**Oregon Coastal Chum Salmon Genetics Pilot Study**

**2019-2021**

Oregon Department of Fish and Wildlife

Conservation and Recovery Program

**Background**

Chum salmon in Oregon coastal basins are part of the Pacific Coast ESU, which includes all populations from the Pacific coasts of Washington and Oregon, as well as populations in the Strait of Juan de Fuca west of the Elwha River (Johnson et al. 1997). Although there have been genetic studies of populations in the Pacific Coast and neighboring ESUs (e.g. Johnson et al. 1997; Small et al. 2011; Johnson et al. 2012), historical and contemporary population structure in the Oregon portion of the ESU remains poorly understood. Only three basins on the Oregon coast (Nehalem, Tillamook, and Yaquina) have consistent annual returns of at least several hundred spawners, but smaller numbers of chum are observed regularly or intermittently in at least 10 other basins. It is unknown how many of these locations historically supported independent populations, or how they are currently functioning as dependent or independent populations. The *Coastal Multi-Species Conservation and Management Plan* (ODFW 2014) identified current and historical population structure of coastal chum salmon as a critical uncertainty to address through research. Genetic techniques have the potential to provide insight into chum population structure, but sample quality has hindered previous investigations along the Oregon coast (Johnson et al. 2012). In 2019, ODFW initiated chum tissue sample collection in several coastal basins to support a new analysis of genetic relationships among the largest chum populations of the Oregon coast. Understanding relationships among these larger populations is a first step toward understanding population structure among all coastal basins where chum currently occur.

**Objectives**

The objectives of our work are to:

1. Collect and analyze samples from the three largest coastal chum salmon populations (Nehalem, Tillamook, and Yaquina), and two additional basins (Siletz and Netarts) that often have a substantial number of spawners, to investigate genetic structure of coastal chum salmon populations.
2. Collect and analyze samples from two major Tillamook sub-basins (Kilchis and Miami) to investigate whether there is significant genetic structure within the basin.
3. Collect tissue samples from different anatomical locations of chum carcasses to investigate whether certain tissues are more likely to provide higher quality samples for analysis.
4. Analyze a small number of archival chum scale samples to evaluate the potential for investigating historical population structure, using the large number of chum scale samples ODFW has collected through spawning grounds surveys over time.

**Approach**

Tissue samples were collected from chum carcasses (Objectives 1-3) in spawning reaches of the Nehalem, Tillamook, Netarts, Siletz, and Yaquina basins in November-December 2019. The target sample size for each basin (or Tillamook sub-basin) was 50 fish, but we could not locate that many carcasses in the Siletz or Netarts basins (see Table 1). Samplers collected 1-2 caudal fin samples with a single hole punch, or sampled the most intact fin, muscle, or bone tissue available on a carcass.

Table 1. Number of chum salmon carcasses (*n*) sampled, and tissue type collected in Oregon coastal basins in November-December 2019.

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| **Basin** | **Sample Site** | ***n*** | **Tissue Type** |
| Nehalem | Foley Cr, East Foley Cr | *50* | caudal fin (50) |
| Tillamook | Kilchis R | *50* | caudal fin (49), pectoral/dorsal fin (1), operculum (1) |
| Miami R | *50* | caudal fin (50) |
| Netarts | Whiskey Cr | *26* | operculum (22), various (7) |
| Siletz | Bear Cr | *3* | pelvic fin (2), pectoral fin (1) |
| Yaquina | Mill Cr | *64* | operculum (30), muscle posterior to operculum (21), various (13) |
| Simpson Cr | *10* | operculum (7), various (5) |

All samples were transferred to the [State Fisheries Genomics Laboratory](https://agsci.oregonstate.edu/state-fisheries-genomics-lab) at Oregon State University for analysis. Archival scales samples (*n = 20*) collected from chum carcasses in Mill Creek (Yaquina basin) between November 27, 2013 and December 4, 2013 were also transferred to the State Fisheries Genomic Laboratory (Objective 4). Scale samples were in their original scale envelopes and no scales had been removed from the envelopes since collection in the field.

In 2021, the State Fisheries Genomic Laboratory will genotype a subset (~90) of the chum salmon sampled in the Nehalem, Tillamook, and Yaquina basins to test out Washington Department of Fish and Wildlife’s GT-seq SNP panel. Results will inform decisions about testing additional samples from 2019, as well as any future field sampling.

Coastal basins where chum salmon are observed regularly or intermittently, and which were not sampled in 2019, include the Necanicum, Nestucca, Salmon, Alsea, Siuslaw, Coos, Coquille, and Chetco. Obtaining sufficient sample sizes to support a robust genetic analysis of chum salmon in these basins will be challenging due to low or highly variable abundance and the resulting difficulty in reliably recovering carcasses (note results in Siletz in 2019). The current pilot study will provide information about population structure and sample quality that will help inform decisions about investing additional sampling resources in these basins.

**References**

Johnson, O.W., W.S. Grant, R.G. Kope, K. Neely, F.W. Waknitz, and R.S. Waples. 1997. Status review of chum salmon from Washington, Oregon, and California. U.S. Dep. Commerce, NOAA Tech. Memo. NMFS-NWFSC No. 32.

Johnson, O.W., A. Elz, J. Hard, and D.S. Stewart. 2012. Why did the chum cross the road? Genetics and life history of chum salmon in the southern portion of their range. North Pacific Anadromous Fish Commission Technical Report No. 8: 135-137.

ODFW. 2014. Coastal Multi-Species Conservation and Management Plan. Oregon Department of Fish and Wildlife, Salem, OR. Available at: <http://www.dfw.state.or.us/fish/CRP/coastal_multispecies.asp>

Small, M.P., B. Glaser, T. Hillson, and C. Bowman. 2011. Population genetic structure and recovery of chum salmon in the Lower Columbia River*.* Washington Department of Fish and Wildlife Molecular Genetics Laboratory, Olympia, WA. Available at: <https://pisces.bpa.gov/release/documents/documentviewer.aspx?doc=P122957>