

RUN-TYPE COMPOSITION OF JUVENILE CHINOOK SALMON IN THE UPPER CHEHALIS RIVER BASIN, 2020 - 2022

Study Goals and Objectives

This summary includes information collected for a 3-year study covering field work done in 2020 to 2022. Genetic samples collected in 2022 have not yet been processed as of June 30, 2023. Issues arose in having them done at UC-Davis. The samples are being processed by the WDFW genetics lab. Results are expected in mid-July.

Two types of Chinook salmon produced in the Chehalis Basin are classified as spring-run or fall-run depending on timing of river entry and spawning. Recent research indicates these differences have a genetic basis. Genetic methods now exist to identify whether a Chinook salmon is a spring, fall, or hybrid (heterozygote) of the two types.

Data for Chehalis spring Chinook salmon exhibit a sharply declining trend over the past 20 years. This decline is a concern for the development of the Aquatic Species Restoration Plan (ASRP) for the Chehalis Basin. High priority has been placed on restoring habitats important to spring Chinook.

Understanding the decline of Chehalis spring Chinook is confounded by changes in the spawning escapement methodologies over the past several decades and a shift to later timing of spawning by these fish. Later spawning timing could be leading to increased interbreeding of the Chinook run-types and/or could be due to an increased frequency of hybrids relative to true spring Chinook. Consequently, there is a need for additional information to determine the status of spring Chinook and to help understand the extent of interbreeding.

In winter and spring of 2020, the Quinault Indian Nation (QIN) completed a pilot study in the upper Chehalis Basin to sample emergent Chinook fry and to assess the run-type composition using genetic analysis. The study was conducted in collaboration with the University of California Davis (UC-Davis). The project was successful in carrying out the intended sampling and in determining the genotypes of the sampled fry. QIN funded the study.

Subsequently, QIN proposed two more years of sampling to complete a 3-year study to assess run-type composition of emergent Chinook fry in areas of the upper Chehalis Basin. The Office of Chehalis funded the two additional years of sampling.

The goal of the project is to help determine the status of spring Chinook in the upper Chehalis Basin and to understand the extent of interbreeding between spring-run and fall-run Chinook where both run types are believed to be spawning. Interbreeding of the run types is believed to

be a significant threat to the long-term viability of spring Chinook in the basin (based on Thompson et al. 2019a and b and Waples et al. 2022).

Project objectives are:

- Sample newly emerged Chinook fry over the period of Chinook fry emergence (mid-January to mid-May) on a weekly basis for tissue samples to assess genotype;
- Operate fry traps within the areas where spring Chinook historically spawned in the upper basin;
- Process all sampled tissues to determine genotype (spring, fall, hybrid); and
- Estimate weekly and seasonal genotype frequencies of Chinook emergent fry moving past each site during the trapping period.

Methods / Study Design

Acquiring non-biased tissue samples and doing genetic assays for individual Chinook spawners would be the most direct method for estimating genotype frequencies of the adult population. However, it is logistically extremely difficult and expensive to collect sufficient tissue samples from live or dead spawners on the spawning grounds.

In lieu of sampling spawners, another way of assessing run-types of the population is to sample the newly emerged fry that survive from egg deposition. The sampling design employed to accomplish this was to place inclined-plane traps in the lower ends of the major spawning areas where spring Chinook historically spawned and where evidence exists that some spawning has continued to recent years. The traps are easily deployed and operated by a two-person crew.

Natural Chinook salmon fry on the Washington coast emerge from their incubation habitats beginning in January and extending into May. Upon emergence, the fry begin their seaward emigration and can be easily caught in the inclined-plane traps.

The inclined-plane traps were deployed at five locations in the upper basin and operated over the entirety of the fry emergence period. The sites were lower Skookumchuck River, middle mainstem Newaukum River, lower South Fork Newaukum River, lower North Fork Newaukum River, lower South Fork Chehalis River, and the upper mainstem Chehalis River just upstream of the confluence with the South Fork.

The underlying assumption in the study design is that fry being sampled at each site represent unbiased samples of genotypes of the fry migrants that emerge from spawning areas upstream of the traps and that are moving downstream past the sites.

Trapping and sampling occurred on a weekly schedule at all of the sites throughout the period of fry emergence. In each week at each site, the traps were set and then checked on consecutive days at approximately 20-24 hr intervals. Each time a trap was checked the fish caught were

identified and recorded. Chinook fry were anesthetized, measured (fork length (FL) in mm) and small tissue samples taken. The effort aimed to acquire tissue samples from 50 Chinook fry each statistical week and, once this objective was met, trapping ceased until the next week.

Chinook salmon fry captured were classified as emergent fry if they were ≤ 45 mm FL and rearing fry if they were > 45 mm FL. All tissue samples were transferred to the genetics lab at the Department of Animal Sciences UC-Davis for processing and classification into run-type genotypes. Methods used were identical to those described in Thompson et al. (2019b). In the analysis, weekly genotype frequencies were combined by weighting the weekly values by trap catch per unit effort (CPUE).

Summary of Results

Gilbertson et al. (2021) and Gilbertson (2022) reported on results for 2020 and 2021, respectively. Processing of genetic samples for 2022 (year 3 of study) is being handled by the WDFW genetics lab and will be completed by mid-July, 2023. Therefore, those results cannot be presented here.

Table 1 summarizes total weekly catches of emergent Chinook fry for the five sampling sites used over the three-year periods, together with the amount of fishing effort (in hours) expended in each week. Weekly catches and effort in the table are totaled for all of the sites combined. Table 2 summarizes the number of tissue samples taken each week from emergent fry for the five sampling sites combined.

Table 3 summarizes genotype frequencies for all weeks combined for all sites in 2020 and 2021.

Discussion

Findings to date can be summarized as follows:

- The objectives of the emergent fry study were achieved in all three years, though genetic processing has not yet been completed for the final year of the study.
- Project catch and effort data indicate the study design and duration covered a large majority of Chinook fry emergence timing in the upper Chehalis basin in areas reported to have spring Chinook spawning.
- Fry captured at the trap locations were dominated by emergent fry from mid-January (week 4) through mid-April (week 17). Catches transitioned to a majority of rearing fry in late April (week 18) through mid-May (week 20).
- FALL was the most common emergent fry genotype followed by HET individuals in both 2020 and 2021. Emergent fry of the SPRING genotype were least frequent in both years.
- These results suggest Chehalis Chinook currently conform more closely to a model of random mating than to a scenario of strong reproductive isolation between the run-types.

This indicates that the extent of interbreeding among run-types is significant and a valid concern in the basin.

- These results can inform the Skookumchuck flow study that has been initiated in that river to assess how flow management might be used to reduce hybridization.

Adaptive Management

The study shows that the abundance of true spring Chinook in the upper Chehalis Basin based on fry sampling is a small percentage of the total aggregate Chinook population. Preliminarily, the fry study indicates that the percentage comprised of spring Chinook is less than 10% and probably closer to 5%. The substantial percentage of fish that are hybrids indicates that significant interbreeding between run-types is occurring in the upper Chehalis Basin.

Table 1. Weekly Emergent Chinook fry catch and total trapping effort (Trap-Hours) in 2020-2022.

Stat Week	Catch			Effort		
	2020	2021	2022	2020	2021	2022
1	-	-	-	-	-	-
2	-	-	-	-	-	51.6
3	-	-	1	-	-	3.2
4	-	244	66	-	678.0	509.0
5	-	163	116	-	1,168.9	1,289.9
6	1	25	127	18.5	27.8	1,170.3
7	-	262	475	-	472.5	1,245.5
8	216	42	265	538.6	172.4	1,281.3
9	376	247	213	1,134.3	46.7	1,050.2
10	494	875	-	552.2	997.0	-
11	668	1,252	237	1,169.9	1,474.0	389.0
12	588	765	94	1,588.9	869.5	527.5
13	250	99	173	1,506.6	356.5	594.1
14	86	575	203	205.0	475.0	1,398.0
15	205	304	137	1,025.6	658.0	483.9
16	274	344	22	905.1	1,534.7	475.5
17	215	333	13	766.0	1,248.5	355.3
18	63	58	19	990.8	1,694.2	1,378.5
19	7	30	4	818.9	1,300.9	1,269.0
20	1	17	-	109.2	561.6	-
21	-	-	-	-	288.6	-

Table 2. Emergent fry tissue samples for genotyping; 2020-2022.

Site	2020	2021	2022
MSC	308	369	169
SFC	84	167	38
MSN	112	566	411
SFN	398	440	154
NFN	174	419	159
SKO	533	737	591
TOTAL	1,609	2,698	1,522

MSC - Mainstem upper Chehalis R.
SFC - South Fork Chehalis R.
MSN - Mainstem lower Newaukum R.
SFN - South Fork Newaukum R.
NFN - North Fork Newaukum R.
SKO - Lower Skookumchuck R.

Table 3. Estimated annual genotype frequencies for each site in 2020 and 2021.

Site	2020			2021		
	FALL	HET	SPRING	FALL	HET	SPRING
MSC	0.720	0.217	0.063	0.832	0.142	0.026
SFC	0.782	0.185	0.033	0.773	0.201	0.026
MSN	0.388	0.493	0.119	0.639	0.224	0.137
SFN	0.814	0.138	0.048	0.618	0.203	0.179
NFN	0.974	0.026	-	0.793	0.187	0.020
SKO	0.799	0.180	0.021	0.859	0.118	0.023
All sites	0.792	0.181	0.027	0.834	0.133	0.033

References

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