

Drawing the Circles: Nested Analysis of Genetic Variation in Coastal Cutthroat Trout and the Delineation of Distinct Groups in British Columbia

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Extended Abstract—While coastal cutthroat trout (CCT) are an important component of many freshwater aquatic communities on the west coast of North America, our understanding of CCT biology remains extremely limited. The factors most influencing population size, productivity, patterns of movement, and the demographic independence of adjacent populations are not fully understood. The delineation of distinct population segments (and the factors which structure them) is an essential part of any conservation program and a clear rationale for defining distinct groups of CCT that will ultimately be required for legal protection under Canada's *Species at Risk Act (SARA)*. Current conservation initiatives in Canada may, therefore, be proceeding without a realistic understanding of what exactly constitutes a "typical" CCT population.

Methods

The process of defining distinct population segments (or "drawing the circles") synthesizes a host of disparate information, including patterns of species incidence, the distribution of unique morphologies or other traits, physiogeographic factors, and increasingly, genetic information. Concordance between different types of data can lend strong support to inferred population structure. Because the distribution of biological diversity is hierarchical in nature, this study employs a nested sampling design to target different scales of CCT diversity (Figure 1). Specifically, the ongoing project has three objectives:

- i. Investigate a "representative" CCT population to determine the degree of annual variation in the composition and success of cutthroat spawners. This is being accomplished by means of a fish enumeration fence on a typical spawning stream and genetic parentage analysis of young-of-the-year (YOY) fry produced over several years. The location chosen for the study was Chonat Lake on Quadra Island. This simple system has one main spawning stream (Chaos Creek, <3 m wetted width and ~700 m total length) that supports a healthy population of

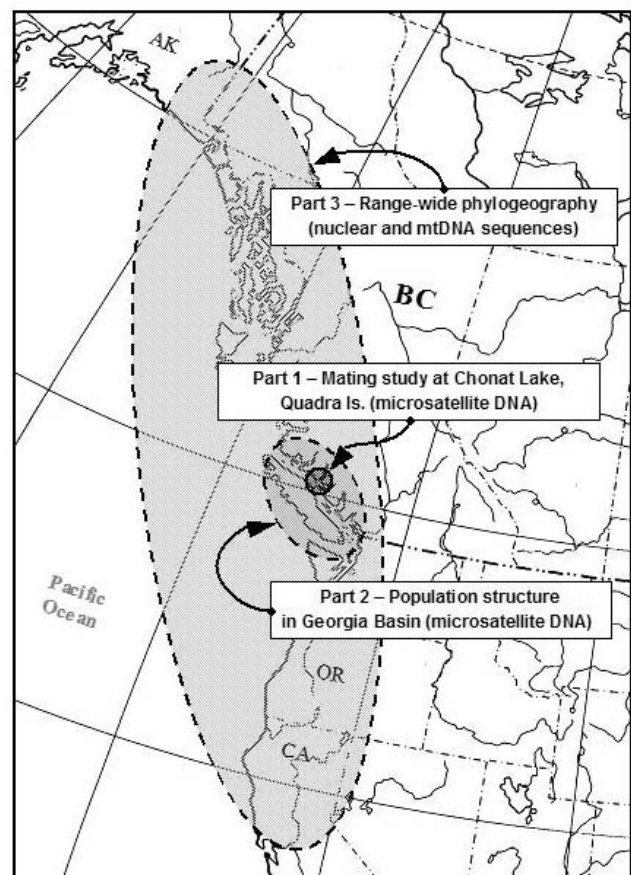


FIGURE 1.—Overview of the nested design of the study targeting coastal cutthroat trout diversity over different spatial scales.

CCT with lacustrine, anadromous, and resident components (total N ~570 ±160 based on mark-recapture, unpublished data).

- ii. Generate an understanding of population structure in CCT by using genetic markers to infer patterns of isolation, migration, and gene flow between adjacent streams. While evidence from other areas suggests

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that populations may ultimately be structured at the level of individual streams (e.g., Wenberg and Bentzen 2001), limits to anadromous dispersal suggest that localized groups of populations (i.e., metapopulations) may exist in British Columbia. We are examining patterns of gene flow among 48 populations from Vancouver Island and the Lower Mainland to determine the geophysical factors which may influence anadromous movement.

- iii. Describe regional patterns of CCT genetic diversity at nuclear and mitochondrial markers to delineate the distribution of evolutionary lineages in the province which could act as the primary conservation units beneath the subspecies level.

Results

i. Chonat Lake parentage study.—The number of female spawners observed at the Chonat Lake fish fence varied considerably from 57 in 2001 to just 21 in 2002. The number of males was not significantly different between years ($n = 24, 23$ respectively). Males generally appear to follow a lacustrine life history and may be less subject to variable ocean mortality. Many fish exhibited a pattern of up and down movement past the fish fence, some leaving the system without apparently mating (i.e., females with full complement of eggs). In contrast, no such movements were observed in year 2. Parentage analysis using microsatellite DNA confirms that the overall percentage of successful spawners was low in Year 1: just 16/24 (67%) males and 31/57 (54%) females were assigned YOY fry. A much higher percentage of spawners appear to have successfully mated in the low density year: 22/23 (96%) Year 2 males and 20/21 (95%) Year 2 females were assigned YOY offspring.

ii. Population structure in Georgia Basin.—Analysis of microsatellite DNA data suggest that all 48 populations sampled in the Georgia Basin are significantly differentiated (in terms of allele frequencies); some over very small spatial scales (<1 km, overall $F_{st} = 0.245$). For example, Chef, Cook, and McNaughton creeks—which essentially share a common confluence into Deep Bay on the east coast of Vancouver Island—are all genetically differentiated. At larger spatial scales, however, regional structure becomes apparent and populations form distinct groups loosely corresponding to geographic areas (e.g., Sechelt Inlet, Strait of Juan de Fuca, and Georgia Basin including the Sunshine Coast, eastern Vancouver Island, and the Gulf Islands). Interestingly, populations in Clayoquot Sound are more similar to populations in the Queen Charlotte Islands (added for comparison) than to other Vancouver Island populations (Figure 2). Similarly, Sunshine Coast populations are more similar to east Vancouver Island populations (across the Georgia Strait) than to Sechelt Inlet populations despite the greater geographic distance.

iii. Range-wide phylogeography.—Initial results from the sequencing of mitochondrial (ND1 and D-loop) and

nuclear encoded DNA markers (type 2-growth hormone) suggest that the complexity of cutthroat trout phylogeography may be on par with the complexity of its ecology and life history forms (see also Williams 2004). Nuclear data suggests the existence of three primary lineages of coastal cutthroat trout, one of which is prevalent only on the Queen Charlotte Islands. Mitochondrial data suggests the existence of at least two groups of cutthroat trout: a monophyletic group and a second group of cutthroat which cluster with rainbow trout. Whether this is the result of the introgression of rainbow trout DNA into hybrid fish or a remnant of some type of ancestral polymorphism is not clear at this time (Costello et al. 2001). Again, populations on the west coast of Vancouver Island appear more similar to those on the Queen Charlotte Islands than to other Vancouver Island populations.

Discussion

Preliminary findings suggest that successful spawning populations of CCT may vary considerable from year to year and be small compared to total population sizes. The ratio of successful breeders to total population size (N_b/N) averaged just 8% at Chonat Lake, which is less than values reported for other salmonids (up to 20% in Pacific salmon; Allendorf et al. 1997). Initial results suggest that high spawner densities and competition for spawning habitats may have a particularly strong effect in CCT populations because of the limited habitat available in smaller CCT streams. It may also suggest that the amount of available spawning habitat in small CCT streams can potentially set an upper limit on the number of spawners able to reproduce in even robust populations. Conversely, a form of “genetic compensation” (where a greater proportion of available individuals contribute during low spawner densities) appears to operate in the Chonat Lake population. This type of compensatory mechanism has been observed in other salmonid species, including steelhead and sockeye salmon (e.g., Chebanov 1991).

There appears to be little geneflow between adjacent systems (<1 migrant per generation), but populations appear loosely grouped into regional clusters. For example, Sechelt Inlet, Georgia Basin, and Strait of Juan de Fuca populations cluster (likely originated from a Chehalis/Columbia refuge) and are possibly an extension of the Puget Sound evolutionarily significant unit (ESU). Populations on the west coast of Vancouver Island north of Barkley Sound show stronger affinities with the Queen Charlottes and may instead represent the southern extreme of an Outer British Columbia Coast Designatable Unit under SARA (Costello and Rubidge 2005). Given the large number of inlet and fjord complexes along coastal British Columbia, it is likely that the number of genetically distinct, demographically isolated population segments of CCT could be quite large. Cutthroat trout likely colonized British Columbia from more than one glacial refuge and many British Columbia populations may represent a mix of refugial races. This

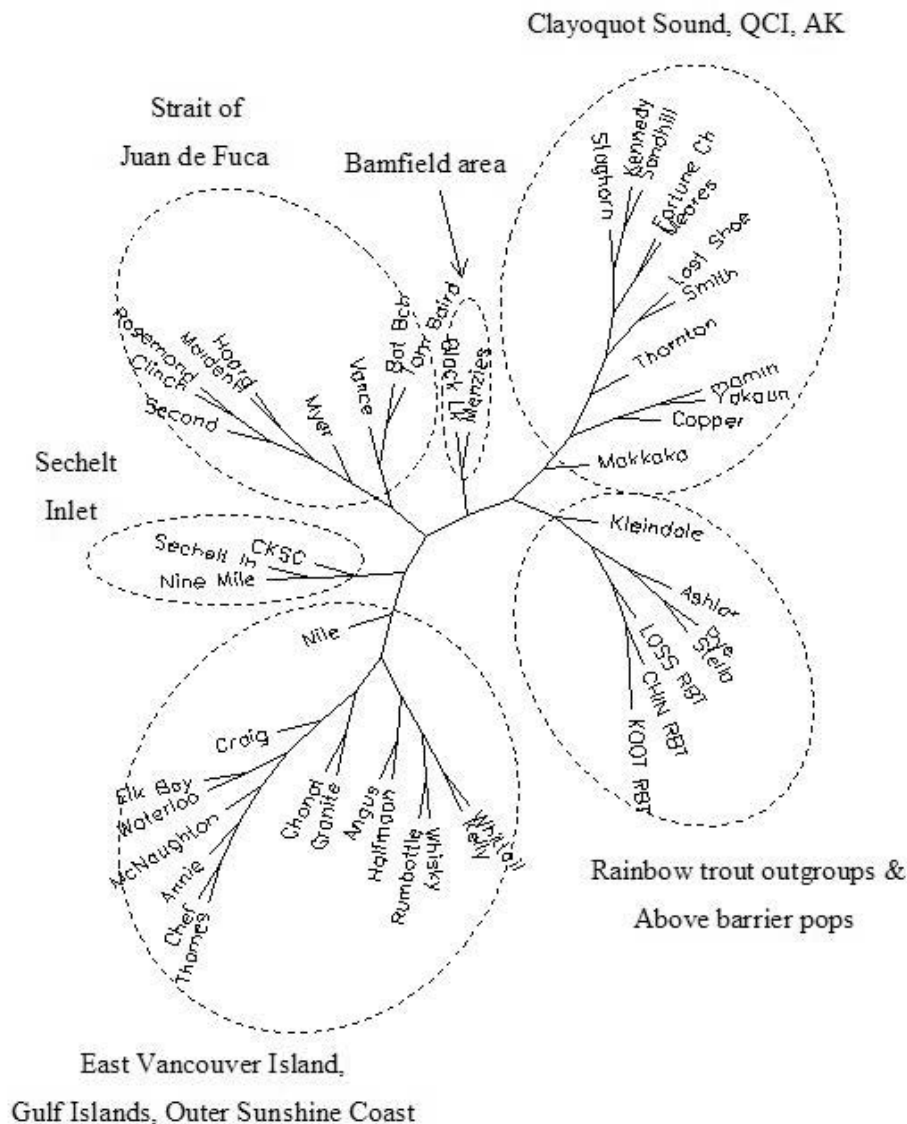


FIGURE 2.—Consensus UPGMA network of genetic relationships between cutthroat trout populations sampled in British Columbia based on Cavalli-Sforza and Edward’s chord distances. Regional groupings are highlighted and hybrids have been removed prior to analysis. Note that the Chonat Lake population is located centrally within the Georgia Basin group.

would represent a significant component of the subspecific biodiversity in the province and have obvious implications for conservation and fisheries management.

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