

Comparison of Genetic Diversity between Chum and Coho Salmon in the Yukon River

Potential Impacts of Land-Use Activities

Introduction

Loss of freshwater habitat is a common factor associated with the decline in abundance and genetic diversity of Pacific salmon throughout their range. The impact of localized habitat degradation on genetic diversity may vary among species depending on how populations are structured. Species composed of populations that occupy large geographic regions and exhibit moderate to high levels of genetic exchange are less likely to lose genetic diversity as a result of local habitat degradation than those composed of isolated populations occurring on small geographic scales with low rates of genetic exchange. Therefore, species-specific population structure is a critical factor in assessment of the potential loss to genetic diversity for a given species when habitat is impacted by land-use activities (e.g., mining, logging, development).

The Conservation Genetics Laboratory of the U.S. Fish and Wildlife Service, Alaska Region, initiated a study to examine genetic diversity and population structure of chum (*Oncorhynchus keta*) and coho (*O. kisutch*) salmon that co-occur in the Innoko and Tanana Rivers, tributaries of the Yukon River in Alaska (Figure 1). This study was part of a comprehensive assessment designed to evaluate the possible environmental and biological impacts of a gold mine on a Yukon River tributary near the Innoko National Wildlife Refuge.

Previous genetic analyses indicate that chum salmon populations, with some exceptions, appear to be organized on large geographic scales encompassing multiple river systems. In contrast,

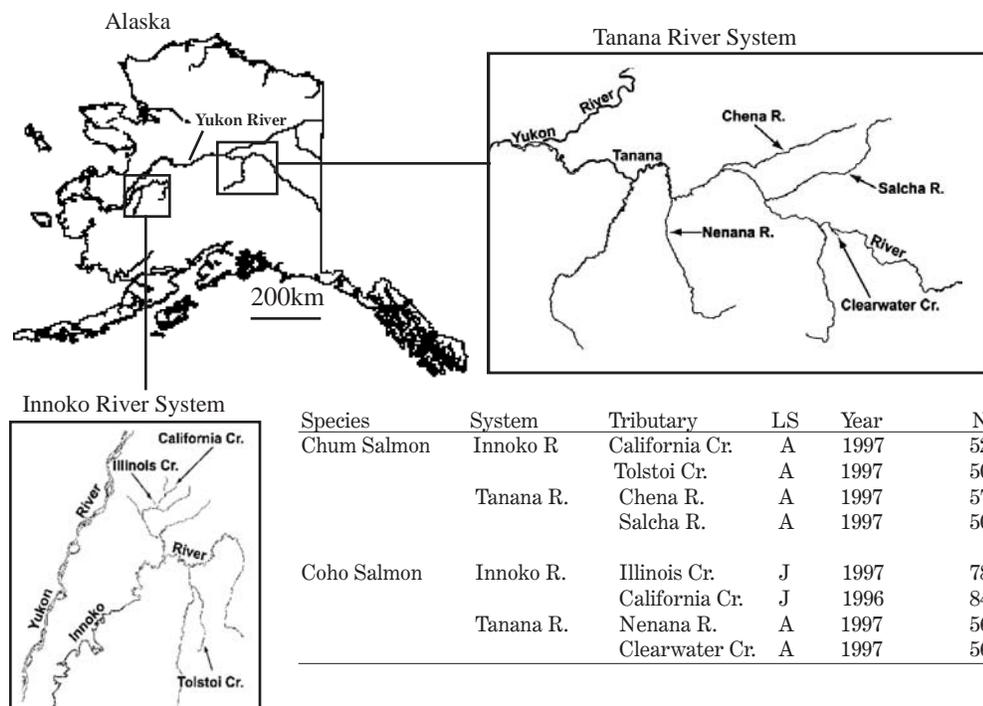


Figure 1. Map of sampling areas in the Yukon River drainage.

populations of coho salmon have been detected at both small and large geographic scales in river systems of the Pacific Northwest and Alaska. In this study, we test the hypothesis that chum and coho salmon in the Yukon River exhibit population structure at different spatial scales. If this hypothesis is true, then the risk of losing genetic diversity because of localized habitat degradation in the Yukon River drainage could differ between these species.

Methods

Fin tissue samples (non-lethal) were collected (1996 and 1997) from chum and coho salmon in both the Innoko and Tanana River tributaries (Figure 1). We

used microsatellites and mitochondrial DNA (mtDNA) to estimate the degree of population structure within and among the four collections made for each species.

The statistic F_{ST} is a relative measure of population structure ranging between zero (no population structure) and one (completely isolated populations). This statistic was used to quantify the amount of genetic variation resulting from population divergence. Variation was hierarchically partitioned into three components: 1) among all eight collections; 2) between the two tributary collections within each of the two rivers, and 3) between the two rivers.

Results

Our study indicates that genetic diversity is structured at different spatial scales for chum and coho salmon in the Yukon River (Figure 2). Genetic diversity in Yukon River chum salmon appears to be distributed over a relatively broad geographic area. The estimate of overall population structure from the microsatellite loci ($F_{ST} = 0.021$) while significant, is low, and due entirely to genetic differences between the two rivers and not to genetic differences within rivers (i.e., between tributaries). This large-scale population structure should serve to buffer chum salmon from the loss of genetic diversity if some spawning aggregations are lost because of localized habitat degradation. However, it must be emphasized that regardless of whether or not overall genetic diversity is lost, the loss of chum salmon from a tributary would likely reduce the overall abundance of Yukon River chum salmon. Such a loss would have other negative impacts (e.g. ecological, cultural, or economic).

In contrast, the data indicate that coho salmon collections in the Yukon River are highly differentiated, suggesting that population structure occurs on a much smaller geographic scale than for chum salmon (Figure 2). Because coho salmon populations are relatively small and discrete, the likelihood of localized habitat degradation affecting an entire population is greater with coho salmon than with chum salmon. It appears that gene flow between populations is extremely low and, if exterminated, the vacant habitat is unlikely to be re-colonized rapidly by other coho salmon populations.

Conclusions

This study suggests that habitat degradation resulting from land-use activities in the Yukon River drainage,

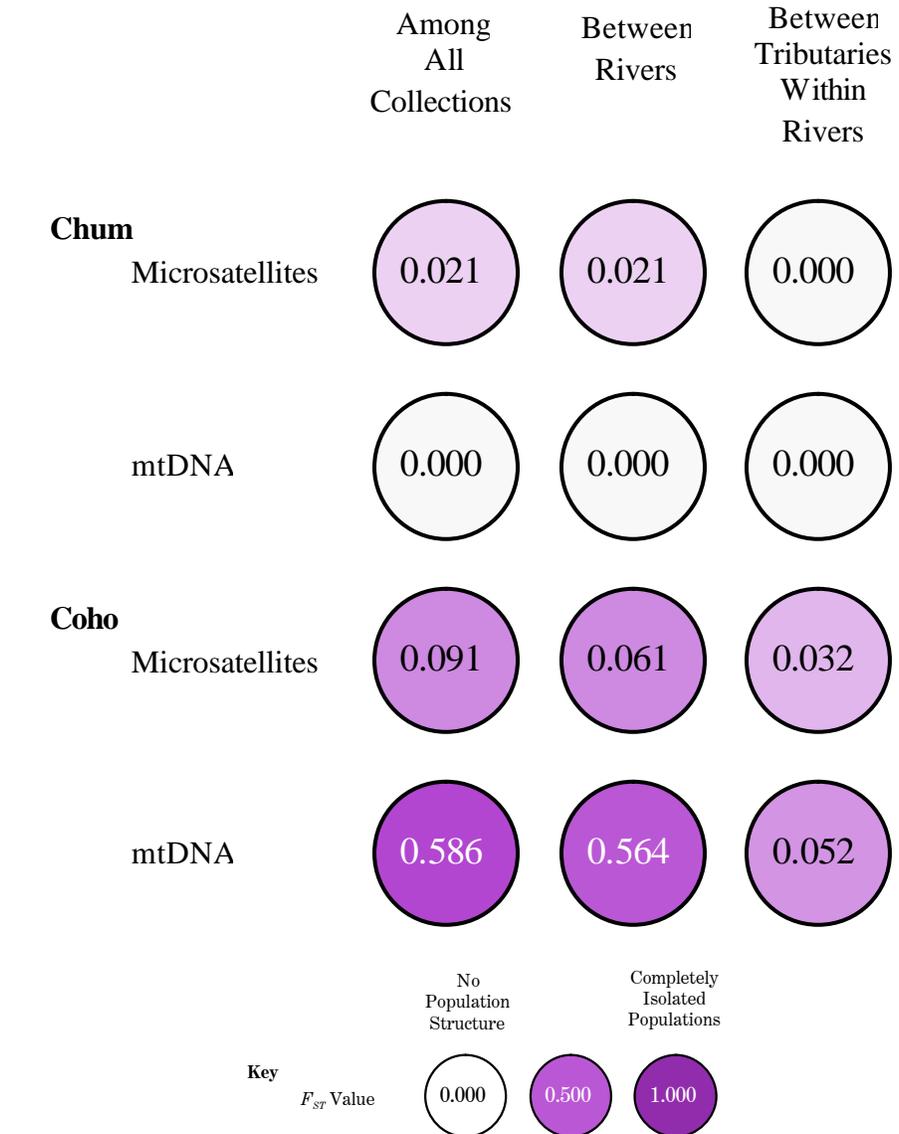


Figure 2. Genetic diversity comparisons for chum and coho salmon in Yukon River tributaries.

such as mining in the Innoko River drainage, would impact the genetic diversity of coho salmon to a much greater degree than chum salmon. Similarly, the geographic scale of management units will differ between these two species. Species-specific

conservation plans may be required to maintain genetic diversity of salmon species occupying the same geographic area. Thus, a multi-species approach is recommended for evaluating the potential impact of localized habitat degradation on the genetic diversity of Pacific salmon.

For additional details, see:

Olsen JB, Spearman WJ, Sage GK, Miller SJ, Flannery B, Wenburg JK (2004) Variation in the population structure of Yukon River chum and coho salmon: evaluating the potential impact of localized habitat degradation. Transactions of the American Fisheries Society 133, 476-483.

For more information contact:

Jeff Olsen
 U.S. Fish and Wildlife Service
 Conservation Genetics Laboratory
 1011 E. Tudor Road
 Anchorage, Alaska 99503
 907/786 3598
 jeffrey_olsen@fws.gov
 alaska.fws.gov/fisheries/genetics

