

Why Did the Chum Cross the Road? Genetics and Life History of Chum Salmon in the Southern Portion of Their Range

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The objectives of the study are to identify spawning chum salmon (*Oncorhynchus keta* Walbaum in Artdi, 1792) in the portion of their range south of the Columbia River, document the history of these populations, and characterize their genetics and life history. We hoped to determine if these fish were remnants of populations originating in California and southern Oregon that have migrated northward, strays from hatcheries that flourished in the 1970s and 1980s, strays from the Columbia River, or indigenous natural populations. Further, we attempted to determine if these fish display any unique genetic, behavioral, or morphological (small body, lower jaw, or kype size) characteristics that may provide a survival advantage in present or future environmental conditions.

We know that chum salmon historically had the widest distribution of any anadromous Pacific salmonid (Bakkala 1970; Salo 1991; Johnson et al. 1997). In the 1900s, chum spawned southward to the San Lorenzo River in Monterey, California, (Scofield 1916) and at least as far inland as 322 river kilometer (rkm) upstream in the Sacramento River (37° 50'N 122°W; Hallock and Fry 1967; Bakkala 1970; Fredin et al. 1977; Groot and Margolis 1991). On the Columbia River, chum salmon migrated at least as far inland as Celilo Falls near the present-day Dalles Dam (309 rkm), and there are newspaper reports that in some years this range reached 628 rkm to the mid-Snake River near Walla Walla, Washington, and the present-day Lower Granite Dam (Nehlsen et al. 1991; Johnson et al. 1997).

Early surveys reported that chum salmon were present in all streams from San Francisco to the Bering Straits (Jordan and Gilbert 1881; Jordan and Jouy 1881). In a series of early surveys of streams between the Sacramento and Columbia rivers in the early 1900s, Snyder (1908) reported that chum salmon were widely distributed and the most abundant salmon present. Adult chum salmon were also “said to be abundant in the fall, from Sacramento northward” (Eigenmann 1890). However, it should be noted that the surveys by Snyder’s party were primarily conducted in June, not a time when chum juveniles or adults would be found today. More recently, chum salmon were reported by Kostow (1995) to spawn at least as far south as Oregon’s Coquille River, while Nehlsen et al. (1991) suggested that relic chum salmon populations may occur as far south as the Elk and Sixes rivers, Oregon, at 42.8°N.

Thus, an understanding of the life history, genetics, and other biological information of chum salmon in the southern portion of their range are very important as climate change and human development begin to impact critical chum salmon habitat further north.

Recovery plans for Columbia River and Hood Canal chum salmon are presently being implemented and Oregon and other southern stocks may provide information and/or donor populations to help in the restoration and survival of other depleted populations.

Tissue samples were collected along the Oregon and Washington coasts and the Columbia River between November 15 and December 15 in 2004-2009 (Table 1). Samples in Washington State between 1995 and 2001 are from archived collections stored at the Washington Department of Fish and Wildlife (WDFW) labs in Olympia. Samples collected in the field were placed in vials containing alcohol in the field and stored at the Northwest Fisheries Science Center (NWFSC) in Seattle, Washington.

We genotyped 452 chum salmon from 14 streams collected over multiple years using 17 microsatellite DNA loci (Table 1) as described in Hillis et al. (1996), Small et al. (2006) and by L. Park (NWFSC, personal communication). Analyses were performed with sample sets from different year classes separated for each population and repeated with the year classes pooled for each population. Relationships among multiple and combined year classes for each of the sample populations were constructed. Overall tree topologies were similar, so we present the combined-years data set. Genetic analysis was conducted at the NWFSC, and standard genetic protocols and statistical analyses were employed using FSTAT2.9.3 (Goudet 2001) and GENEPOP 3.3 (Raymond and Rousset 1995) with genetic distances plotted in a neighbor-joining (NJ) tree using Populations 1.2.30 (Langella 1999).

Table 1. Location and year of chum salmon tissue samples collected along the Washington (WA) and Oregon (OR) coasts and the Columbia River. LCR is Lower Columbia River; S. OR is southern Oregon; N. OR is northern Oregon; SPS is southern Puget Sound.

Population	Drainage	Region	Year	No. Samples
Moss Cr.	Miami R.	S. OR	2004	9
Mill Cr.	Yaquina R.	S. OR	2006-09	60
Yaquina R.	Yaquina R.	S. OR	2004-09	55
Bear Cr.	Siletz R.	Mid-coast OR	2006-08	8
Coal Cr	Kilches	Mid-coast OR	2004, 2006	37
Tillamook R.	Tillamook R.	Mid-coast OR	2006, 07, 08	88
E. Foley Cr.	Nehalem R.	N. OR	2004-09	100
Necanicum R.	Necanicum R.	N. OR	2006	17
Ives Island	LCR	Columbia R.	2002	27
Lewis R.	LCR	Columbia R.	2003	22
Hardy Cr.	LCR	Columbia R.	1997	18
Grays R.	LCR	Columbia R.	2001	25
Hamilton Cr.	LCR	Columbia R.	1992, 1996	34, 22
Chinook River	Coastal CR	Columbia R.	1998	50
Dewatto R.	Hood Canal	Hood Canal (fall run)	1998	39
Blackjack Cr.	SPS	SPS (Summer run)	1996	36
Ellsworth Cr.	Willapa Bay	WA coast	1998	50
Bitter Cr.	Willapa Bay	WA Coast	1996	50
Satsop R.	Grays Harbor	WA Coast	1996	60

Preliminary results indicate that the majority of collections in the study deviated from Hardy-Weinberg equilibrium (HWE) with homozygote excess indicative of their small population numbers and small effective population sizes. There was little heterozygote excess observed, which suggests there was little outbreeding in these coastal groups. The genetic data revealed little heterogeneity among samples of chum collected in different Oregon and Washington coastal rivers. Differences between the coastal fish and Columbia River fish are small and reflect a close relationship. Kilchis River samples appear to be most closely related to Columbia River fish, although the Kilchis River is not geographically as near the mouth of the Columbia River as several other coastal rivers in this study. Preliminary analysis indicates there are few unique or private alleles in the coastal populations, and this suggests there are not “unique populations” from further south migrating into northern regions, but that these coastal fish are natural, indigenous populations.

In our genetics analysis we found heterogeneity among regional groups (e.g., Puget Sound and Oregon Coast) and some spatial structure among Washington and Oregon coastal samples. However, poor sample quality precludes more detailed conclusions at this time. Columbia River chum salmon samples also showed genetic differences from coastal chum salmon, but at a lower level than from other areas.

Life history data collected followed protocols established by Oregon Department of Fish and Wildlife (ODFW) and in the NOAA chum salmon status review (Johnson et al. 1997). The ODFW and WDFW staff collected historical run-timing and other life history data. Preliminary results of size, age, and meristic fin counts did not indicate any differences among chum salmon on the coast, or in the Columbia River and Puget Sound. Preliminary results of run timing analysis from datasets provided by WDFW and ODFW indicate that there is a narrower time of return for the Oregon coastal fish than for Washington fish. However, analyses are ongoing and often observers did not use consistent methods, so comparisons among rivers are difficult.

From historical records it appears that chum salmon once ranged in healthy numbers from southern Oregon to the Columbia River, and they were present in significant numbers south to mid-California. Populations began a decline in the southern-most portion of the range in the mid 1880s, and by the 1960s the only consistent populations in this region were in northern Oregon. However, even in northern Oregon chum salmon have declined dramatically since the 1950s.

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