**2017**	**2018**	**2020**	**AVG**
CK-029	**Nimpkish R**	**HO**	325	161	122	100	341	839	–
		NO	2075	1290	1874	917	531	2123	–
pNOS	–	–	0.86	0.89	0.94	0.90	0.61	0.72	**0.82**
$pHOS_{local}$	–	–	0.14	0.11	0.06	0.10	0.39	0.28	**0.18**
$pHOS_{stray}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

*Table E50. Total expanded recoveries of southern BC Chinook returning to **Lang Cr** for return years 1998–2001, based on **CWT sampling**. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: LANG CR						
Donor CU	**Donor River**	**Origin**	**1998**	**2000**	**2001**	**AVG**
CK-9007	**Lang Cr**	**HO**	**122**	**99**	**188**	–
		NO	**437**	**795**	**986**	–
pNOS	–	–	0.78	0.89	0.84	**0.84**
$pHOS_{local}$	–	–	0.22	0.11	0.16	**0.16**
$pHOS_{stray}$	–	–	0.00	0.00	0.00	**0.00**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	**0.00**

*Table E51. Total expanded recoveries of southern BC Chinook returning to **Harrison R** for return years 1998–2021, based on **CWT sampling**. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: HARRISON R

Donor CU	Donor River	Origin	'98	'99	'00	'01	'02	'03	'04	'05	'06	'07	'08	'09	'10	'11	'12	'13	'14	'15	'16	'17	'18	'19	'20	'21	AVG
CK-22	Cowichan R	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	113	–	–	18	–	19	–	–	–	–
CK-03	Harrison R	**HO**	17486	6674	2813	8518	3801	7509	7474	9388	5010	2718	358	1905	1573	2249	2002	2931	1581	1635	2194	1141	2783	1909	1963	2289	–
		NO	217267	102028	114687	121654	123147	251422	143712	84353	55627	118940	44056	154658	112669	142552	54098	80384	48173	104466	56945	33723	61601	45986	44863	44670	–
CK-31	Robertson Cr	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	194	–	–	–	–	–
CK-9006	Stave R	–	–	–	484	244	126	447	236	199	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-9007	Capilano R	–	69	86	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	89	63	71	42	116	119	–
CK-9008	Chilliwack R	–	469	2276	1152	36	–	904	77	–	196	–	105	248	198	–	–	114	138	282	109	360	1104	415	168	138	–
pNOS		–	0.92	0.92	0.96	0.93	0.97	0.97	0.95	0.90	0.91	0.98	0.99	0.99	0.98	0.98	0.96	0.96	0.97	0.98	0.96	0.95	0.94	0.95	0.95	0.95	**0.96**
$pHOS_{local}$		–	0.07	0.06	0.02	0.07	0.03	0.03	0.05	0.10	0.08	0.02	0.01	0.01	0.01	0.02	0.04	0.04	0.03	0.02	0.04	0.03	0.04	0.04	0.04	0.05	**0.04**
$pHOS_{stray}$		–	0.00	0.02	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.02	0.01	0.01	0.01	**0.01**
$pHOS_{stray,OCU}$		–	0.00	0.02	0.01	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	0.02	0.01	0.01	0.01	**0.01**

Table E52. Total expanded recoveries of southern BC Chinook returning to ***Chehalis R*** *for return years 2014–2020, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: CHEHALIS R						
Donor CU	**Donor River**	**Origin**	**2014**	**2017**	**2020**	**AVG**
CK-003	**Chehalis R**	**HO**	**151**	**166**	**223**	–
		NO	**133**	**52**	**124**	–
pNOS	–	–	0.47	0.24	0.36	**0.35**
$pHOS_{local}$	–	–	0.53	0.76	0.64	**0.65**
$pHOS_{stray}$	–	–	0.00	0.00	0.00	**0.00**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	**0.00**

Table E53. Total expanded recoveries of southern BC Chinook returning to ***Stave R*** *for return years 1998–2003, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: STAVE R									
Donor CU	**Donor River**	**Origin**	**1998**	**1999**	**2000**	**2001**	**2002**	**2003**	**AVG**
CK-22	**Cowichan R**	–	–	76	–	–	–	–	–
CK-03	**Harrison R**	–	55	66	–	31	16	–	–
CK-9007	**Capilano R**	–	–	24	–	–	–	–	–
CK-9008	**Chilliwack R**	–	–	109	–	–	–	–	–
CK-9006	**Stave R**	**HO**	593	299	208	828	105	682	–
		NO	453	301	231	148	51	488	–
pNOS		–	0.41	0.34	0.53	0.15	0.30	0.42	**0.29**
pHOS$_{local}$		–	0.54	0.34	0.47	0.82	0.61	0.58	**0.67**
pHOS$_{stray}$		–	0.05	0.31	0.00	0.03	0.10	0.00	**0.04**
pHOS$_{stray,OCU}$		–	0.05	0.31	0.00	0.03	0.10	0.00	**0.04**

Table E54. Total expanded recoveries of southern BC Chinook returning to ***Chilliwack R (Fall Run)*** *for return years 1998–2011, based on* ***thermal mark*** *sampling. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: CHILLIWACK R - FALL

Donor CU	Donor River	Origin	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	AVG
CK-9008	**Chilliwack R**	**HO**	62437	73835	68369	65969	58340	51412	52126	30060	38152	18106	31299	10926	69824	44131	–
		NO	16343	1110	2614	2278	256	2564	1910	1039	3043	5373	4433	3190	5123	3855	–
CK-031	**Robertson Cr**	–	–	–	–	–	–	–	449	–	117	–	–	–	–	–	–
pNOS		–	0.21	0.01	0.04	0.03	0.00	0.05	0.04	0.03	0.07	0.23	0.12	0.23	0.07	0.08	**0.09**
$pHOS_{local}$		–	0.79	0.99	0.96	0.97	1.00	0.95	0.96	0.97	0.92	0.77	0.88	0.77	0.93	0.92	**0.91**
$pHOS_{stray}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray,OCU}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

*Table E55. Total expanded recoveries of southern BC Chinook returning to **Chilliwack R (Fall Run)** for return years 1998–2021, based on **CWT sampling**. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners (pHOS$_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers (pHOS$_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU (pHOS$_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: CHILLIWACK R - FALL

Donor CU	Donor River	Origin	‘98	‘99	‘00	‘01	‘02	‘03	‘04	‘05	‘06	‘07	‘08	‘09	‘10	‘11	‘12	‘13	‘14	‘15	‘16	‘17	‘18	‘19	‘20	‘21	AVG
CK-3	**Harrison R**	–	–	–	–	–	–	52	–	66	–	–	–	1	–	–	1	49	–	–	25	4	24	19	–	–	–
CK-7	**Maria Sl**	–	–	–	–	25	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-9006	**Stave R**	–	309	1146	555	19	–	–	59	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-9007	**Capilano R**	–	–	8	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	3	23	45	6	4	–	–
CK-9008	**Chilliwack R**	**HO**	38738	43556	60137	18401	23908	18611	24698	52174	21104	28717	24536	19673	64174	47803	15566	30017	29706	19769	27759	12363	23740	45164	30067	40234	–
		NO	52572	33342	29902	36911	43415	39431	43902	31714	25481	45800	58339	28854	107495	5926	4667	32325	37671	17255	18272	10286	15849	34559	14129	29383	–
CK-17	**Spius Cr**	–	–	–	22	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
CK-22	**Cowichan R**	–	–	–	–	–	10	–	–	–	–	–	–	34	–	–	–	15	–	–	1	–	–	–	–	–	–
CK-31	**Robertson Cr**	–	–	–	–	–	–	–	462	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
No CU	**US Hatcheries**	–	–	–	–	–	–	–	–	–	1	–	–	–	–	–	–	–	–	–	–	–	–	–	–	19	–
pNOS		–	0.57	0.43	0.33	0.67	0.64	0.68	0.64	0.38	0.55	0.61	0.70	0.59	0.63	0.11	0.23	0.52	0.56	0.47	0.40	0.45	0.40	0.43	0.32	0.42	**0.49**
pHOS$_{local}$		–	0.42	0.56	0.66	0.33	0.36	0.32	0.36	0.62	0.45	0.39	0.30	0.41	0.37	0.89	0.77	0.48	0.44	0.53	0.60	0.55	0.60	0.57	0.68	0.58	**0.51**
pHOS$_{stray}$		–	0.00	0.01	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
pHOS$_{stray,OCU}$		–	0.00	0.01	0.01	0.00	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

Table E56. Total expanded recoveries of southern BC Chinook returning to ***Nicola R*** *for return years 1998–2021, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: NICOLA R																											
Donor CU	**Donor River**	**Origin**	**‘98**	**‘99**	**‘00**	**‘01**	**‘02**	**‘03**	**‘04**	**‘05**	**‘06**	**‘07**	**‘08**	**‘09**	**‘10**	**‘11**	**‘12**	**‘13**	**‘14**	**‘15**	**‘16**	**‘17**	**‘18**	**‘19**	**‘20**	**‘21**	**AVG**
CK-17	**Coldwater R**	–	5	46	–	7	75	181	19	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Nicola R	**HO**	406	4397	2570	2926	3136	3029	638	489	626	123	806	144	2216	590	504	1392	384	1323	760	945	1164	2173	1467	3039	–
		NO	1313	3752	5569	5985	9812	11420	9600	2879	4585	1003	3728	550	3194	2290	5338	2220	6805	3570	1361	908	607	2353	2707	1166	–
	Deadman R	–	–	–	–	4	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	Spius Cr	–	–	86	170	173	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
pNOS		–	0.76	0.45	0.67	0.66	0.75	0.78	0.94	0.85	0.88	0.89	0.82	0.79	0.59	0.80	0.91	0.61	0.95	0.73	0.64	0.49	0.34	0.52	0.65	0.28	**0.70**
$pHOS_{local}$		–	0.24	0.55	0.34	0.34	0.25	0.22	0.06	0.15	0.12	0.11	0.18	0.21	0.41	0.20	0.09	0.39	0.05	0.27	0.36	0.51	0.66	0.48	0.35	0.72	**0.30**
$pHOS_{stray}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray,OCU}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

Table E57. Total expanded recoveries of southern BC Chinook returning to ***Spius Cr*** *for return years 1998–2004, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners (pHOS*$_{local}$*), proportion of strayed hatchery-origin spawners from all donor rivers (pHOS*$_{stray}$*), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU (pHOS*$_{stray,OCU}$*), are provided, along with averages for the time series.*

RECIPIENT RIVER: SPIUS CR										
Donor CU	**Donor River**	**Origin**	**1998**	**1999**	**2000**	**2001**	**2002**	**2003**	**2004**	**AVG**
CK-17	**Spius Cr**	**HO**	5	146	487	287	6	–	–	–
		NO	260	20	155	164	846	1113	1920	–
	Coldwater R	–	9	–	–	12	18	102	30	–
	Nicola R	–	27	–	125	246	–	27	–	–
CK-15	**Shuswap R Low**	–	–	–	61	–	–	–	–	–
pNOS	–	–	0.87	0.12	0.19	0.23	0.97	0.90	0.98	**0.77**
pHOS$_{local}$	–	–	0.02	0.88	0.74	0.41	0.01	0.00	0.00	**0.29**
pHOS$_{stray}$	–	–	0.00	0.00	0.07	0.00	0.00	0.00	0.00	**0.01**
pHOS$_{stray,OCU}$	–	–	0.00	0.00	0.07	0.00	0.00	0.00	0.00	**0.01**

Table E58. Total expanded recoveries of southern BC Chinook returning to ***Coldwater R*** *for return years 1998–2004, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: COLDWATER R									
Donor CU	**Donor River**	**Origin**	**1998**	**1999**	**2000**	**2002**	**2003**	**2004**	**AVG**
CK-17	**Coldwater R**	**HO**	72	267	–	945	557	91	–
		NO	224	69	487	451	733	997	–
	Nicola R	–	4	–	–	–	–	–	–
	Spius Cr	–	–	–	10	–	–	–	–
pNOS	–	–	0.75	0.21	0.98	0.32	0.57	0.92	**0.60**
$pHOS_{local}$	–	–	0.24	0.79	0.00	0.68	0.43	0.08	**0.40**
$pHOS_{stray}$	–	–	0.01	0.00	0.02	0.00	0.00	0.00	**0.00**
$pHOS_{stray,OCU}$	–	–	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

*Table E59. Total expanded recoveries of southern BC Chinook returning to **Shuswap R (Low)** for return years 1998–2021, based on **CWT sampling**. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners (pHOS$_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers (pHOS$_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU (pHOS$_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: SHUSWAP R LOW

Donor CU	Donor River	Origin	‘98	‘99	‘00	‘01	‘02	‘03	‘04	‘05	‘06	‘07	‘08	‘09	‘10	‘11	‘12	‘13	‘14	‘15	‘16	‘17	‘18	‘19	‘20	‘21	AVG
CK-14	**Salmon R/ TOMF**	–	7	1	7	10	17	–	–	7	–	–	–	–	4	–	–	–	–	–	–	–	–	–	–	–	–
CK-15	**Shuswap R Low**	**HO**	2123	5317	4783	6996	5397	7320	2495	1799	3796	1192	3042	2308	2484	1716	1372	5568	2579	3466	1404	1784	3555	5655	5047	4055	–
		NO	27800	41066	33979	32677	53184	32121	26899	17752	58118	19076	34538	25205	70283	18517	9384	28442	45958	39584	11201	14258	21978	37842	28628	53446	–
	Shuswap R Mid	–	79	–	16	9	–	–	8	–	–	–	–	–	–	–	4	25	7	118	2	9	14	57	33	12	–
CK-22	**Cowichan R**	–	–	86	170	173	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	2	–	–	–	–	–
pNOS		–	0.93	0.88	0.87	0.82	0.91	0.81	0.91	0.91	0.94	0.94	0.92	0.92	0.97	0.92	0.87	0.84	0.95	0.92	0.89	0.89	0.86	0.87	0.85	0.93	**0.90**
***pHOS**$_{local}$*		–	0.07	0.11	0.12	0.18	0.09	0.19	0.08	0.09	0.06	0.06	0.08	0.08	0.03	0.08	0.13	0.16	0.05	0.08	0.11	0.11	0.14	0.13	0.15	0.07	**0.10**
***pHOS**$_{stray}$*		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
***pHOS**$_{stray,OCU}$*		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

Table E60. Total expanded recoveries of southern BC Chinook returning to ***Shuswap R (Middle)*** *for return years 1998–2021, based on* ***CWT sampling****. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners (pHOS$_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers (pHOS$_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU (pHOS$_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: SHUSWAP R MIDDLE

Donor CU	Donor River	Origin	'98	'99	'00	'01	'02	'03	'04	'05	'06	'09	'10	'11	'12	'13	'14	'15	'16	'17	'18	'19	'20	'21	AVG
CK-15	**Shuswap R Low**	–	116	–	–	58	–	–	–	–	83	10	65	2	–	83	46	74	–	16	11	63	79	170	–
	Shuswap R Mid	**HO**	3474	2513	2837	3555	6534	3677	1615	1746	–	–	–	53	159	1162	751	1515	232	320	985	951	1297	546	–
		NO	2509	889	791	351	1299	2847	434	900	5037	1707	4972	1019	229	1148	1483	1571	416	560	1355	1105	1165	1312	–
pNOS		–	0.41	0.26	0.22	0.09	0.17	0.44	0.21	0.34	0.98	0.99	0.99	0.95	0.59	0.48	0.65	0.50	0.64	0.63	0.58	0.52	0.46	0.65	**0.53**
pHOS$_{local}$		–	0.59	0.74	0.78	0.91	0.83	0.56	0.79	0.66	0.02	0.01	0.01	0.05	0.41	0.52	0.35	0.50	0.36	0.37	0.42	0.48	0.54	0.35	**0.47**
pHOS$_{stray}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
pHOS$_{stray,OCU}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

*Table E61. Total expanded recoveries of southern BC Chinook returning to **Maria Sl** for return years 2000–2003, based on **CWT sampling**. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: MARIA SLOUGH							
Donor CU	**Donor River**	**Origin**	**2000**	**2001**	**2002**	**2003**	**AVG**
CK-07	**Maria Sl**	**HO**	2	148	632	44	–
		NO	15	96	707	761	–
pNOS	–	–	0.89	0.40	0.53	0.95	**0.69**
pHOS$_{local}$	–	–	0.11	0.60	0.47	0.05	**0.31**
pHOS$_{stray}$	–	–	0.00	0.00	0.00	0.00	**0.00**
pHOS$_{stray,OCU}$	–	–	0.00	0.00	0.00	0.00	**0.00**

*Table E62. Total expanded recoveries of southern BC Chinook returning to **Salmon R/TOMF** for return years 1998–2012, based on **CWT sampling**. Estimates are separated by hatchery- (HO) and natural-origin (NO) spawners for the recipient river. Annual estimates of the proportion of natural-origin spawners (pNOS), proportion of local (homed) hatchery-origin spawners ($pHOS_{local}$), proportion of strayed hatchery-origin spawners from all donor rivers ($pHOS_{stray}$), and the proportion of strayed hatchery origin spawners from donor rivers outside the CU ($pHOS_{stray,OCU}$), are provided, along with averages for the time series.*

RECIPIENT RIVER: SALMON R/TOMF																
Donor CU	**Donor River**	**Origin**	**1998**	**1999**	**2000**	**2001**	**2002**	**2003**	**2004**	**2005**	**2006**	**2009**	**2010**	**2011**	**2012**	**AVG**
CK-14	**Salmon R/ TOMF**	**HO**	18	136	91	562	427	48	154	82	165	26	187	17	106	–
		NO	266	175	335	803	544	103	284	344	425	45	467	157	246	–
pNOS		–	0.94	0.56	0.79	0.59	0.56	0.68	0.65	0.81	0.72	0.63	0.71	0.90	0.70	**0.71**
$pHOS_{local}$		–	0.06	0.44	0.21	0.41	0.44	0.32	0.35	0.19	0.28	0.37	0.29	0.10	0.30	**0.29**
$pHOS_{stray}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**
$pHOS_{stray,OCU}$		–	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**

APPENDIX F. INVESTIGATION INTO CWT–THERMAL MARK BIAS

Note: the following Appendix was originally provided to Angus Mackay of the Northern Fund Committee to report on observed discrepancies between otolith and CWT based estimates of Robertson Creek Hatchery (RCH) contributions to fisheries and escapement.

September 24, 2018

To: Angus Mackay, Northern Fund Committee

This note is in response to the February 22, 2018 letter requesting additional info regarding discrepancies between CWT based and otolith based estimates of hatchery contributions in 2015 and 2016 (the request is excerpted below).

> *… as a component of the 2017 report the proponent is requested to provide a specific explanation for the discrepancies observed (see 2016 annual report – page 20 (bottom)). For example, are these differences due to sample design, inadequate tagging rates, bias from CWT awareness factors, or some combination of these or other factors? The underlying interest is to ensure that the Robertson Creek run reconstructions are based on the best possible information and are producing reliable estimates. This is particularly important given the dependency of the PSC's CTC model on CWT data for this important "driver" stock of Chinook salmon.*

The tables (2015 tables 39 and 40, 2016 tables 44 and 45) and related to this request are attached and summarized in the following Table 1. These tables indicate that, in these 2 years, CWT significantly underestimated (by about 50%) the catch and escapement of RCH chinook (45% underestimate in 2016 and 57% underestimate in 2015). Catch along the WCVI was underestimated by 66% and 61% respectively for 2016 and 2015. Escapement of RCH chinook was underestimated by 34% and 55% in 2016 and 2015 respectively.

Table F1. Summary of Robertson Creek Hatchery contributions to fisheries and escapement along the WCVI in 2015 and 2016.

Mark comparison	**All fisheries/locations**		**Catch Only**		**Escapement Only**	
	2015	**2016**	**2015**	**2016**	**2015**	**2016**
Total abundance based on otoliths and CWT	79 314	77685	21 449	27 473	57 865	50 392
Total abundance based on expanded CWT only	34 155	42598	8 401	9 458	25 754	33 140
Difference: CWT-based - otolith-based	-45 159	-35 267	-13 048	-18 015	-32 111	-17 252
Percent difference relative to otolith based	-57%	-45%	-61%	-66%	-55%	-34%

It is not clear at this time what the cause or origin of these differences between otolith based and CWT based estimates is. Some potential possibilities include:

Adult salmon stage

- Sample design
- Sampling biases during implementation
- Bias from CWT awareness factors
- Differential homing (straying) of CWT'ed and unmarked chinook

Juvenile salmon stage

- Inadequate tagging rates
- Errors in the estimation of releases of both CWT'ed and unmarked chinook
- Differential mortality or loss of CWT'ed vs unmarked chinook

At this time we don't have an answer but recognize it is a significant issue which we are investigating (e.g. stray rates for WCVI chinook are being assessed). But we are able to provide the following insights. First, the letter indicates an underlying intent of producing reliable numbers, to which we agree. Reliability can be described based on the level and consistency of sampling effort and consistency of results. To this end, 2 separate sample groups have operated in the same manner over many years, with relatively high sample rates, with the objective of estimating contribution to escapement of RCH into the Stamp River: 1) swim-ins into the hatchery, and 2) river spawners. About 100% of hatchery swim-ins are observed for adipose clips (and so CWT) and 400 randomly sampled for otoliths. In the river dead pitch the average sample rate has been 16% since 2000 ranging between 5-33%. The results are for the complete brood year returns from 1998 to 2012.

These two sampling groups have the same result, CWT underestimate RCH contribution by about 30%. For swim-ins the CWT underestimated the RCH contribution to the total abundance by on average 31.0% (n=15 years, 1 st dev= 12.5%, range 16%-63% difference). For the river deadpitch the CWT underestimated the RCH contribution to the total abundance by on average 32.0% (n=15 years, 1 st dev= 14.4%, range 5%-56% underestimate). The following graphs show the estimated return abundance of RCH chinook from the two methods and the level of bias. Figure 1 includes the swim-in sample and Figure 2 the Stamp River deadpitch.

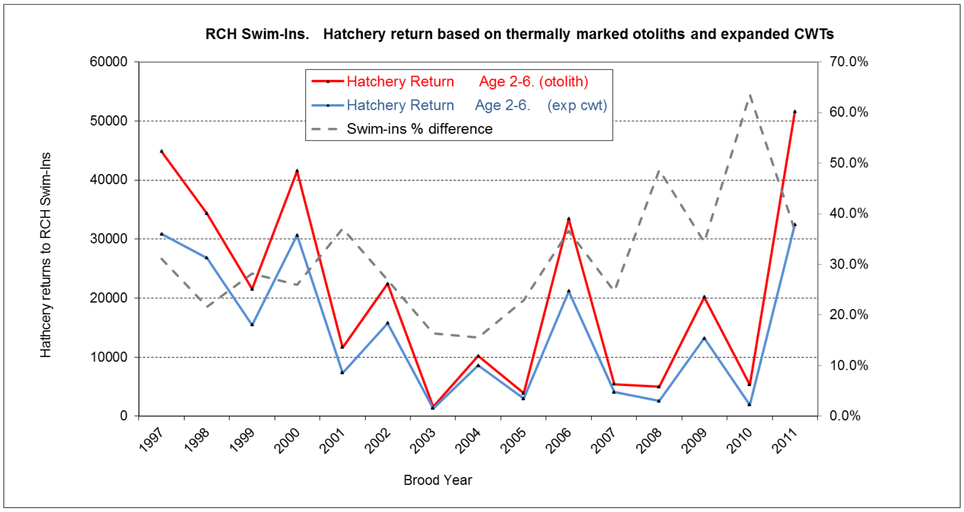

Figure F1.A. Abundance of RCH chinook in the swim-in population 1998–2012. Over these years CWT estimate of hatchery contribution was on average 31% lower than otolith based estimates.

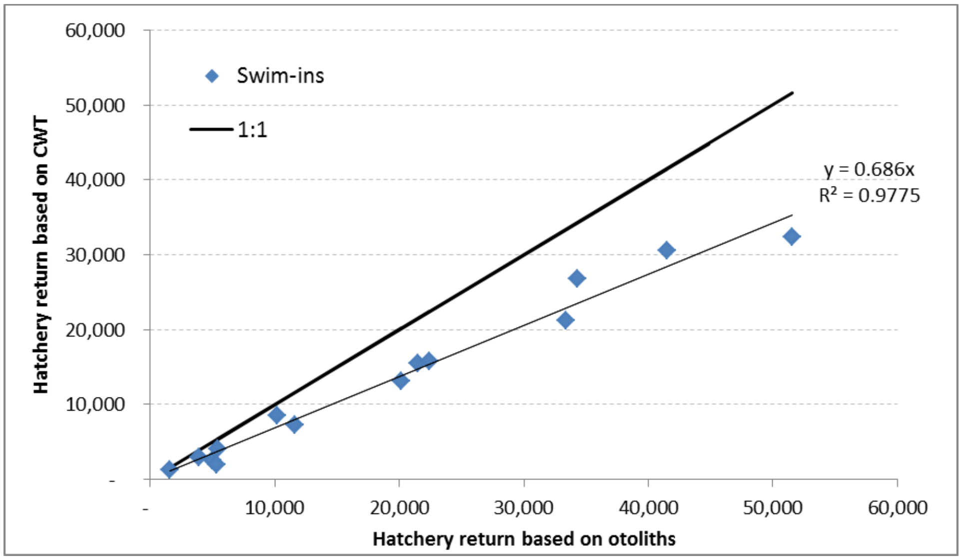

Figure F1.B. Relationship between otolith and CWT based estimates of abundance of RCH chinook in the swim-in population 1998–2012.

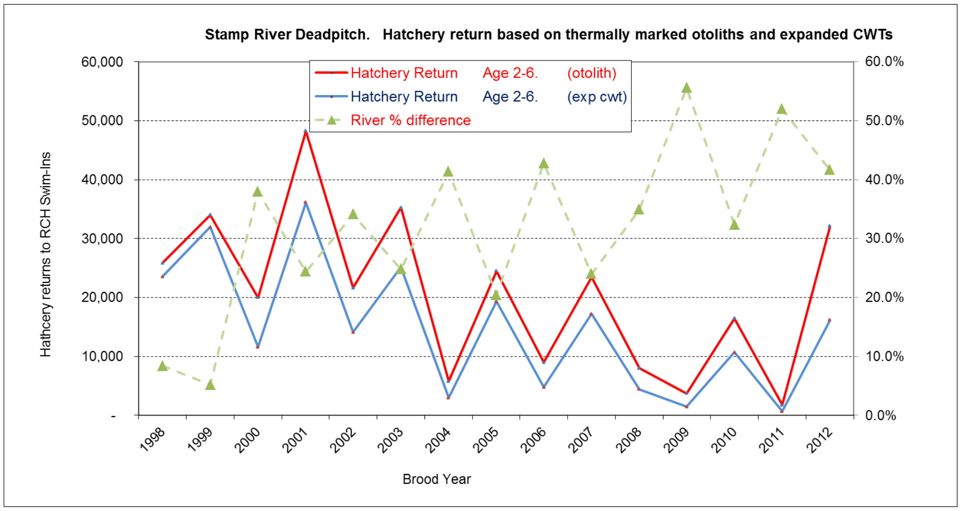

Figure F2.A. Abundance of RCH chinook in the Stamp River 1998–2012 based on CWT and otolith. Over these years CWT estimate of hatchery contribution was on average 32% lower than otolith based estimates.

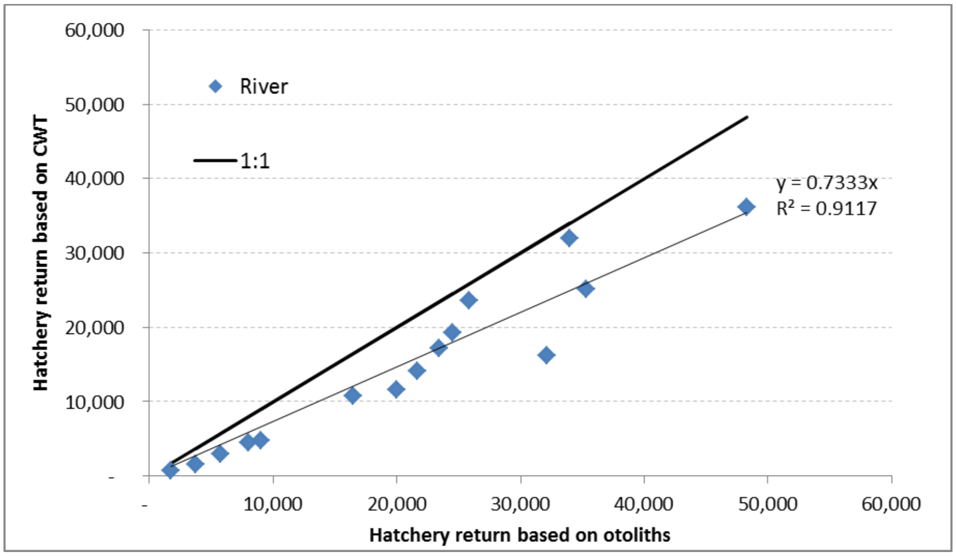

Figure F2.B. Relationship between otolith and CWT based estimates of abundance of RCH chinook in the Stamp River dead pitch sample 1998–2012.

Due to lack of otolith sampling in ocean salmon fisheries outside this project we are not able to assess the extent of this bias in the fisheries. We expect there to be increased uncertainty in the fishery results due to factors such as lower sample rates and increased uncertainty in CWT expansion factors in the fishery. We do not expect higher bias in the fishery relative to the escapement samples. The limited data from 2015 and 2016 (Table 1) do show higher differences in the catch (66% in 2016 and 61% in 2015) compared to escapement samples (34% in 2016 and 55% in 2015). The 2017 data checking is almost complete and 2018 just getting organized before going into the labs, so it is too early to tell if the bias in fishery samples is higher than in escapement. This is one of the reasons to continue this project for another year.

We do note that there appears to be a negative bias in CWT based estimates for other Chinook indicator stocks, but the extent of the bias appears inconsistent between hatcheries. These results will be prepared for the straying report expected in early 2019.

The relative consistency in the bias suggests that the causal factors are likely working at the juvenile life stage. We are testing this hypothesis with Cowichan Chinook. The Cowichan River hatchery began marking otoliths about 5 years ago and also CWT and Adipose Fin Clipping almost 100% of their production.

Additional Reference Tables:

Table F2. (2015 report Table 6) Return of Somass/Robertson Creek Hatchery chinook to the WCVI terminal area in 2015. Note: hatchery origin fish are determined by otolith, DNA and CWT marks.

Terminal Area	**Fishery/Location**	**Age**					**Total**
		2	**3**	**4**	**5**	**6**	
Barkley-Alberni Area 23	FSC/Treaty	51	1090	111	19	-	1271
	First Nation Comm	42	5372	708	83	-	6205
	Recreational	31	7172	1133	169	-	8505
	Commercial GN	5	383	19	-	-	407
	Commercial SN	-	-	-	-	-	-
	Escapement	1782	50295	4288	887	7	57259
	Total	**1911**	**64312**	**6259**	**1158**	**7**	**73647**
Other WCVI Areas	Catch	1	2121	2491	447	2	5062
	Escapement	2	483	88	35	-	608
	Total Terminal Return	**1914**	**66916**	**8838**	**1640**	**9**	**79317**

Table F3. (2015 report Table 7) Terminal return of CWT-associated Robertson Creek Hatchery fish to Area 23 (Barkley Sound and Alberni Inlet) in 2015.

Terminal Area	**Fishery/Location**	**Age**					**Total**
		2	**3**	**4**	**5**	**6**	
Barkley-Alberni Area 23	FSC/Treaty	-	-	-	-	-	-
	First Nation Comm	103	4368	-	-	-	4471
	Recreational	-	3249	44	41	-	3334
	Commercial GN	-	-	-	-	-	0
	Commercial SN	-	-	-	-	-	0
	Escapement	1501	22753	1018	482	-	25754
	Total	**1604**	**30370**	**1062**	**523**	**0**	**33559**
Other WCVI Areas	Catch	-	553	44	-	-	597
	Escapement	-	-	-	-	-	-
	Total Terminal Return	**1604**	**30923**	**1106**	**523**	**0**	**34156**

Table F4. (2016 report Table 8) Return of Somass/Robertson Creek Hatchery chinook to the WCVI terminal area in 2016. Note: hatchery origin fish are determined by otolith, DNA and CWT marks.

Terminal Area	**Fishery/Location**	**Age**					**Total**
		2	**3**	**4**	**5**	**6**	
Barkley-Alberni Area 23	FSC/Treaty	-	189	2222	-	-	2411
	First Nation Comm	231	3403	8250	-	-	11884
	Recreational	626	2445	5645	201	-	8917
	Commercial GN	55	489	764	-	-	1308
	Commercial SN	-	-	-	-	-	0
	Escapement	6528	17751	24665	157	-	49101
	Total	**7440**	**24277**	**41546**	**358**	**0**	**73621**
Other WCVI Areas	Catch	106	735	1932	179	-	2952
	Escapement	-	298	959	34	-	1291
	Total Terminal Return	**7546**	**25310**	**44437**	**571**	**0**	**77864**

Table F5. (2016 report Table 9) Terminal return of CWT-associated Robertson Creek Hatchery fish to Area 23 (Barkley Sound and Alberni Inlet) in 2016.

Terminal Area	**Fishery/Location**	**Age**					**Total**
		2	**3**	**4**	**5**	**6**	
Barkley-Alberni Area 23	FSC/Treaty	-	-	-	-	-	-
	First Nation Comm	107	668	3660	136	-	
	Recreational	13	985	2571	-	-	
	Commercial GN	-	-	-	-	-	-
	Commercial SN	-	-	-	-	-	-
	Escapement	4355	13098	15687	-	-	
	Total	**4475**	**14751**	**21918**	**136**	**-**	**0**
Other WCVI Areas	Catch	108	137	1307	103	-	1655
	Escapement	-	-	-	-	-	-
	Total Terminal Return	**4583**	**14888**	**23225**	**239**	**-**	**1655**