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# THE MAGNITUDE AND EXTENT OF CHINOOK SALMON STRAYING FROM HATCHERIES IN SOUTHERN BRITISH COLUMBIA

*Chinook Salmon adult spawning phase. Image credit: Fisheries and Oceans Canada (DFO).*

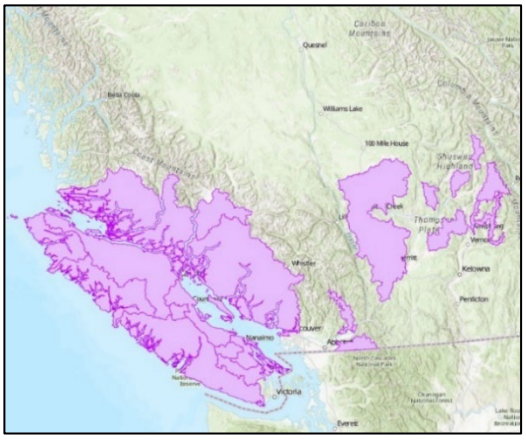

*Figure 1. Southern British Columbia Chinook Conservation Units examined in this analysis. Map courtesy of Chelsea Greenberg (DFO).*

## Context:

*Safeguarding the genetic diversity of Chinook, a key objective of Canada's Wild Salmon Policy, is required under the Fish Stocks Provisions of Canada's* Fisheries Act. *Although most 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. Understanding the risks associated with hatchery straying has been identified as in important factor in preserving genetic diversity in natural Chinook 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, Assessment, or Stewardship. Hatcheries attempt to balance benefits of production against ecological and genetic risks. In this report, we focus on one component of this risk associated with the straying of hatchery-origin Chinook Salmon into non-natal spawning populations.*

*To date, the magnitude of straying from hatchery production in SBC has not been assessed. The purpose of this report is to review and assess available data for an evaluation of the rate, 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 SBC.*

*This Science Advisory Report is from the September 12–13 and December 14, 2023 regional peer review on Assessment of Hatchery Chinook Salmon Straying in Southern British Columbia. Additional*

*publications from this meeting, including the full research document[1], will be posted on the Fisheries and Oceans Canada (DFO) Science Advisory Schedule as they become available.*

## SUMMARY


- Hatchery-origin salmon provide significant socio-economic benefit as well as conservation value in some cases, but high levels of hatchery production can create fishery, ecological, and genetic risks for natural populations.
- The risks of hatchery-origin Chinook straying into non-natal rivers was the focus of this assessment. Straying was described from two distinct perspectives: from the populations in which strays originate, i.e., donor populations, and from the populations that receive them, i.e., recipient populations.
- This report describes first generation, hatchery-origin straying of 19 ocean-type populations and one stream-type Chinook Salmon population into non-natal rivers in Southern British Columbia using Coded Wire Tag (CWT) and otolith thermal mark data.
- Based on in-river samples, average hatchery donor stray rates were estimated at approximately 4% based on otolith thermal marks and 2% based on CWT samples.
- The donor stray rate to non-natal Conservation Units (CUs) was lower—less than 2% across populations and years—and was negligible between Stock Management Units (SMU).
- Lower stray rates from large hatchery releases can still result in a large magnitude of strays observed in smaller non-natal systems.
- Conuma Hatchery on the West Coast of Vancouver Island (WCVI) had a substantially higher donor stray rate; the highest among large-scale production hatcheries, which resulted in the greatest magnitude of strays to other rivers.
- Local and regional variability in environmental factors made separating their causal effect on stray rate from hatchery practices difficult. While the influence of hatchery practices from potential environmental factors were not statistically delineated in this work, the need for hatcheries to prioritize imprinting to reduce stray rates was emphasized.
- The contribution of strayed, hatchery-origin spawners ($pHOS_{stray}$) in the escapement was identified as a metric to assess the impact of strays on natural-origin populations; observed values were compared to a 0.03 benchmark established for wild populations.
- Average $pHOS_{stray}$ was highest on the WCVI with most strays originating from Conuma Hatchery. Lower values, mostly below the 0.03 benchmark were observed on the East Coast of Vancouver Island (ECVI), and a negligible hatchery stray contribution was observed in Fraser River populations.
- Proportionate natural influence (*PNI*) is a metric used to evaluate and monitor the level of natural influence and genetic risk in integrated populations. On the WCVI, particularly in northern populations, *PNI* was low; ECVI had more populations with moderate to high *PNI* values; and the Fraser River contained many populations with consistently high *PNI*s.


[1] Weil, J., Luedke, W., Healy, T.M., Withler, R.E., Brown, N., Bokvist, J., and Porszt, E. The Magnitude and Extent of Chinook Straying from Hatcheries in Southern British Columbia. DFO Can. Sci. Advis. Sec. Res. Doc. In Prep.

- Genetic analysis indicated that genetic variation remained consistent for the three major hatchery populations within the WCVI from 1985–2015.
- On the WCVI, genetic results indicated that hatchery populations contributed significantly to natural spawners and resulted in increased genetic homogenization among non-natal rivers.
- The persistence of natal genetic signals in WCVI rivers that have experienced some level of homogenization suggests that enhanced contribution management, using *PNI*, is important to preserve wild influence and associated genetic diversity.
- Withler et al. (2018) and US Hatchery Scientific Review Group (HSRG; 2009) publications indicated a need for the adaptive and scientifically defensible management of hatcheries. The results presented in this report support this view, and suggest that the inclusion of a stray management framework would support these principles.

# INTRODUCTION

Anadromous Pacific salmon (*Oncorhynchus spp.*) have a life cycle that begins in freshwater, then includes extended periods of in-ocean rearing and migration, before returning as maturing adults to spawn in freshwater where they originated. Each species, Wild Salmon Policy (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. Chinook Salmon (*O tshawytscha*) have a lower stray rate than Pink, Chum, and some Coho Salmon, 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). While straying to non-natal rivers is known to occur in natural populations, this study focused on straying in hatchery populations and the associated genetic risks.

Most estimates of Chinook Salmon straying come from hatchery populations 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 34.9% and 3.4% for ocean-type and stream-type Chinook Salmon respectively. 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 consistently had higher stray rates than stream-type Chinook.

Hatchery programs in Southern BC (SBC), coordinated by the Salmonid Enhancement Program (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 over 40 million Chinook, the majority of which are allotted to harvest programs throughout BC. In the scope of this study, we examine straying from 20 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.

## Definition of Straying in Hatchery Chinook

Straying in Salmon is described as spawning at a 'non-natal' site (Quinn 1993). 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.

We define a Chinook Salmon stray as an individual that spawned naturally or was taken as broodstock in a non-natal river basin, or simply an **out-of-basin stray**. 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. In this study, strays do not include hatchery-origin Chinook Salmon that spawned naturally within the natal river basin. These hatchery-origin spawners pose a separate genetic risk to natural-origin salmon and are included within an enhanced contribution management framework developed by the US Hatchery Scientific Review Group (HSRG 2009) and further developed in advice for British Columbia hatcheries by Withler et al. (2018).

In the Fraser R watershed, we propose following the definitions of home and strayed individuals outlined in the Columbia R (e.g., Ford et al. 2015), that 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 Conservation Units (CUs), reflecting similar genetic, ocean distribution, and life history characteristics. We define a Chinook Salmon from one CU spawning in another as an **out-of-CU stray**. In this report, the words 'population' and 'stock' are used synonymously, reflecting the variable nomenclature used in the literature.

In the literature (e.g., Quinn 1993), 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/or 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, the contribution of strays to natural spawners within a river population, and the contribution of hatchery fish to specific SBC rivers.

# ASSESSMENT

## Data Sources and Methods Used to Assess Straying

Data used in this report were collected mostly as a result of monitoring efforts conducted under a framework for Chinook assessment in fisheries management. 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. In addition, escapement indicators were identified for each stock management unit to track trends in Chinook escapement over time against Pacific Salmon Treaty rebuilding objectives.

In addition to CWT indicator stocks, thermally marked populations were used to determine the extent of hatchery straying. Thermal marking, a process of manipulating the water temperature during the early life stages of the fish, is used to uniquely mark the otolith with a hatchery-specific mark. This method is commonly applied to non-indicator hatchery release groups.

Using expanded recoveries, stray rates and magnitudes for samples marked at 15 hatchery facilities (associated with 20 SBC stocks between 1998–2021) were estimated. These stocks 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 the 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.

The proportion of hatchery-origin spawners in each system that were of local origin, $pHOS_{local}$, and were of out-of-basin strays, $pHOS_{stray}$, were determined using the following equations:

$$pHOS_{local} = \frac{N_{H,local}}{(N_{H,local} + N_{H,stray} + N_N)} \quad (1)$$

$$pHOS_{stray} = \frac{N_{H,stray}}{(N_{H,local} + N_{H,stray} + N_N)} \quad (2)$$

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:

$$pHOS = pHOS_{local} + pHOS_{stray} = \frac{(N_{H,local} + N_{H,stray})}{(N_{H,local} + N_{H,stray} + N_N)} \quad (3)$$

In this report, the term $pHOS$ is used synonymously with $pHOS_{census}$. $pHOS$ was estimated from natural spawner samples (deadpitch or carcass recovery) when possible; otherwise samples taken from broodstock capture events were used. Where multiple sample types were available, natural spawner samples were prioritized. Although Withler et al. (2018) distinguished $pHOS_{census}$ from the proportion of effective hatchery-origin spawners in the wild ($pHOS_{eff}$; corrected for spawning effectiveness and selection pressure), the present study focused on census estimates.

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 and control the relative adaptive influence of each environment on the integrated population as a whole. The HSRG (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 ($pNOB$), with designations provided for the hatchery influence on the population at prescribed values of *PNI* (Table 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 *pHOS* ≤ 0.03** for out-of-basin hatchery strays per year to safeguard *PNI* and the long-term fitness of the wild population.

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 $pHOS_{local}$and $pHOS_{stray}$, and report $pHOS_{stray,OCU}$ to specifically consider and highlight the proportion of recovered stray hatchery spawners that originated from outside the CU of the assessed population.

*Table 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<br>≤ 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<br>>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<br>≤ 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<br>≤ 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<br>> 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 $h^2$ and $\omega^2$, not reported here.

Since 2017, hatcheries in SBC initiated genetic sampling of nearly all broodstock, which serves as the baseline for parentage-based tagging (PBT) analysis. PBT was not used to assess hatchery straying in this report, but it may be used in the future to better understand the differences between CWT and otolith estimated contributions and potentially improve straying assessments with finer temporal and spatial scales data (see Beacham et al. 2017).

## Donor Stray Rate and Magnitude in Southern BC

Mean annual donor stray rates from hatchery-origin, ocean-type Chinook Salmon returning to SBC rivers, estimated from expanded CWT or thermal mark recoveries are presented in Table 2.

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 to 17%) was estimated at the basin scale (that is, straying between river systems).

Considerable variation between populations and across years was 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 to 50%), Gold R (13%; range 0 to 37.8%), Burman R (4.3%; range 0 to 26.3%), and Conuma R (3.7%; range 0 to 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.

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 to 7.6%) at the basin scale.

Similar to thermal mark data, there was 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%).

A low stray rate from a large production hatchery facility can still result in a high number of strays, which can overwhelm a small population of natural spawners. Note that the magnitude of strays spawning in each non-natal river basin are reviewed separately in the recipient rivers section of this report.

Between 1998–2021, the average magnitude of stray recoveries in SBC, estimated from 12 donor hatcheries that used thermal marking and sampling in 49 recipient rivers, was approximately 2,000 Chinook. More than 50% of this average magnitude originated from Robertson Cr Hatchery and strayed into the Gold R (see Candy and Beacham 2000). The average magnitude of strays estimated from 17 donor stocks that used CWT marking was 810 Chinook. 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 Figure 2 as a chord diagram.

Straying from rivers outside the CU can affect the genetic distinctiveness of these groups. 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 3.

Based on CWT recoveries from 1998–2021, in 17 donor stocks and 49 sampled rivers in SBC, a mean annual donor stray rate to systems 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%.

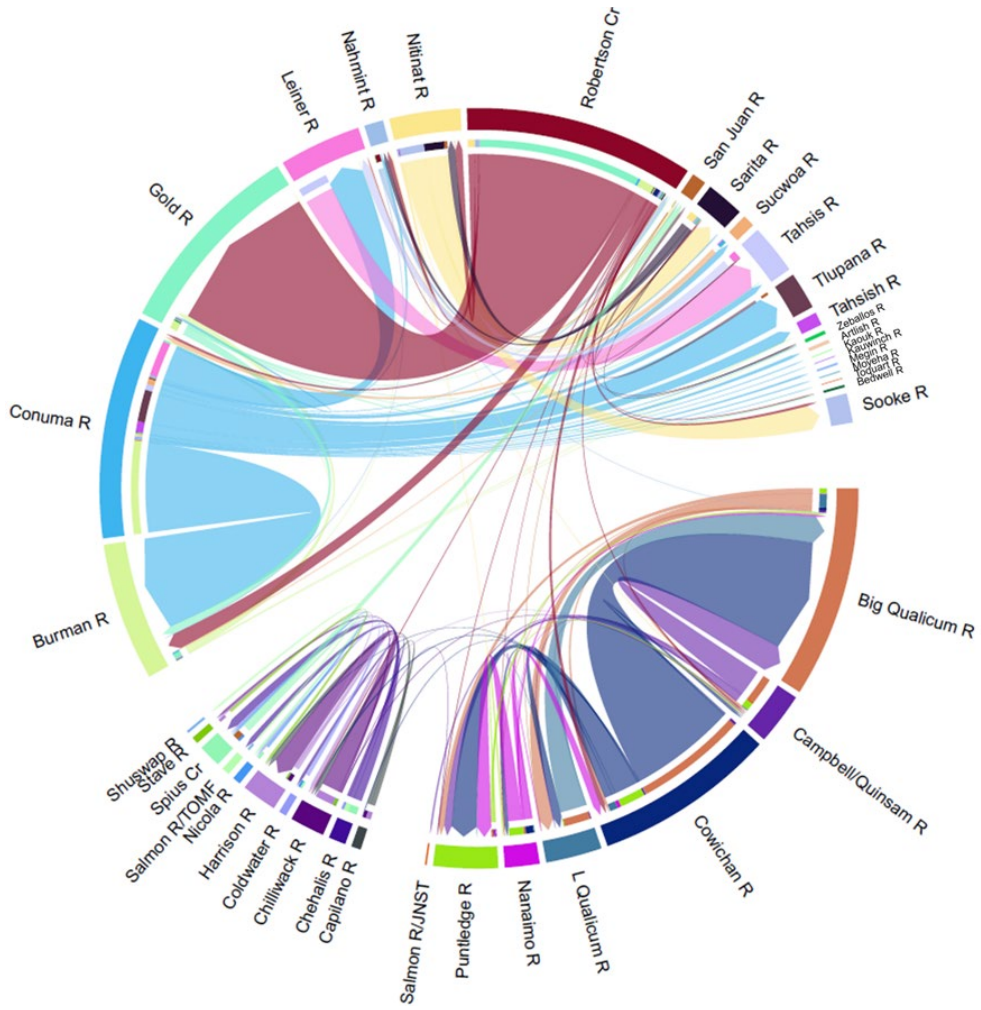


*Figure 2. Chord diagram of total expanded stray recoveries observed in SBC (using both thermal and CWT data) between 1998–2021 for recipient systems. The outer most band displays donor rivers in SBC; the interior band is colour matched to the recipient system, and arrows direction and thickness indicate 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.*

*Table 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.*

| | | **STRAY RATE (SR)** | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | **CWT** | | | | **THERMAL MARK** | | | |
| **Donor River** | **CU** | **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 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.*

| | | **STRAY RATE OUTSIDE THE CU ($SR_{OCU}$)** | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | | **CWT** | | | | **THERMAL MARK** | | | |
| **Donor River** | **CU** | **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%** | - | - | - |

## Recipient Rivers: Hatchery Stray Contribution to Spawners in Southern BC

Mean estimates of $pHOS_{stray}$, $pHOS_{stray,OCU}$, $pHOS_{local}$ and the proportion of natural-origin spawners (*pNOS*) in SBC Chinook Salmon escapements, estimated from expanded CWTs or thermal mark recoveries are presented in Figure 3 and in Tables 4a and 4b.

On the WCVI, of the six river populations which had no local hatchery enhancement, all had an average $pHOS_{stray}$ > 0.18, which far exceeded the benchmark set out by Withler et al. (2018) for wild-stray influenced populations ($pHOS_{stray}$ > 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.

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.

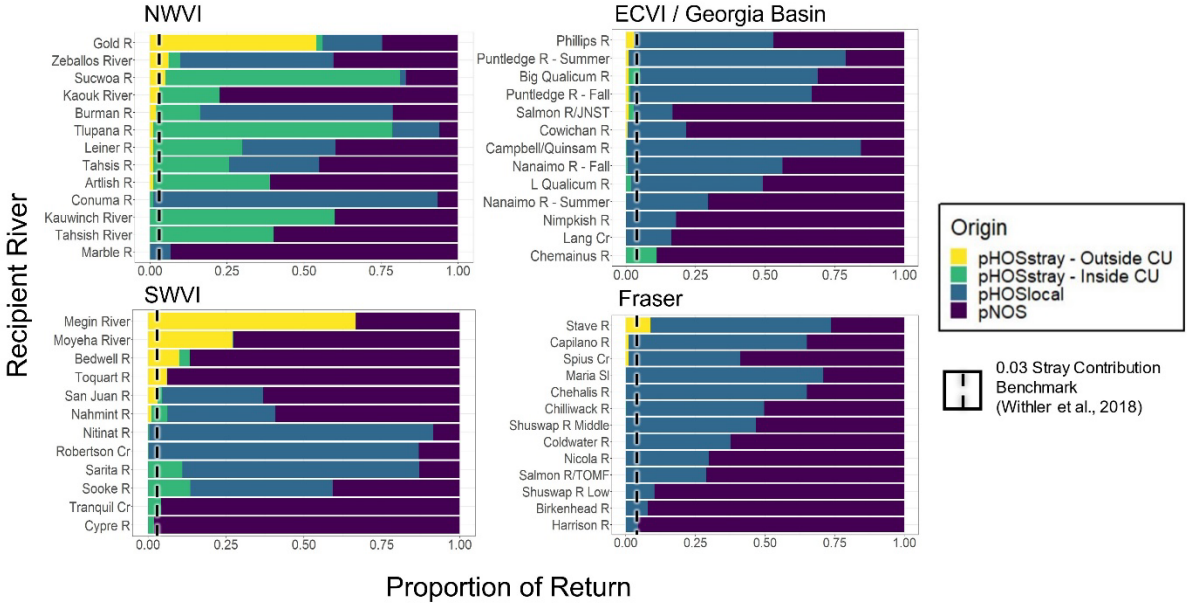


*Figure 3. Mean (1998–2021) proportion of spawners returning to 49 recipient river populations from four regions of southern BC. Different coloured bars correspond to the respective origin of spawners observed; hatchery-origin strays (Yellow = $pHOS_{stray,OCU}$, Green = $pHOS_{stray}$), local hatchery-origin returns that homed to the natal rivers (Teal = $pHOS_{local}$) or natural-origin spawners based on no adipose clip, CWT, or otolith thermal mark (Dark Purple = pNOS).*

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 ($pHOS_{stray}$) in the escapement, as a 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 $pHOS_{stray}$ was highest on the WCVI, with most strays originating from Conuma R Hatchery. Lower values, mostly below the 0.03 benchmark were observed on the ECVI, and a negligible stray contribution was observed in Fraser R populations.

*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.

## Genetic Assessment of Chinook Straying Along the WCVI

Genetic analysis of microsatellite loci, collected from 2013 to 2016 (Withler et al. 2017), was used to (1) provide a parallel assessment of hatchery straying, and (2) estimate the cumulative genetic introgression associated with stray Chinook from enhanced populations. This 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 approach enabled an examination of the degree and stability of population structure in WCVI Chinook Salmon and an investigation into the effects of hatchery-wild interactions since the inception of enhancement efforts in the late 1970s.

Genetic variation among populations on the WCVI is summarized in Figure 4. 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 consistently since the initiation of enhancement. Comparisons to the variation observed in other WCVI populations suggests that genetic variation from these major facilities (Robertson Cr, Conuma R and Nitinat R) has been introduced into the majority of populations in the same CU as the hatchery, resulting in a degree of 'genetic homogenization' across populations. This pattern is consistent with the described impacts of straying based on marked recoveries in recipient rivers presented above.

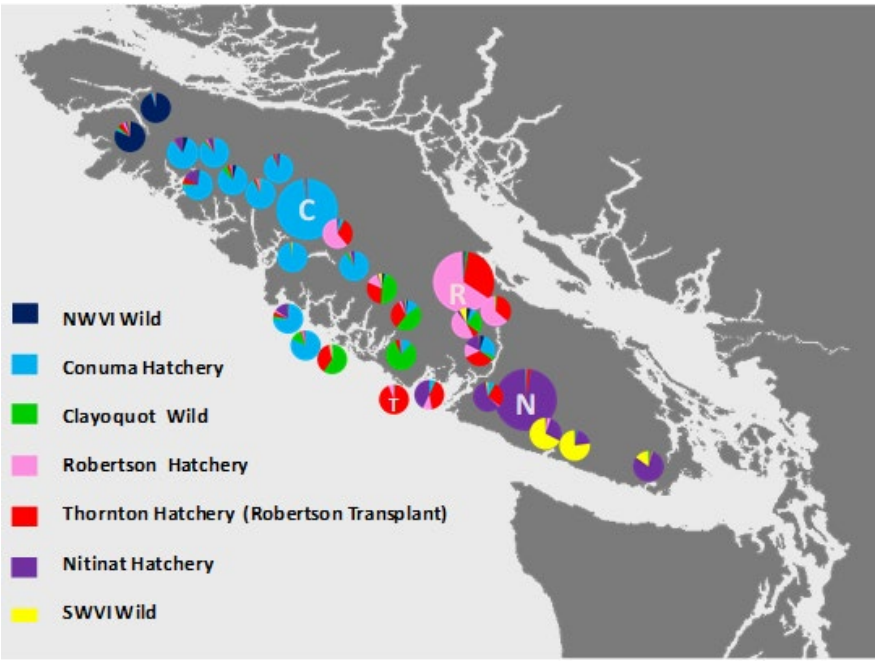


*Figure 4. Genetic ancestries of Chinook populations sampled between 2013–2015 along the West Coast of Vancouver Island. The size of the pie slice indicates the average proportion of the sample identified by STRUCTURE analysis to be of a given genetic ancestry corresponding to the colour in the legend.*

## Factors Affecting Stray Rate

Delineating the effect of environmental conditions and hatchery practices as causal factors influencing stray rate is difficult considering environmental variability, especially with local and regional variation. 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.

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 specific 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 was due to most thermal marking being implemented only to the level of hatchery-of-origin and not to the finer resolution of different release groups from a single hatchery. 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 the 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.

### Sources of Uncertainty

Throughout this study, various sources of uncertainty were identified that could affect the interpretation of the results. Key sources of uncertainty are outlined in the following list.

- Low precision and/or accuracy of data associated with:
  - Spawner composition
  - Recovery expansion factors
- Incomplete sampling and assessment of rivers in Southern BC
- Unknown straying contribution from hatchery production that was not marked or tagged
- Lack of environmental data at the appropriate spatial and temporal scales to relate to hatchery rearing strategies
- Tagging errors associated with thermal marking
- Observed discrepancy between thermal mark and CWT estimates of hatchery contribution
- As calculated, *PNI* may under estimate the impact of hatchery strays

## CONCLUSIONS AND ADVICE

Hatchery programs attempt to balance the benefits of production against fishery, ecological, and genetic risks. In this report we focus on one component of this risk, associated with the straying of hatchery-origin Chinook Salmon into non-natal spawning populations. Both annual donor straying rates and hatchery contributions into recipient rivers were provided in this analysis. Although donor stray rates from hatchery enhancement are generally low, the magnitude of Chinook strays can be substantial and is important to monitor. Rearing strategy may be an important contributing factor to straying, however no specific conclusions were drawn within this analysis. Although monitoring donor stray rates will support the prioritization of management actions, the recipient stray contribution ($pHOS_{stray}$) is the critical measure of hatchery stray influence. Generally, hatchery stray contribution was found to be under the 0.03 benchmark, with the exception of the WCVI.

The work by Withler et al. (2018), HSRG (2017, 2020), and Anderson et al. (2020) provide principles and a framework to preserve genetic diversity within and among enhanced salmon populations. The research in this paper focuses on a small component of their principles, namely the degree to which hatchery straying represents a risk to achieving genetic diversity objectives. 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.

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(*) identifies individuals who participated in the follow-up meeting on December 14th, 2023

## SOURCES OF INFORMATION

This Science Advisory Report is from the September 12–13 and December 14, 2023 regional peer review on the Assessment of Hatchery Chinook Salmon Straying in Southern British Columbia. Additional publications from this meeting will be posted on the Fisheries and Oceans Canada (DFO) Science Advisory Schedule as they become available.

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.

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