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Conservation Units for Pacific Salmon under the Wild Salmon Policy

Unités de conservation du saumon du Pacifique en vertu de la Politique concernant le saumon sauvage

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Abstract

The initial steps in protecting biological diversity and the primary roles of scientific research, are to identify the diversity and then take inventory of the units of diversity that require conservation[1]. Consequently, the first of six strategies in the *Wild Salmon Policy*[2] concerns the identification of the units and determining their conservation status. The primary purpose of this document is to describe the method that was developed to identify the "Conservation Units" for the five species of Pacific salmon in British Columbia. The description of units in most of the Yukon[3] and Northwest Territories will proceed using this method once the ecotypology of those areas is completed.

The approach of Waples et al.[4] was modified to characterize diversity in Pacific salmon along three major axes: ecology, life history, and molecular genetics, and then to compartmentalize that diversity into Conservation Units. The three descriptive axes are used to map local adaptation in a variety of ways. The maps are then examined and combined to locate and describe the Conservation Units. The first stage in the description of the Conservation Units is based solely on ecology. The ecotypologies used include a characterization of the near-shore marine environment in addition to one for fresh water. The second stage of the description involves the use of life history, molecular genetics, and further ecological characterizations to group and partition the first stage units into the final Conservation Units. The result is Conservation Units that are described through the joint application of all three axes.

There is a high degree of concordance between ecotypic, biological (life history) and genetic characterizations of intraspecific diversity, confirming the principal conclusions of Waples et al.[4] Molecular genetics was essential in areas of high genetic diversity but once identified, ecotypology appeared capable of mapping the genetic diversity. Similarly, there were instances where life histories differed and where ecological descriptors mapped that diversity. The high levels of concordance between the three axes strongly suggest that the Conservation Units describe real and presumably adaptive diversity.

In addition to the pragmatic advantages of a method that uses all available information to describe intraspecific diversity, an ecotypic approach has benefits stemming from characterizations of salmon habitat in its broadest sense. Importantly, the method supports the intent of the WSP to use CUs for the conservation of both pattern and process[5].

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[1] see Wood, C.C. 2001. Managing biodiversity in Pacific salmon: The evolution of the Skeena River sockeye salmon fishery in British Columbia. Blue Millennium: Managing Global Fisheries for Biodiversity, Victoria, British Columbia, Canada, pp. 1-34. Proceedings of the Blue Millennium International Workshop, June 25-27, 2001, Victoria, BC, Canada. Papers available at http://www.worldfish.org/bluem-reports.htm

[2] DFO. 2005. Canada's policy for conservation of wild Pacific salmon. Fisheries and Oceans Canada, 401 Burrard Street, Vancouver, BC V6C 3S4. p. 49+v.

[3] Several of the ecotypic zones straddle the Yukon-British Columbia border and are described in this document.

[4] Waples, R.S., Gustafson, R.G., Weitkamp, L.A., Myers, J.M., Johnson, O.W., Busby, P.J., Hard, J.J., Bryant, G.J., Waknitz, F.W., Nelly, K., Teel, D., Grant, W.S., Winans, G.A., Phelps, S., Marshall, A., and Baker, B.M. 2001. Characterizing diversity in salmon from the Pacific Northwest. J. Fish. Biol. **59**: 1-41.

[5] Pattern is the diversity that currently exists. Process refers to the evolutionary processes that create and maintain diversity. (see Moritz, C. 2002. Strategies to protect biological diversity and the evolutionary processes that sustain it. Systematic Biology **51**(2): 238 - 254.)

One general conclusion from this exercise is that Pacific salmon in Canada are very diverse. This diversity is reflected in the estimated numbers of CUs by species shown in the following table:

species	number of CUs
pink-odd	19
pink-even	13
chum	39†
coho	43
chinook	68†
sockeye-river	24
sockeye-lake	214

† Additional CUs will be described in the Yukon River. Additional CUs are possible in the Mackenzie River, although currently they would be outside of the geographic purview of the Wild Salmon Policy.

Résumé

Les premières étapes de protection de la diversité biologique et les premiers rôles de la recherche scientifique consistent à déterminer l'étendue de la diversité et de recenser ensuite les unités de diversité que nécessite la conservation[6]. Par conséquent, la première des six stratégies de la Politique concernant le saumon sauvage[7] consiste à identifier les unités et à évaluer leur état. L'objet principal du présent document est de décrire la méthode mise au point pour définir les « unités de conservation » des cinq espèces de saumon du Pacifique, en Colombie-Britannique. La description des unités dans une grande partie du Yukon[8] et des Territoires du Nord Ouest sera effectuée au moyen de cette méthode une fois l'écotypologie de ces zones terminées.

La démarche de Waples et coll. a été modifiée afin de caractériser la diversité du saumon du Pacifique selon trois grands axes : écologie, cycle biologique et génétique moléculaire, puis de compartimenter cette diversité en unités de conservation. Les trois axes descriptifs servent à cartographier l'adaptation locale, en d'autres mots, ce qui est réellement à conserver, de diverses façons. Les cartes sont ensuite examinées et combinées en vue de situer et de décrire les unités de conservation. La première étape de la description des unités de conservation est fondée uniquement sur l'écologie. L'écotypologie comprend une caractérisation du milieu marin semi-côtier en plus de celui de l'eau douce. La deuxième étape de la description suppose le recours au cycle biologique, à la génétique moléculaire et à d'autres caractérisations écologiques afin de regrouper et de diviser les unités de la première étape en unités de conservation finales. Il en résulte des unités de conservation qui sont décrites au moyen de l'application commune des trois axes.

Il existe un haut degré de concordance entre les caractéristiques écotypiques, biologiques (cycle) et génétiques de la diversité intraspécifique, confirmant les principales conclusions de Waples et coll.[9] La génétique moléculaire a été essentielle dans les situations de grande diversité génétique, mais une fois l'identification faite, l'écotypologie a semblé suffire à cartographier la diversité génétique. De même, il y avait des cas où le cycle biologique différait et où les descripteurs écologiques ont pu servir à cartographier la diversité. Le haut niveau de concordance entre les trois axes semble indiquer assez certainement que les unités de conservation décrivent une diversité réelle et présumément adaptative.

En plus des avantages pragmatiques d'une méthode qui fait appel à toute l'information disponible pour décrire la diversité intraspécifique, une approche écotypique a des avantages qui découlent des caractérisations de l'habitat du saumon dans son sens le

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[6] voir Wood, C.C. 2001. Managing biodiversity in Pacific salmon: The evolution of the Skeena River sockeye salmon fishery in British Columbia. Blue Millennium: Managing Global Fisheries for Biodiversity, Victoria, British Columbia, Canada, pp. 1-34. Compte rendu du Blue Millenium International Workshop, du 25 au 27 juin 2001, Victoria, C.-B., Canada. Documents accessible à http://www.worldfish.org/bluem-reports.htm

[7] DFO. 2005. Canada's policy for conservation of wild Pacific salmon. Fisheries and Oceans Canada, 401 Burrard Street, Vancouver, BC V6C 3S4. p. 49+v.

[8] Plusieurs des écotypes chevauchent la limite entre le Yukon et la Colombie-Britannique et sont décrites dans ce document.

[9] Waples, R.S., Gustafson, R.G., Weitkamp, L.A., Myers, J.M., Johnson, O.W., Busby, P.J., Hard, J.J., Bryant, G.J., Waknitz, F.W., Nelly, K., Teel, D., Grant, W.S., Winans, G.A., Phelps, S., Marshall, A., and Baker, B.M. 2001. Characterizing diversity in salmon from the Pacific Northwest. J. Fish. Biol. **59**: 1-41.

plus large. Fait important, la méthode appuie le but de la Politique d'utiliser les UC pour la conservation de la tendance et des processus[10].

Une des conclusions générales de cet exercice est que le saumon du Pacifique au Canada est très diversifié. Le nombre approximatif d'UC par espèce, indiqué dans le tableau qui suit, témoigne de cette diversité :

espèce	nombre d'UC
rose-ann. impaires	19
rose-ann. paires	13
kéta	39†
coho	43
quinnat	68†
rouge-rivière	24
rouge-lac	214

† D'autres UC seront décrites dans le fleuve Yukon. Bien que d'autres UC soient possibles dans le Mackenzie, elles n'entreraient pas dans le champ d'application géographique de la Politique concernant le saumon sauvage.

[10] La tendance correspond à la diversité qui existe actuellement. Les processus désignent les processus évolutionnaires qui créent et maintiennent la diversité. (voir Moritz, C. 2002. Strategies to protect biological diversity and the evolutionary processes that sustain it. Systematic Biology **51**(2): 238 - 254.)

1. Context

Pacific salmon (genus *Oncorhynchus*) are the most ecologically, morphologically and behaviorally diverse vertebrate species in Canada, with many thousands of more or less distinctive "populations". To conserve their biodiversity and to manage the species for the benefit of all Canadians the Canadian Department of Fisheries and Oceans (DFO) adopted and is now implementing Canada's Policy for the Conservation of Wild Salmon Policy (the WSP) (DFO 2005). Implementation of the WSP consists of six strategies, the first of which stipulates the standardized monitoring of wild salmon status. Standardized monitoring begins with the identification of species-specific Conservation Units or CUs. The CUs serve two roles under the WSP. First, each CU is, in some sense, a significant element of biodiversity that the WSP seeks to conserve and manage. Second, each CU is a unit for reporting on the success (or failure) of actions taken under the WSP to conserve wild Pacific salmon. Subsequent steps in the Policy's implementation, including the characterizing of the biological, habitat and ecological status of each CU are contingent on providing a consistent, objective, defensible and operational definition of the CU that is both practicable and will insure that the important elements of salmon biodiversity can be conserved and managed.

Any scheme to compartmentalize biodiversity in Pacific salmon will be, at best, an approximation. In addition to all of the usual difficulties caused by limited and incomplete information, the highly dynamic nature of the interactions between salmon and their diverse habitats means that their diversity is continually evolving. Only 10000 years ago there were no salmon in western Canada at all because the entire region was glaciated and now virtually all accessible habitats are full. Humans, with their alterations to habitat on all scales and their often intense predation, are creating conditions that can only serve to accelerate adaptive change in salmon. Consequently, the characterizations of diversity in salmon that we present are imperfect and will be subject to change as new information becomes available and as our interpretations of that information are refined. For current information about the WSP, including the current lists of Conservation Units and their statuses as well of details of the processes in place to review and modify the lists of Conservation Units, the interested reader is referred to the DFO, Pacific Region's web portal, http://www.pac.dfo-mpo.gc.ca/pages/default_e.htm (en français, http://www.pac.dfo-mpo.gc.ca/pages/default_f.htm).

2. Introduction

Pacific salmon occur throughout coastal British Columbia and deep into the interior of BC and the Yukon along the drainages of the Fraser, Skeena, Nass, Stikine, Taku, Alsek, Yukon, and Mackenzie Rivers. There are seven *Oncorhynchus* species in Canada, five Pacific salmon and two anadromous trout. All seven of the species are anadromous, meaning that their eggs are laid in freshwater but that juvenile fish enter the sea at some point in their life cycle. Only sockeye salmon, *O. nerka,* has an obligate freshwater form, the kokanee. The timing of sea-entry is one of the most useful descriptors of intraspecific diversity. All of the Pacific salmon are semelparous, which means that individuals spawn once and then die. Both species of anadromous trout are iteroparous. All of the species can complete their life cycle within fresh water, although, with the exception of kokanee, this is seldom observed within their native range. This document applies only to the anadromous forms of the five Pacific salmon species. Our method could be applied, with some modifications, to kokanee and the anadromous trout, but those species are beyond the purview of the Wild Salmon Policy and were excluded from our consideration.[11]

Perhaps the most phenomenal characteristic of Pacific salmon is their ability to return or "home" to their natal river, even after spending several years in the Pacific Ocean thousands of kilometers away. This homing ability is so refined that in some circumstances adults return to their natal nest site (Quinn et al. 1999)! Complex traits such as homing arise because they confer a survival advantage. Fish that spawn close to their natal redds tend to produce more offspring that survive to reproduce than those individuals that spawn distantly from their natal redds. Many of the biological traits of Pacific salmon that vary from one population to the next, such as where and when to spawn, egg size and number, body size and shape, whether fry should migrate upstream or downstream after emerging from the nest, etc., have been shown to be site-specific[12]. Since a particular set of traits or phenotype confers a survival advantage in a particular place but not necessarily in other places, mechanisms that link a phenotype to the places where it survives well have evolved. That evolution has occurred in a vast geography that has both pattern, due to geology, latitude, and climate, and tremendous heterogeneity at the scales on which individual salmon interact with their environment. The results are levels of <u>intra</u>specific diversity unparalleled in any other vertebrate species in Canada.

Intense fisheries for Pacific salmon began about 140 years ago (e.g. Sprout and Kadowaki 1987) but our understanding of the nature of the resource is much more recent. For example, our understanding of the diversity of sockeye salmon in the Skeena River was very limited prior to the mid-1940's even though the watershed has the largest natural lake in British Columbia and the single largest population of sockeye (Wood 2001). Salmon research began in earnest in the 1940's and culminated with Ricker and the stock concept (Ricker 1954), which allowed biologists to estimate "optimal" stock-specific harvest rates and appreciate for the first time the impacts that mixed-stock fisheries were having on unproductive populations. The threat that over-exploitation posed to the diversity of wild salmon was recognized nearly immediately. For example, McDonald (1981) warned that unproductive stocks could be extirpated due to the typical fishing rates in river-mouth fisheries at the time.

Concerns about the loss of biodiversity through extinctions of <u>species</u> have been with us for decades and Canada, along with many other countries, acknowledged the importance of diversity by ratifying the 1992 United Nations Convention on Biological Diversity (UN United Nations 1992). Canada subsequently adopted a federal law, the Species at Risk Act or SARA (Canada 2002). SARA substantially broadened the concept of species, i.e., those biological entities that could be afforded protection under the Act, by defining the term "wildlife species" to include not only species and subspecies but also races, varieties and <u>distinct populations</u>.

Concern for intraspecific diversity in Pacific salmon was first formalized at the policy level in 1998 by the Honourable David Anderson, PC, then the Minister of Fisheries and Oceans, through the release of a discussion paper titled "A New Direction for Canada's Pacific Salmon Fisheries" (DFO 1998). This policy document listed 12

[11] Please see Appendix 8 for the purpose and scope of this document.

[12] What actually has been demonstrated is that these characteristics have a genetic basis (are passed to offspring), that traits vary in a predictable way across time and space, and that having a particular set of traits (the phenotype) confers a survival advantage compared to other phenotypes (e.g.)

general principles for conservation, sustainable use, and improved decision-making that set out a broad policy framework under which specific operational policies and guidelines for managing Pacific salmon would be developed. The first and fifth principles clearly identify that conservation of stock diversity would be the first priority of the regulatory agency (emphasis ours):

- Principle 1: "Conservation of Pacific salmon <u>stocks</u> is the primary objective and will take precedence in managing the resource".
- Principle 5: "The long term productivity of the resource will not be compromised because of short term factors or consideration–tradeoffs between current harvest benefits and long term <u>stock</u> well being will be resolved in favour of the long term".

Canada's Policy for Conservation of Wild Pacific Salmon (the WSP) was released in 2005 following six years of discussion, consultation, review, and revision (DFO 2005). The WSP is one of several policies whose provenance was the New Directions discussion paper. The goal of the WSP is to "restore and maintain healthy and diverse salmon populations and their habitats for the benefit and enjoyment of the people of Canada in perpetuity".

The WSP introduced the biological concept of the "Conservation Unit" or CU and described how the diversity of wild Pacific salmon would be safeguarded by protecting CUs. CUs are conceptually defined as mutually interchangeable groups of wild salmon with similar adaptations that are reproductively coupled. Under the WSP CUs have the dual roles of firstly being, in some sense, fundamental units of biodiversity and secondly, of being the accounting units for documenting progress in achieving the policy goals of the WSP.

The initial steps in protecting biological diversity and also the primary roles of scientific research, are to identify the diversity and then take inventory of the units of diversity that require conservation (Wood 2001). Consequently, the first of six strategies in the WSP concerns the identification of the units and determining their conservation status. The primary purpose of this document is to describe the method that was developed to identify the CUs of the five species of Pacific salmon under federal jurisdiction.

3. Defining units for the conservation of biodiversity

Why focus on the Conservation Unit as the new unit for conservation and management of Pacific salmon in Canada? The Wild Salmon Policy defines conservation as "the protection, maintenance, and rehabilitation of genetic diversity, species, and ecosystems to sustain biodiversity and the continuance of evolutionary and natural production processes" (DFO 2005). People benefit from natural production processes in a number of ways but primarily through harvest – a use that can be sustained only if harvested populations are able to persist through both natural ranges of environmental variability as well as human induced stresses and produce a harvestable surplus. Pacific salmon habitat varies in both time and space and the species are adapted to those variations at a remarkably fine spatial scale. Geographic variation in life history characteristics known to be associated with individual fitness and, presumably, productivity, is known to occur in many exploited species and is characterized as local adaptation (Allendorf and Waples 1996, Schaffer and Elson 1975, Taylor 1991). The preservation of local adaptation is therefore one of, if not the most important, objective of conservation.

A second important objective of conservation is the preservation of genetic diversity (Allendorf et al. 1997). The viability and future productivity of a species are dependent on its genetic diversity because, on the time scales of interest to people, that is the only source of future adaptation. For example, Bristol Bay AK sockeye, an aggregate of hundreds of very diverse spawning populations has remained productive through periods of dramatic changes in freshwater and marine conditions. Under each successive environmental regime one or other of the many stock components has thrived (Hilborn et al. 2003).

The protection of diversity that was important in Bristol Bay is conceptually simple. The lakes in the complex had a wide array of slightly different sockeye some of which did well at one time or another and there was a very beneficial result to protecting that diversity. Not so simple is the concept of genetic diversity as developed by Moritz (2002). He casts the problem of conservation in terms of protecting both 'pattern' and 'process'. Pattern is equivalent to existing local adaptation, and its conservation can be accomplished by the identification and protection of groups of populations, at least over the short-term. For example, it was the protection of such 'pattern' that yielded benefits in Bristol Bay. In contrast, protecting process requires maintaining what Moritz terms the "context" for natural selection to operate, namely habitat integrity and connectedness and viable populations. In this context, natural selection allows the constituent diversity of the population to express itself with the result that local adaptation is maintained.

Some authorities have suggested that the dual objectives of protecting pattern and process can be achieved by conserving 'healthy' populations in all historically accessible habitats (Healey and Prince 1995, MacLean and Evans 1981, Riddell 1993). This approach would not seem to require a detailed understanding of either pattern or process presumably because comprehensive protection would by definition look after pattern, while process would be protected by eliminating or limiting human impacts. Such an approach would have the additional benefit of directing considerable attention to habitat protection and restoration, a need that was a recurrent theme during consultations on the Wild Salmon Policy (see Appendix 7). However, if all populations are maintained in all habitats, this approach might so severely constrain human activities (Redford and Richter 1999) that many would consider its cost unnecessarily high.

The approach embodied in the Wild Salmon Policy to conserving both pattern and process is to operationally separate these two objectives of conservation. The WSP clearly identifies the importance of protecting evolutionary process for the viability of the resource, and the protection of both habitat and ecosystems are the foci of other strategies in the policy. Essentially, that leaves Conservation Units as the vehicle for achieving the first objective of conservation, the identification, and protection of pattern or extant local adaptation. Nevertheless, protecting the diversity, integrity, spatial extent and interconnectedness of habitat is probably the best way of guarding against the loss of genetic diversity.

The formal description of local adaptation requires that we identify characteristics such as particular life-history traits or phenotypes that confer a measurable reproductive advantage compared to other traits or phenotypes and then demonstrate that the traits are heritable (Rader et al. 2005). Although feasible, such an approach would be expensive and time-consuming and would not meet the urgencies of implementing the WSP. Three practicable alternatives have been proposed to characterize intraspecific diversity in Pacific salmon: life-history, ecology and biochemical genetics (Waples et al. 2001). We use all three of these approaches as explained in the next section.

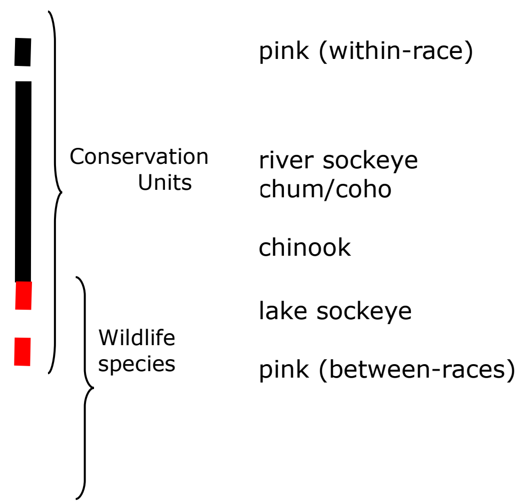
Most discussion about units of conservation at the intraspecific level are based on the concept of the Evolutionarily Significant Unit or ESU, which was introduced by Ryder (Ryder 1986) and elaborated on for Pacific salmon by Waples (Waples 1991b, 1995). The original descriptions of the ESU emphasized a multi-attribute approach that involved demonstration of reproductive isolation coupled with significant adaptive variation (Crandall et al. 2000). Although some have emphasized isolation over adaptive variation, the consensus is that Waples' original emphasis on both isolation and adaptive variation was correct (de Guia and Saitoh 2006).

A great deal has been written about the ESU and other units for conservation with the result that the nomenclature has become so complex that at least one observer has called for its simplification before there is costly confusion on the part of biologists, resource managers and policy makers (Cronin 2006). The clarification and consistent use of terms for units of conservation is important because of the costs, lost opportunities and frustrations caused by imprecision and lack of clarity (Adamowicz and Purvis 2005, Agapow et al. 2004, Cronin 2007, de Guia and Saitoh 2006, Dillon and Fjeldsa 2005, Isaac and Purvis 2004, Mace 2004, Zink 2004). Accordingly, we think it important to attempt to clarify what is meant by the term "Conservation Unit."

The WSP defines a Conservation Unit as "a group of wild salmon sufficiently isolated from other groups that, if extirpated, is very unlikely to recolonize naturally within an acceptable timeframe." (DFO 2005). This definition embodies the concepts of isolation, adaptive variation and ecological exchangeability that underlie Waples'(1995) definition of the ESU with the modifications of Crandall et al. (2000). However, CUs are not ESUs, although the two units of diversity are closely related as shown by the scheme of Wood and Holtby (1998). Their scheme, illustrated in the following table, uses a theoretical model to predict from levels of gene flow when local adaptation is likely to exist. The scheme also provides a consist nomenclature that is similar to the simplifications proposed by Cronin (2006) and provides an approximate quantitative definition of a Conservation Unit.

In the terms of this scheme, a Conservation Unit is typically a LOCAL population. This scheme also provides an approximate quantitative definition of a CU, at least in terms of the objective of describing local adaptation. Units that are more isolated are termed CLOSED populations and could be considered distinct population segments (ESUs) under the American ESA or wildlife species under the Canadian SARA. At least some lake sockeye populations would be considered closed populations, raising the possibility that multiple sockeye CUs might exist within single lakes. This definition of LOCAL and CLOSED populations also means that every CLOSED population comprises at least one LOCAL population. In other words, the sockeye population of a lake can be both a Conservation Unit and a SARA wildlife species. If the effective size of a population is large and/or selection is strong then local adaptation can persist even in the presence of considerable gene flow. This appears to be the case with pink salmon in at least some situations (Seeb et al. 1999), which would imply that in some circumstances SUBPOPULATIONS would be also considered CUs.

Units of conservation & definitions* from Wood & Holtby (1998)	Correspondence of WSP Conservation Units and species differences
DEME: An interbreeding group of organisms (without genetic connotations)	
GENODEME: The smallest detectable unit of genetic population structure. Gene flow between genodemes is large such that genetic drift and/or migration preclude local adaptation within the genodeme for typical selection coefficients ($\Phi^{\dagger}$)	
SUBPOPULATION: A group comprising one of more genodemes that is partially isolated from other such groups ($N_e m>10$)§. Local adaptation may exist if N_e and Φ are sufficiently high	
LOCAL POPULATION: A group comprising one or more subpopulations that is relatively isolated from other such groups ($N_e m<10$) and that is probably locally adapted.	
CLOSED POPULATION: A group comprising one or more populations that is almost completely isolated from other such groups ($N_e m<1$) such that its genetic diversity is at risk through random genetic drift when reduced to low abundance.	



* The definitions presented here employ estimates of gene flow expressed as the product $N_e m$. Gene flow is a continuous variable and so the boundaries of the different units must be considered as approximations or guidelines rather than as inflexible

† Φ is a measure of the "strength" of natural selection. Selection produces a directional or non-random change in gene frequencies to produce a locally-adapted genotype. Selection is obscured by random or non-directional changes that are produced either by migration (gene-flow) or by random genetic drift.

§ N_e is the genetically effective population size, a number usually substantially lower than the number of reproductive organisms. m is the migration rate. Their product, $N_e m$, is the effective number of migrants per generation and is a measure of gene flow.

It is not necessary, however, to define the Conservation Unit quantitatively, although such a definition does serve to position, approximately, the CU in the continuum of relatedness that exists between genodemes. For example, the operational definition of the Designatable Unit of COSEWIC involves expert consensus on demonstrable distinctiveness along axes of taxonomy, phylogeny, biochemical genetics, and/or biogeography.

The WSP's definition of the Conservation Unit also includes a temporal constraint by stipulating that a loss of diversity should be reversible within a reasonable time. After an extirpation occurs, recolonization and evolution of an adapted genotype would take time. We know that the diversity of salmon now present within Canada has appeared since the last glaciation or within the last 15,000 years (McPhail and Lindsey 1970). In Tustumena Lake, an Alaskan lake that has essentially been created through glacial rebound within the last two thousand years, invading sockeye have quickly adapted to the new habitat, perhaps to the extent of becoming a local population (Burger and Spearman 1997). While in geological time, local adaptation has taken the proverbial blink of an eye, in human terms it has required a third of our species' recorded history. There are other examples involving sockeye that indicate much more rapid adaptation, but in all cases these involved repeated human intervention (Burger et al. 2000, Hendry 2001). Pink, coho and chinook salmon have been successfully introduced into the Great Lakes and now reproduce naturally in many areas but only pink appear to be self-perpetuating. Chinook salmon were successfully introduced into New Zealand over a century ago and are now self-perpetuating (McDowall 1994). However, attempts to introduce Pacific salmon elsewhere, both within and outside their natural range have generally met with consistent failure (Withler 1982).

This and similar evidence led Waples et al. (2001) to concluded that "*<u>local</u> populations of Pacific salmon are not replaceable over ecological time frames. Empirical evidence indicates that if a local population is lost, it is not likely to be replaced (even with active human intervention) within a time span of interest to humans*" (p. 20). The amount of time necessary is likely dependent on a large number of factors but would almost certainly be proportional to the degree of isolation that existed prior to the loss. In other words, a SUBPOPULATION should reestablish more quickly than a LOCAL population. If so, then the definition of the Conservation Unit implies that the intent of the WSP is to protect diversity at as "fine" a level in the diversity continuum as is possible. This suggests that when possible, diversity should be characterized and protected below the level of the LOCAL population.

In summary, the Conservation Unit is a tool for describing diversity at a level for practicable implementation of the Wild Salmon Policy. While it would be possible to define the CU quantitatively in terms of levels of gene-flow, degree of reproductive isolation and local adaptation, we think it will ultimately be more useful to provide a method that positions the CU approximately on the biological continuum and facilitates the provision of consistent, objective and transparent advice about the state of diversity and the significance of salmon populations to that diversity.

4. Methodology

Waples et al. (2001) characterized diversity in Pacific salmon in the American Pacific Northwest along three major axes: life history, ecology and biochemical genetics. Our task, as we laid it out in the previous sections, is somewhat different, in that we want to use characterizations of intraspecific diversity to compartmentalize that diversity into units for conservation. From our perspective, the axes of Waples et al. (2001) are more akin to tool sets that allow us to map local adaptation, which is what we actually want to conserve, in a variety of ways. We then examine and combine the maps to locate and describe the units of conservation. Waples et al. (2001) have demonstrated that the three tool sets provide very similar results for Pacific salmon at least at the geographic scales that both they and we are considering. That is important because each tool has both strengths and weaknesses and often data limits the application of at least one of the tools in a particular area. Those shortcomings can be overcome with a toolbox outfitted with interchangeable and complimentary tools.

Life histories or more broadly phenotypic characters <u>are</u> adaptations and intraspecific variations in these characters, if genetically determined, are local adaptations. Phenotypic variation can also result from interactions between the environment and the genotype (Adkison 1995) although recent studies suggest that genotypic effects predominate (e.g. Keeley et al. 2007, Marcil et al. 2006). Within the Pacific salmon some forms of intraspecific variation in life history, such as whether your young rear in a lake, a river or the ocean, aren't so much local adaptation as they are high-level strategies for survival. Such distinctive variants could readily be recognized as species or subspecies. For example, the stream-type and ocean-type chinook in the Columbia River have all of the attributes of distinct species (Waples et al. 2004) and were consequently considered to be ESUs (Myers et al. 1998, Waples et al. 2001). Certainly, adaptations of such magnitude must be described and protected. However, there are many other forms of variation that constitute direct evidence of local adaptation and which are worthy of consideration as defining characteristics of Conservation Units.

The other two axes use different approaches to detect the conditions in which local adaptation is likely to persist. Neither approach actually demonstrates local adaptations. The ecological approach hypothesizes that since local adaptation is adaptation to local conditions that determine survival and reproduction, where there are differences in those conditions there will also be local adaptation. Therefore, the ecotypic approach seeks to describe "ecological adaptive zones". The biochemical genetics approach seeks to identify populations that are either sufficiently isolated reproductively from other populations for local adaptations to persist or are behaving genetically as if such local adaptations do exist.

Wood and Holtby (1998) applied the biochemical genetics approach to chinook and coho salmon in the Skeena River drainage. They concluded that the spatial extent of CUs for both species were the major subdrainages and subsequently showed that that spatial scale is concordant with an ecotypic characterization of the drainage (unpubl. data LBH). Although such observations are supportive of the conclusion of Waples et al. (2001) that the three approaches are interchangeable, the strength of any argument is increased wherever multiple approaches suggest the same population structure.

4.1 Diagrammatic overview of the methodology

Figure 1is a diagrammatic summary of our methodology. The first step of the method involves the description of freshwater and marine ecological adaptive zones for Pacific salmon. These two ecotypic characterizations are then merged to form a third ecotypic characterization that we termed the Joint Adaptive Zone. (JAZ) (Section 4.2).

The second step of our procedure involved excluding the JAZ where a species was not found (Section 4.3). Each of the remaining JAZ would be considered a putative Conservation Unit. This determination was straightforward where there were well-documented records of continuous presence of spawners. However, in some cases we could not be certain if a species was present within the JAZ. We used a categorical approach to the determination of a species within a JAZ as shown in the following table. In those cases where the presence of a species was characterized as "probable" but where there were no identified sites within the JAZ for that species, a site (an Annual Escapement Waterbody[13] or AEW) was assigned to the species. This situation most commonly arose in the smaller northern transboundary rivers and so the assigned AEW was the mainstem of the largest river.

For sockeye and pink salmon, we partitioned the populations into the two major life-history types found in each of those species. Odd- and even-year pink salmon have been nearly completed isolated reproductively that they have many of the characteristics of subspecies. The lake- and river/ocean-types of sockeye are not nearly so isolated but our characterization of the diversity within the two types is quite different. Consequently, partitioning them at this point in the analysis facilitated their different treatment. We do not seek to impute any taxonomic stature to the two life history types. These divisions are discussed more fully in the sections on the two species. At this point in the analysis, we also considered separating chinook salmon into its two major life history types, ocean- and stream-types (Waples et al. 2004). We decided not to make such a split in part because many populations in Canada are mixtures of the two types and because those situations where the two types are distinctive are fully captured in the subsequent analysis.

categorization of species presence	description	Sufficient to consider the JAZ a CU?
unlikely	We were unable to find any evidence that the species spawns within the JAZ on a persistent basis <u>and</u> the presence of spawning populations would be surprising because of the characteristics of the FAZ. For example, most species are not found in the inland portions of Arctic rivers.	no
possible	We were unable to find evidence that the species persistently spawns within the JAZ <u>but</u> there was no basis to exclude the possibility that the species is present. An example is even-year pink salmon in the Fraser River.	no
probable	There are anecdotal or non-quantitative records indicating the presence of the species <u>or</u> the JAZ is well within the species range but has not been surveyed. The Unuk and Whiting Rivers are examples of such systems.	yes
documented	There are well-documented records of persistent presence. This category was the usual case.	yes

[13] Annual Escapement Waterbodies are geographic descriptors to which escapement counts are associated and are part of the SEDS data system. The AEW are indexed by the GFE_ID.

The result of the second step was a list of known "species"-populations by Joint Adaptive Zone, the most comprehensive of our ecotypic classifications. Each of these species-JAZ units was considered a putative ecotypic Conservation Unit. In the third step of our method, each of those ecotypic CUs was examined for genetic and ecological evidence that might warrant their modification.

First, the ecotypic classification was compared to a biochemical genetic classification (Section 4.4). This comparison was used to detect instances where the ecotypic classification subsumed significant genetic diversity, in which case the ecotypic CU might be partitioned. Conversely, the ecotypic classification might have separated populations where there was no evidence of reproductive isolation, in which case two or more ecotypic CUs could be merged. The ecotype-genetic comparison was also used to examine whether the ecotypic CUs adequately separated major lineages and whether the ecotypic boundaries matched the genetic groupings. Other than partitioning to capture major lineages, partitioning and merging of the ecotypic CUs required additional evidence that the resultant CUs were distinctive and were required to describe local adaptation. That evidence came from an examination of life history differences, differences in spawning time, and other ecological differences (Section 4.5).

Application of these considerations led to species-specific adjustments to the JAZ-ecotypes producing for each species a list of recommended Conservation Units.

4.2 Adaptive Zones and Ecotypology

Environmental typology has been used extensively in plant ecology to describe species assemblages or communities that are co-adapted to particular habitats (e.g., the Biogeoclimatic Zones of British Columbia). The habitats themselves can be characterized using properties that define the principal environmental and biological forces that shape the adaptive environment. For plants, these forces include temperature (minimum and maximum temperatures, length of the growing season) and aridity (amounts, form and pattern of rainfall). Similar arguments can be used for aquatic species such as Pacific salmon. In fresh water, stream temperature, gradient, substrate and hydrology that act in concert to form aquatic habitat types. In the ocean both physical factors such as temperature, depth, and currents and ecological factors such as plankton species assemblages could be used for typology (Longhurst 1998).

Our hypothesis is that Pacific salmon populations found within each adaptive zone, whether it is in freshwater or the ocean, are more likely to be ecologically interchangeable than with populations in different adaptive zones. This assumption is in accordance with both Waples' definition of distinct population segments for application of the American Endangered Species Act (Waples 1991a, 1995) and with subsequent definitions of units for conservation that emphasize ecological exchangeability (Crandall et al. 2000)

The following section discusses a typology of freshwater and marine adaptive zones for Pacific salmon and their use in the delineation of conservation units for Pacific salmon.

4.2.1 Pacific Salmon Freshwater Adaptive Zones

One of the principal challenges in classifying freshwater habitat types is that these systems are dynamic and flowing. The characteristics of a particular stream or lake result from some combination of influences from the local environment and those upstream and upslope. Classifying freshwater habitat types from a Pacific salmon species perspective is additionally challenging as many of these species move over large distances during their year or two in freshwater, exploiting a wide variety of habitats.

The development of freshwater adaptive zones for Pacific salmon was based primarily on a hierarchical ecological classification of freshwater ecosystems in British Columbia - Ecological Aquatic Units for British Columbia (EAU BC) (Ciruna and Butterfield 2005). Hierarchical classifications mirror the generalization that freshwater habitats and their biological components are shaped by a hierarchy of spatial and temporal processes (Angermeier and Schlosser 1995, Angermeier and Winston 1999, Frissell et al. 1986, Imhof et al. 1996, Mathews 1998). Use of a hierarchical scheme allows the classification to capture the multitude of spatial and temporal scales on which structuring processes operate. For example, patterns of continental and regional freshwater zoogeography result from drainage connections that change over time in response to climatic and geologic events (Bussing 1985, Hocutt and Wiley 1986). Importantly, regional patterns of climate, drainage, and physiography influence river ecosystem characteristics such as morphology and hydrology, temperature and nutrient regimes, which in turn influence biotic patterns of community composition and species abundance (Hamilton 1999, Hughes and James 1989, Moyle and Ellison 1991, Pflieger 1989, Poff and Ward 1989, Poff and Allan 1995, Swanson et al. 1988). At finer spatial scales, patterns of stream, lake and wetland morphology, size, gradient, and drainage network position result in distinct freshwater assemblages and population dynamics (Angermeier and Schlosser 1995, Angermeier and Winston 1999, Frissell et al. 1986, Higgins et al. 2005, Hyatt et al. 2000, Labbe and Fausch 2000, Mathews 1998, Maxwell et al. 1995, Pringle et al. 1993, Seelbach 1997, Tonn and Magnuson 1982).

The use of hierarchical classification schemes for freshwater ecosystems is widespread and has an extensive literature. Some of the important concepts and frameworks developed for freshwaters can be found in Warren (1979), Frissell et al. (1986), Cupp (1989), Pflieger(1989), Moyle and Ellison(1991), Leach and Herron(1996), Hudson et al. (1992), Naiman et al.(1992), Townsend and Hildrew (1994), Ward and Palmer (1994), Angermeier and Schlosser(1995), Maxwell et al. (1995), Rosgen (1994), Seelbach et al. (1997), Pahl-Wostl (1998), Haberack(2000), and Higgins et al. (2005).

The theoretical basis for the EAU BC hierarchy assumes that environmental factors act in a hierarchical manner such that habitat characteristics at lower levels of the classification are, in part, determined by those at higher levels. For example, the morphology of a stream reach may determine whether the hydrologic conditions provide for a particular fish habitat. This factor varies over short sections of the broader river ecosystem. However, the overarching factor, climate, determines water temperature and broadly identifies large-scale areas that are generally suitable for the species. Geology determines whether water chemistry and channel bed material (substrate) are suitable for spawning. Accordingly, the mapped patterns are a spatial hierarchy with patterns at higher levels of the classification becoming fragmented by lower levels of the classification (e.g. Snelder et al. 2004).

EAU BC classifies freshwater ecosystems at four spatial scales (freshwater ecoregions, ecological drainage units, river ecosystems, and lake and stream reaches), based on measurable environmental features and processes. Freshwater ecoregions and ecological drainage units (EDUs) take into account continental and regional zoogeographic, climatic, and physiographic patterns respectively. River ecosystems (mesoscale units), take into account dominant fluvial and geomorphic patterns and processes. Lake and stream reach ecosystems (local scale units), account for local environmental patterns and processes.

EAU BC subdivides continuously varying environmental gradients into independent categories. However, these groups and patterns do not usually exist as distinct separate entities in nature – they are more often a continuum with no discrete boundary or edge. The mapped pattern of classes is a simplification of highly complex ecological patterns and this simplification of reality is important to bear in mind when considering a spatial ecological classification.

4.2.2 Ecological Drainage Units (EDUs)

The development of freshwater adaptive zones for Pacific salmon is based primarily on the second level of the EAU BC - the ecological drainage units (EDUs). EDUs are comprised of river ecosystems that share a common *zoogeographic history* and therefore likely have a distinct set of freshwater assemblages and habitats. Zoogeography is the science that deals with patterns of species distribution and the processes that result in such patterns. The processes important to salmon distribution are primarily glaciation (ice ages), the interactions of land and water (fluvial geomorphology), and climate. These same processes are also the source of habitat variation that drives adaptive variation in organisms and underlies intraspecific diversity in the Pacific salmon. They are therefore central to the concept of the CU.

Our hypothesis is that Pacific salmon populations found within each EDU are more likely to be ecologically interchangeable than with populations in different EDUs (Crandall et al. 2000).

British Columbia is the third largest province in Canada. North to south, it extends over 11 degrees of latitude and has a land area of almost 1,000,000 km^2. Summarizing the distribution of plants and animals in this vast area is a major task. For terrestrial organisms, B.C. uses a system of biogeographic regions based on topography, climate, and plant communities. Unfortunately, such terrestrial biogeographic systems rarely work for freshwater fish because of the limited dispersal abilities of freshwater fish (Abell et al. 2000, Hughes et al. 1987). In a recently glaciated region like B.C., the single most important factor governing what species reached what rivers is the postglacial sequence of drainage connections. Thus, to understand the present distribution of freshwater fishes in B.C., it is first necessary to understand both where the fishes came from and the dispersal routes they followed in achieving their present distributions. Obviously, other factors also are involved. *Physiography* – especially topography features like mountain ranges, canyons and waterfalls, and *climate* profoundly influence the distribution of fishes within the province. Nonetheless, the nature and timing of postglacial drainage connections governed which fishes reached which drainage system, and the presence or absence of primary freshwater fish species define EDUs. Once fish reached a drainage system, their present distribution within the system was determined by factors like barriers, gradient, hydrograph, temperature, water chemistry, and biotic interactions.

Not surprisingly, the Pleistocene expansion and contractions of ice sheets had important impacts on B.C.'s fish fauna. As the late Pleistocene ice sheets expanded to cover most of northern North America, the interglacial fish fauna in B.C. was either destroyed or pushed into unglaciated regions called *refugia*. Thus, the freshwater fish that were present in B.C. during the last interglacial period probably survived the last glaciation – the Fraser glaciation, in one or more of the three major ice-free refugia adjacent to the province. The unglaciated region south of the ice and west of the Continental Divide is referred to as the Columbia Refugium. The unglaciated portions of the Columbia River system were major contributors to B.C.'s freshwater fish fauna. However, the coastal areas south of the ice sheet, and south of the Columbia River, also were important for euryhaline fishes such as Pacific salmon. The combined Columbia River and south coastal unglaciated areas are collectively referred to as the *Pacific Refugium*. Similarly, McPhail (2006) refers to the unglaciated regions south of the Laurentide Ice Sheet and east of the Rocky Mountains as the *Great Plains Refugium*. This is a combination of two semi-independent refugia: the Missouri Refugium and the Mississippi Refugium. The third unglaciated area adjacent to B.C. is the *Bering Refugium* (the ice-free regions of Alaska and the Yukon). A small number of species found in the north-western part of our province dispersed into B.C. from this refugium (McPhail 2006).

EDUs contain one or more species that unequivocally align them with one of the five major aquatic ecoregions, and at least one species that is not found in adjacent EDUs within the same ecoregion or subregion. Hocutt and Wiley (1986), Haas (1998), McPhail and Carveth(1993), and McPhail (2006) were used to delineate EDUs based on zoogeographic patterns of freshwater fishes in BC. Subsequently EDUs were further refined based on physiography and climate such that each EDU contains sets of freshwater system types with similar patterns of *climate, drainage density, gradient, hydrological characteristics and connectivity.* Physiographic and climatic patterns were derived from the analysis of BC provincial watershed atlas and associated hydrologic, climatic and physiographic information for third order watersheds throughout the province.

Thirty-six EDUs were delineated in BC but not all of them have populations of Pacific salmon. For that reason the Similkameen, Kettle, Clark Fork – Flathead, Upper and Lower Kootenay, Great Lakes – Columbia Mountains, and Columbia – Kootenay Headwaters Upper Liard, Upper Stikine, Lower and Upper Peace, and the Hay EDUs were unnecessary for our classification. Some EDU boundaries were further refined based on finer-scale hydrology and temperature data to conform more closely to what we think salmon specifically are responding to in their freshwater habitats. The Lower Fraser EDU was split into the Lower Fraser FAZ and the Lillooet FAZ. The Rivers-Smith FAZ, the Hecate Lowlands FAZ and the Unuk River FAZ were all split out of the large and geographically heterogeneous North Coastal Streams EDU. The result is a scheme with 31 Pacific salmon FAZs in BC. A map and descriptions of these FAZs are found in Appendix 1.

4.2.3 Pacific Salmon Marine Adaptive Zones

Marine environments pose similar challenges in terms of typology as those presented by freshwater systems. They are dynamic and flowing systems influenced by salinity and temperature gradients and underlying physiography. There have been several broad scale marine ecosystem classifications undertaken (Sherman and Duda 1999, Ware and McFarlane 1989). However, only one to date has focused on marine ecosystems from the perspective of typing Pacific salmon habitat. Augerot et al. (1999) developed a four-stage hierarchical classification to divide the North Pacific Rim into *salmon ecoregions.* Salmon ecoregions are defined as watershed-coastal ecosystems of distinct physical characteristics, including the full sequence of riverine, estuarine, and near-short marine habitats used by juvenile anadromous salmonids. They were defined using several existing classifications of marine circulation systems and production domains (e.g., Ware and McFarlane 1989; Sherman and Duda 1999) as well as international expert consensus.

Augerot et al. (1999) used the Environmental Systems Research Institute's (ESRI[14]) digital chart of the world (DCW) to provide a digital geographic representation of the entire North Pacific Ecosystem, to identify the stream networks and spatial boundaries of each salmon ecoregion, and to establish a geographically explicit data management system for stock status information. ESRI's DCW was produced from aeronautical charts produced by the US Defense Mapping Agency[15] at a scale of 1:1,000,000. The geospatial database of the DCW is divided into 2074 "tiles" that represent 5-degree-by-5-degree areas of the globe.

To define the geographic boundaries for each salmon ecoregion in GIS, Augerot et al. (1999) drew digital polygons around the stream networks associated with each of the four levels of the salmon ecoregion hierarchy. Although some inconsistencies in the densities of stream networks were apparent where separate tiles were merged to create the integrated DCW stream layer, these had no significant impact at the resolution of the analysis.

The following are the four levels of the classification:

Level 1. Contains two ecoregions, the Arctic Ocean and the Pacific Ocean with associated freshwater drainages.

Level 2. Semi-enclosed seas and primary ocean circulation systems with distinct processes or bathymetric characteristics in the North Pacific (similar to the Large Marine Ecosystems defined by Sherman and Duda 1999), and associated freshwater drainages. There are two Arctic Ocean and 16 Pacific Ocean regions defined at this level.

Level 3. Finer-scale coastal discontinuities within each semi-enclosed sea or major circulation system including fjords, straits, and areas with distinct production processes (e.g., areas of upwelling and downwelling). There are three Arctic Ocean and 36 Pacific Ocean regions defined at this level.

Level 4. Major drainage basin networks equal to or greater than the area of the Kanchalan River (22,230 km^2) entering each Level 3 coastal area. There are 14 Arctic Ocean and 52 Pacific Ocean ecoregions defined at this level.

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[14] http://www.esri.com; 380 New York Street, Redlands, CA 92373-8100

[15] see http://en.wikipedia.org/wiki/National_Geospatial-Intelligence_Agency

We use level three of the classification to delineate Pacific salmon CUs. To do so we first transferred the geographic boundaries of the ecoregions to a 1:50,000 base map using natural geographic boundaries such as Cape Caution and Brooks Peninsula as necessary.

There are twelve salmon ecoregions in BC. Each salmon ecoregion has at least one CU. For example, the Fraser River, as well as the rivers and streams of SE Vancouver Island and the Sunshine Coast, fall into the Georgia basin salmon ecoregion. Two modifications were made to the level-three salmon ecoregions based on our knowledge of Pacific salmon in BC. First, the eastern boundary of the Vancouver Island Coastal Current ecoregion was moved from just NW of Port Renfrew to approximately Race Rocks in the Strait of Juan de Fuca on the advice of DFO biologists. It was noted that the patterns of survival and run timing of coho and chum in that area were more similar to populations further west on Vancouver Island than they were to populations in the Strait of Georgia. The second change also involved the Georgia Basin ecoregion. A new marine adaptive zone (MAZ) was created in the mainland inlets (Toba Inlet north to Belize Inlet) including Johnstone and Queen Charlotte Straits and the adjacent portions of Vancouver Island. The Puget Sound – Georgia Basin salmon ecoregion was cut in half at the boundary of the Johnston Strait and Georgia Strait to form the Queen Charlotte Strait – Johnston Strait – Southern Fjords MAZ (on Vancouver Island and the mainland) to the north of the Georgia Strait MAZ. The result is a scheme with 13 Pacific salmon MAZs in BC. A map of these MAZs is found in Appendix 2.

We hypothesize that salmon ecoregions characterize the adaptive marine environments for Pacific salmon. This classification describes marine adaptive zones with the same implications to exchangeability as for the FAZs. Populations within a salmon ecoregion are adapted to it and are therefore more fully exchangeable with other populations within that particular zone than with populations from other zones.

4.2.4 Pacific Salmon Joint Adaptive Zones

Pacific salmon Joint Adaptive Zones (JAZ) are the intersection of the freshwater and marine adaptive zones. They are an attempt at capturing the adaptive environment of Pacific salmon populations throughout their full life history. At this point in the analysis, all populations that fall within a JAZ are considered a potential CU (except for lake-rearing sockeye). This means that each JAZ contains at least one CU. There are 33 JAZs in BC. A map of the JAZ ecotypes is found in Appendix 3.

The next step in the process of delineating CUs is the refinement of CU boundaries on a species-by-species basis based on genetic and life history variations including run timing, coast versus interior phenotypic differences, and age at maturity. For sockeye, we examine the dichotomy of rearing habitats and freshwater behaviors dividing the species into lake-type and ocean-types; variations in run timing and spawn timing that reflect adaptations to different spawning locations within single lakes, and age differences due to productivity of the nursery lake.

4.3 Salmon populations

Pacific salmon are (or were) likely found at some time in the year in every stream entering the ocean in British Columbia that does not have an insurmountable barrier, even if the system did not support spawning. For example, during the winter juvenile coho can be found in several small streams near Carnation Creek (in Barkley

Sound, WVI) where no spawning has been observed. These fish apparently move from estuaries and near-shore zones in late fall to over-winter (T. Brown, DFO, Nanaimo, pers. comm.). It would be nearly impossible and certainly not practicable to document all of the locations where salmon are found[16]. We suspect that most of the lake-type sockeye populations and a high proportion of the chinook populations are known. We are far less certain about the remaining species. Since our objective is to describe all of the diversity in Pacific salmon, an ecotypic approach is attractive because it allows us to categorize populations without having to observe them directly. Of course, direct observation is always preferable to any kind of modeling, ecological, genetic, or otherwise.

To describe the distribution of Pacific salmon in BC, we began with the list of "Annual Escapement Waterbodies" (AEW) from the Salmon Escapement Database System or SEDS (E. Grundmann, PBS, pers. comm.) Each of these waterbodies is uniquely identified with a numeric code, the GFE_ID, which we have also used to identify the site. In the snapshot of the SEDS database that we have used there were 2,363 AEW. The persistent presence of Pacific salmon in an AEW was considered documented if one of four conditions was met:

1. SEDS contained at least five escapement records[17] between 1950 and 2006;
2. A genetic sample had been obtained from an identifiable site (i.e., one that could be geo-referenced with confidence). Genetic samples would have been collected from spawning fish in places that individuals with local knowledge knew to support populations.
3. There were records of spawn timing in the stream narrative records housed with SEDS. Field staff often noted the presence of spawning salmon without attempting escapement estimates.
4. Local knowledge presented during public consultations provided evidence of salmon presence in identifiable locations.

There are currently 2,417 waterbodies in our database[18].

The waterbodies themselves are a mix of features, segments of features, groups of features or point locations (e.g. the sites of genetic sampling), where a feature is a stream, a slough or a lake. Counting weirs were also considered waterbodies. Each waterbody corresponds to what has traditionally been considered a population. In our nomenclature adult salmon counted in most of these waterbodies would be considered a topodeme, which is an interbreeding group of organisms occurring in a particular habitat (Wood and Holtby 1998). However, because of historical methods of reporting escapement, some waterbodies are aggregates of topodemes and for some of the lake sockeye sites, the waterbodies are actually closed populations. We did not consider locations where salmon are extirpated. Several of those sites, especially those that are associated with dams, are well documented, but we suspect that others are not. Dealing with the many issues of past extirpations was not within our areas of expertise nor our

[16] It is feasible, however, to develop a GIS-based model capable of predicting which locations could support self-perpetuating populations.
[17] Three records for odd-year and even-year pink salmon. These requirements are approximately 10% of the total durations of the escapement records.
[18] As of 16 January 2008. New sites are being added on a regular basis.

purview. In summary, each AEW should be considered only as a collection of one or more sites where spawning salmon have been regularly present within the last 50 years.

We then georeferenced each of the sites by associating it with its appropriate stream reach or lake and broader third order watershed unit in the BC Watershed Atlas at a map scale of 1:50,000. This scale proved inappropriate for the Queen Charlotte Islands where many of the streams are too small to be captured. Consequently, for the Queen Charlottes we associated each of the sites with its appropriate stream reach or lake and broader third order watershed unit in the Terrain Resource Information Management (TRIM) watershed layer at a map scale of 1:20,000. There are a small number of sites that we were unable to locate precisely because of the inadequacy of the descriptions available to us. These were either georeferenced to a location that we believed to be within a few kilometers of the actual location or, rarely, were excluded from the site list.

Describing sockeye sites required particular attention because of the presence of two distinct life-history types[19]. To determine whether a waterbody likely supported lake- or river-type sockeye, for each known sockeye location we consulted DFO stream catalogues to determine where sockeye had been seen in the system. If sockeye were seen either at the lake outlet, in the lake or above the lake, and if the lake was larger than approximately 50 ha[20], then the population was considered of the lake-type otherwise it was considered river-type. In many cases the stream was either not in the stream catalogue or (more usually), there was no mention of sockeye spawning or presence in the stream narrative. In those cases we then examined a 1:50 000 topographical map of the system. If the lake met the minimum size requirement and if the stream narrative indicated that other species could reach the lake, or, in the absence of such information, that there was no evidence of waterfalls, cataracts, or abrupt elevation changes, then the sockeye were assumed lake-type.

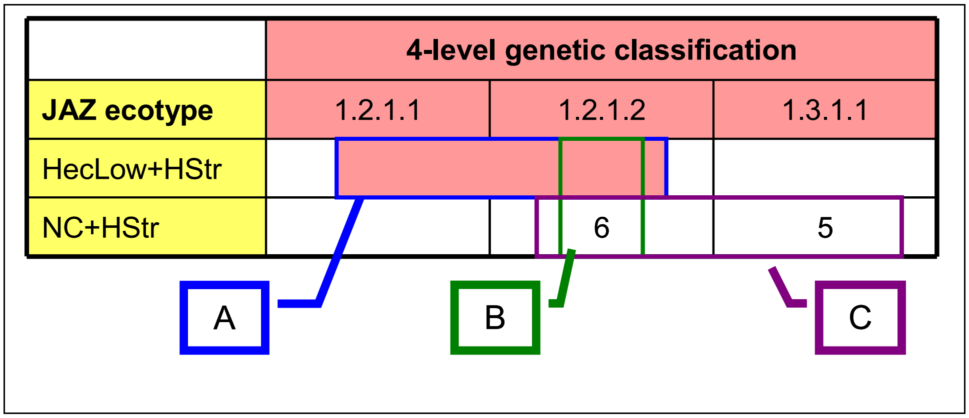
4.4 Crosswalking the ecotypic and genetic population classifications

We compared our ecotypic characterization of Conservation Units with neutral genetic structure for all species. Terry Beacham and the PBS Genetics Lab provided us with unrooted neighbor-joining trees based on Cavalli-Sforza and Edwards (1967) chord distances between populations calculated using 10 or more microsatellite loci. The trees for chinook and sockeye salmon have been published in the primary literature (Beacham et al. 2006a, Beacham et al. 2006b) and complete details of the data sets, genetic and statistical methods used to generate those trees are detailed there. The remaining trees are unpublished and were computed from similar datasets using the same methods (T. Beacham, pers. comm.)

To begin the comparison we first described the major groupings of populations based on genetic relatedness using a hierarchical genetic classification derived from the neighbor-joining trees (dendrograms). This process is illustrated in Figure 3. First, we set the maximum number of levels in the hierarchy to five. We then rearranged the dendrogram to form a stick diagram to make it easier to see site groupings. The unrooted tree was then traversed recursively, assigning a new level at each bifurcation. Where there was clear evidence of a geographic cline a sequence of bifurcations was assigned to a single level in the hierarchy. Such sequences frequently occurred in large river

[19] We did not consider kokanee, the third life-history type.
[20] Considered the minimum area to support a self-perpetuating lake-type population (K. Hyatt, PBS, pers. comm.)

systems where sampled populations were related by distance. Where alternative groupings were plausible we were guided by the relative genetic distances between the groups that would be formed. Those distances were approximately calculated from the sums of chord lengths in the dendrograms. We found that, in general, the third or fourth level of five-level hierarchies captured the major population groupings. We then determined the ecotype (i.e., the JAZ) of each population in the genetic sample and cross-tabulated the ecotypic and genetic classification as shown in the following diagram.



The numbers in the body of the table are the number of genetically sampled populations in each genetic classification (column) that have the ecotype shown in the row. A four-level hierarchical classification was used in this example. All sites were in the same group (group 1.) at the first level while there were two groups at the second level (groups 2 and 3), and so forth. The sites fell into two JAZ ecotypes

The blue box "A" indicates that in the first ecotype (HecLow+HStr) there were four sites (populations) falling into two fourth-level genetic groups. In most circumstances, this was considered strong concordance of the two classifications, although we sometimes examined the two genetic groups to determine if there were ecological and/or life history differences between them. To do that we used our set of ecological variables (see 13) and forward-stepping discriminant analysis (SYSTAT Software 2005, Statistics I, p310-315). If there were significant differences on either axis then the ecotypic CU would be split into two CUs, even though they were genetically similar. The purple box "C" indicates that of the 11 populations in the NC+HStr JAZ ecotype, six were in one level-2 genetic group and five were in another level-2 genetic group. Since a level-2 group would invariably have been considered a major genetic group, this situation represents a lack of concordance in the two classifications where the ecotypic classification was too coarse, i.e., that it had not captured diversity to the level we desired. We would have concluded that two CUs were present. In some cases, there were several level-2 genetic groups present and we concluded that the species was particularly diverse within that JAZ ecozone and that more than two CUs were present. We also determined if we had the situation represented by the green box "B". Here a genetic class, 1.2.1.2, is split between two JAZ ecotypes. In almost every such case the sites within one of the ecotypes were (geographically) close to the adjoining ecotype boundary and that the apparent disagreement between the genetic and ecotypic classifications could be resolved with small species- and, in most cases, site-specific adjustments to the ecotype boundaries.

The ecotypic classifications were also compared to the major lineages for each species as revealed by the genetic classification and the literature. However, since the ecotypic classification considers zoogeographic history there were no instances where there needed to be refinement to the CUs based on genetic lineage.

4.5 Life-history and further ecological considerations

In situations where the biochemical genetics analysis suggested significant population structure within the ecotypic zones used to define CUs, further ecological characteristics were examined to determine if the genetic structure corresponded to ecological patterns.

Ecotypic and biochemical genetic approaches to defining CUs are indirect. Ecotypic approaches describe adaptive environments to which, it is hypothesized, fish are adapted. Biochemical approaches involve inferences about levels of gene flow and to the persistence of local adaptation. Phenotypic variation that, in general, has been shown to be genetically based, can serve as a direct diagnostic of adaptive and heritable diversity.

4.5.1 Further ecological considerations

A set of hydrological, thermal, and physiographic variables was used to describe environmental conditions at the level of the third-order watershed (see Appendix 5). Further ecological considerations were made in the situation where the ecotypic×genetic crosswalk indicated that there were two or more major genetic groups within an ecotypic CU. We used step-wise discriminant analysis to construct environmental models that separated the genetic groups. This step was applied sparingly. In most cases, the sample sizes were usually less than 10 sites in total and the models that resulted were difficult to interpret biologically.

4.5.2 Life-histories

In both sockeye and chinook salmon there are a number of life-history variants that can be used as direct diagnostics of adaptive variation. Chinook variations of interest are smolt age (0^+ vs. $\geq 1^+$) and adult migration timing (spring/summer vs. fall). Unlike variations in smolt age in coho salmon, which appear to be largely environmentally determined, smolt age in chinook is fixed or at least nearly so. In addition, there are other differences between populations with different smolt ages. Sockeye variations of interest are adult migration timing (in the Fraser four timing groups have been the basis for fisheries management) and juvenile life history (three forms, ocean/river rearing [anadromous], lake rearing [anadromous] and lake-rearing [non-anadromous]). The life histories of pink and chum are invariant, and known life history variants in coho are not sufficiently established in the literature to be used at this time. However, lake-type and early migrant types could be recognized later as the basis for describing additional CUs.

4.5.3 Spawn-timing

While counting fish on the spawning grounds, Fisheries Officers and Guardians noted the dates when fish were first observed on the spawning grounds, when spawning ground counts peaked and when spawning had ceased. The SEDS data system contains spawning time records for most of the AEW in British Columbia except for the northern transboundary rivers. Our treatment of these data is outlined in 13.

Spawn timing is clearly a local adaptation. The thermal requirements for hatching and emergence, although somewhat species specific, appear to be relatively invariant (Beacham and Murray 1990). The synchronization of emergence with both local and regional conditions such as food availability or hydraulic conditions is likely highly adaptive (e.g. Holtby et al. 1989). One might suppose then that given inflexible thermal requirements for development and a date for emergence that, on average, maximizes fitness, then selection would act to tune spawn timing to those average and site-specific conditions. Hence, spawn timing is an important component of local adaptation. Although spawn timing might vary among sites, if, under identical conditions, fish from different sites spawned at the same time, then spawning time could be a facultative response to local conditions. If so, then fish moving between sites could spawn at the appropriate times and would be considered ecologically interchangeable on at least this particular axis of adaptation. In the absence of the "common-garden" experiments needed to demonstrate the environmental component of spawn timing, we could not examine this possibility directly. Instead, we fit regression models using spawn time as the independent variable and a suite of physical variables mostly associated with temperature. We reasoned that deviations from that common model were interpretable as site-specific adaptations, and hence that both spawn timing and model residuals could be used together to characterize CUs.

4.5.4 Potentially important diversity that was not considered

Elements of diversity that were not considered were those for which there was no comprehensive data. These components of diversity fall into the three general categories of ocean distributions and ecology, migration (run) timing and small-scale spatial and temporal diversity.

<u>Ocean distribution and ecology.</u> Catch distributions for coho and chinook salmon, the two species that have been widely tagged with site-specific methodologies (principally coded-wire tags (Jefferts et al. 1963) are known for most of the Pacific/Yukon Region and are well known in the south where most of the hatcheries (i.e., tagging and release sites) are located (e.g. Johnson and Thompson 1989). When these data have been analyzed on a coast-wide basis, they suggest broad spatial groupings of sites on scales similar to those of our Marine Adaptive Zones (e.g. Committee 1994, Healey 1978, 1983, Weitkamp and Neely 2002). Despite the massive coded-wire tagging effort for coho and chinook over the past three decades, site-specific information for ocean distributions is far from comprehensive and for that reason, we would have been unable to detect fine-scale spatial diversity except through chance. For example, the lake-type coho of the upper Cowichan (Swain and Holtby 1989) have a catch distribution that is very dissimilar to other coho populations around the Strait of Georgia (Holtby 1993). While the significance of that difference is arguable (see the following section on fine-scale spatial diversity), it was detected only because of a short-term wild-tagging program at Mesachie Creek (Birch and Langston 1989, Burns 1989, Taylor 1987, Taylor and Lane 1990). Such diversity presumably exists elsewhere. Furthermore, catch distributions provide little information about site-specific movements and distributions of juvenile fish in the year or years before maturation. For example, the movements of juvenile coho originating around the Strait of Georgia that underlie the profound shift in

the catch distribution that first occurred in 1991 and every year since 1994 (CoTC 1994) remain unexplained despite considerable speculation (e.g. Beamish et al. 2000). For the other species, for which there have been no coast-wide site-specific tagging programs, little is known about site-specific ocean distributions beyond general migratory patterns.

Migration timing Differences in migration timing, both emigration and immigration, are undoubtedly important components of diversity and where information is available have proven instrumental in demonstrating or elucidating population structure (e.g. Candy et al. 2002, Hodgson and Quinn 2002, Stewart et al. 2006). Where such information was available and comprehensive it was used in combination with the primary ecotypic and genetic information. However, timing information in fisheries was generally not used because the site-specific composition of the catch usually was poorly defined.

Diversity at spatial and temporal scales "finer" than those we have used. Adaptive and heritable variation exists at spatial and temporal scales finer, and perhaps much finer than those that we use in characterizing diversity. For example, Tallman and Healey (1994) demonstrated adaptations by chum salmon to temperature regimes in reaches of small coastal streams and there are now numerous studies showing adaptive spatial and temporal diversity within single rivers (e.g. Hendry and Day 2005, Neville et al. 2006, Primmer et al. 2006, Stewart et al. 2006).

We accept that there is adaptive, heritable diversity that is not taken into account in our characterization of CUs. For us, the question was what to do about it. We note that there are practical constraints that limit the extent to which diversity could be protected. There are limits to the resources available to identify, monitor, and protect fisheries resources, Pacific salmon are but one of many such resources, etc. Since the Wild Salmon Policy commits DFO to report on the status of all CUs, the limits of what is practicable cannot escape our attention. We did not respond to the limits of the practicable by limiting the number of CUs that we identified. Instead, we developed a method that characterizes diversity in a manner that we believe is consistent with currently accepted levels of best practice for both assessment and management. Our method is based on a characterization of the adaptive environment of Pacific salmon coupled with genetic structure and broad and general adaptations to their habitats. Fine-scale diversity is acknowledged but is not used to describe CUs unless such use resolves differences between the ecotypic and genetic characterizations. To that end, we did not generally consider diversity of the sort identified by Tallman and Healey (1994), among others, as sufficient to recognize a CU.

4.5.5 CU names

Names are important not only because they enable communication but also because they facilitate understanding. In most cases CUs were named by geographical location using the FAZ as far as possible and where necessary by life-history type or by some other distinguishing characteristic such as run timing. In some cases where a CU consists of a single site ("population") the river or lake name was used. All known sites were assigned to a CU based on geographical location and known characteristics of the salmon. Lists of sites are unlikely ever to be exhaustive, particularly for chum, pink, and coho salmon. However, the following descriptions of how the method was applied to each of the species should permit novel sites to be readily categorized.

5. Pink Salmon

5.1 Distribution

The pink salmon (*Oncorhynchus gorbuscha*) is the most abundant of the Pacific salmon. Persistent pink salmon populations are found in coastal streams from the Olympic Peninsula and Puget Sound to Point Barrow on the Beaufort Sea (NW Alaska). In North America, the most southerly populations were reported from the Sacramento River of California but pink salmon in California and coastal Oregon and Washington are now believed to be extirpated or nearly so (Hard et al. 1996). Historically, pink salmon have been reported from the Mackenzie delta (McPhail and Lindsey 1970) and while more recent studies cited by Heard (1991) failed to find pink salmon in Arctic Canada, the species is listed as part of the fauna of the area[21]. In Asia, pink salmon have a very similar latitudinal and longitudinal distribution (Heard 1991).

5.2 Life History

Pink salmon have several distinguishing characteristics including small adult size, a single age of maturity, minimal time in fresh water, and dramatic sexual dimorphism as sexually mature adults. The fixed single age at maturity is of particular interest to describing Conservation Units. Throughout North America, pink salmon have a fixed two-year life cycle and because of this “even-year” and “odd-year” brood lines are completely reproductively isolated (Heard 1991). Both races are found throughout most of the species range but there are intriguing and unexplained geographical patterns in their relative abundance. In Puget Sound, SE Vancouver Island and the Fraser River, even-year pink are either absent or quite rare. Even-year and odd-year pink are of generally equal abundance throughout the rest of Pacific Canada with the exception of the Queen Charlotte Islands, where even-year pink predominate. Even-year pink also predominates in NW Alaska. A similar latitudinal pattern seems to occur in Asia (Heard 1991).

Pink salmon are reputed to stray at higher rates than other Pacific salmon (e.g. Horrall 1981) but the evidence to support this assertion is weak. The evidence summarized in Heard (1991) and Hard (1996) strongly indicates that pink salmon home with high fidelity to their natal streams, as do other salmon species. Pink salmon do show a tendency to colonize new habitat when populations are large as they have recently done in the Fraser River but this characteristic is also seen in other species such as coho (e.g. Nickelson and Lawson 1998). In recent studies of straying in pink salmon Mortensen et al. (2002) and Thedinga et al. (2000) found moderate straying rates between local streams (~8%). Much higher straying rates have been observed in Prince William Sound (Seeb et al. 1999), but those are at least partially explained by the preponderance of intertidally spawning populations in the Sound, which apparently have higher straying rates than riverine spawners (Thedinga et al. 2000). We note that these estimates of straying rates are demographic rates and may exaggerate actual gene flow (Tallman and Healey 1994). Importantly, there is considerable stable genetic structure in Prince William Sound pinks that persists in the face of apparently high straying rates (Thedinga et al. 2000). Perhaps most informative about the plasticity of pink salmon is that transplants of this species have proven no more successful than for other species such as sockeye (Heard 1991, Withler 1982).

[21] Pink are present in the Mackenzie River delta: http://www.dfo-mpo.gc.ca/regions/CENTRAL/pub/fact-fait-ogla-rglo/pinksalmon_e.htm

The only other variation in pink salmon that is relevant to the determination of Conservation Units that we are aware of are the morphological differences between pink salmon from small coastal streams and large rivers (Beacham et al. 1988b). Fish from large rivers were larger and more robust compared to individuals from smaller systems. Similar differences have been observed in other species. Such temporally stable differences would seem to further caution against inferring an absence of adaptive variation from the high levels of gene flow that have been estimated (e.g. Olsen et al. 1998).

5.3 Ecotypic CUs

Pink salmon are absent only from the most inland of the JAZ ecotypes (even-year: Figure 4, odd-year: Figure 5) and from the northern rivers including the Alsek. In most of the areas where they are present the species is found in most of the surveyed streams (even-year: Table 1, odd-year: Table 2). The presence of sustaining populations of even-year pink salmon in the Fraser River and its tributaries is uncertain but is certainly possible. Escapement records are lacking but there are spawn timing data and even-year pink salmon are present in 22% of the sites on the mainland side of Georgia Strait (Figure 4, Table 1). There is little doubt that both even- and odd-year pink salmon are present in all of the northern transboundary JAZ except the Alsek River, although there are no SEDS or timing data for most of those sites. We do not know why pink salmon are apparently absent from the Alsek River and its tributaries. Including all of the JAZ where we concluded that presence is probable, there are 25 ecotypic CUs of even-year pink salmon pink salmon (Table 1) and 32 ecotypic CUs of odd-year pink salmon (Table 2).

5.4 Genetic population structure

Beacham et al. (1988b) examined the two broodlines in British Columbia for differences in a small number of morphometric characters. Although some significant differences were found, their general conclusion was that pink were morphometrically more similar within regions than within broodlines. However, gill raker counts were significantly different between broodlines and showed parallel latitudinal variation, with more gill rakers in the odd-year broodline and in both broodlines, more gill rakers in northern populations. These patterns have no obvious explanation but suggest some unknown difference in habitat or prey items that favors differences in gill raker counts.

Numerous studies using allozymes and molecular genetics have confirmed the nearly complete reproductive isolation of the odd-year and even-year broodlines (e.g. Beacham et al. 1985, Beacham et al. 1988b, Churikov and Gharrett 2002, Noll et al. 2001, Shaklee and Varnavskaya 1994). The demonstration by Smoker and Gharrett (1991) of outbreeding depression in the second-generation hybrids of odd-year and even-year pink from Auke Creek Alaska strongly suggests that the two broodlines should properly be considered, if not sister species, then at least races. Consequently, we have decided to treat odd-year and even-year pink as separate races for establishing Conservation Units under the WSP.

Beacham et al. (1988b) concluded that there were three regional groups of even-year pink salmon with British Columbia. The Queen Charlotte Islands group was the most distinctive of the three. One of the other groups was quite large extending from the Nass River in the north to the Bella Coola in the south and included the Skeena and Nass Rivers. The last group included the South Coast (mainland portions around the Strait of

Georgia) and NE Vancouver Island. No populations from the northern transboundary rivers or WVI were included. The one population from the extreme NW of Georgia Strait (Quinsam) grouped with other NE Vancouver Island populations. For the odd-year race, no samples were included from the Queen Charlotte Islands and two regional groupings were found, which corresponded roughly to the two groups in even-year pink salmon. The southern group included the Fraser and Thompson Rivers, NE Vancouver Island and the south coast to Loughborough Inlet. The third group included the central and north coasts from Knight Inlet north.

The latest microsatellite dataset (Figure 6; Beacham et al. unpublished data) seems to present a population structure that is largely unstructured geographically for even year pink (Figure 7, Figure 8) but similar to previous descriptions for the geographic structure of the odd-year race (Figure 9, Figure 10). Furthermore, the genetic population structure does not have the characteristics that one associates with episodic extirpation associated with glaciation and recolonization (i.e., high levels of latitudinal or longitudinal geographic structure), or with high levels of gene flow inversely related to distance (i.e., direct relationship of genetic and geographical distances).

In even-year pink salmon, we identified eight genetic clusters (Figure 7). Our genetic cluster D corresponds to the Queen Charlotte group identified by Beacham et al. (1988b). The remaining clusters correspond to the northern and central group of Beacham et al (1988b), but it would be misleading to call this a cohesive group since most of the clusters span the coast (Figure 8).

When the genetic groups are compared to the JAZ ecotypes (i.e., when the geographical extent of the genetic clusters is examined), there is very little commonality between the ecotypic and genetic population structures (Table 4). Only the sites on the Queen Charlotte Islands are largely distinctive both genetically and geographically (Table 4, Figure 8). The NC+HStr and HecLow+HStr JAZ ecotypes are particularly diverse genetically having representatives from almost all of the genetic clusters (Table 4). Except for the clusters with single members, cluster membership is widely spread across the coast (Table 4, Figure 8).

We identified 16 genetic clusters in odd-year pink (Figure 9). One of the clusters (A) has a large number of members that span the coast from Smith Inlet to Portland Canal (Figure 10). The other clusters are in what could be termed a northern group (clusters B to K), and are similarly widely dispersed along the coast. Consequently, there is little coherence between the genetic and ecotypic classifications. All of the sites but one in the Skeena River were from cluster J and the only two sites from the Queen Charlotte Islands were from cluster B (Table 5, Figure 10) but most of the other JAZ had members of two or more clusters. As with even-year pink, the two mainland JAZ bordering Hecate Strait were particularly diverse.

In the south, there is considerable geographic genetic structure. South of Kingcome Inlet all but two of the sites are members of clusters L to P (Table 5, Figure 10). Clusters L, M and N were found in the southern fjords, cluster O occupies the Strait of Georgia and cluster P was found in the Fraser River (Figure 10, Table 5). consisting of AEW in the southern fjords (groups L, M and P, , Figure 9), AEW around the Strait of Georgia (group O, , Figure 9), and AEW in the Fraser River (group P, Figure 9). The three groups, B, A & C to K, and L to P, correspond to the three genetic groups found by Olsen et al. (1998)

The absence of a close correspondence between ecotypic and genetic structure, is entirely unlike that for the other species, and more importantly is not what one would expect if the population structure of pink salmon resulted from episodic extirpation due to glaciation and recolonization. Two hypotheses have been advanced to explain this lack of regional structure. Olsen et al. (1998) attribute the lack of structure to high levels of gene flow. Churikov et al. (2002) studied phylogeny of both broodlines over most of the Pacific rim using mitochondrial DNA and also found only weak regional structure. The only geographical structure was the clear separation of Alaskan and Asian populations in the even-year race. These authors suggest that the genetic similarities observed among the geographic regions are the result of post-glacial colonization from numerous common sources rather than from extensive gene flow.

Pink salmon are the least dependent on freshwater of all the *Oncorhynchus* and the ability to spawn in the lower reaches of coastal streams that are tidally inundated has been documented in several regions (e.g. Hunter 1959). One might suppose therefore that pink salmon could have persisted in many northern areas during periods of glaciation at the edges of ice fields, although their apparent sensitivity to low temperatures during incubation (Beacham and Murray 1990) seems surprising if that were the case. The ability to persist in small streams at the interface of ice and the ocean might explain the observations of Churikov et al. (2002) if during periods of glaciation pink salmon populations were not strongly isolated in a small number of refugia but maintained a population structure much as it is today.

5.5 Ecotypic X Genetic Classification

Our preliminary description of Conservation Units for pink salmon asserted that adaptation to fresh water was likely to be far less important than adaptation to the marine environment. Furthermore, the broad scale of the geographical population structure suggested by molecular genetics and allozymes is more consistent with the population structure that would be inferred from adaptation to marine habitats. However, the geographical structure of variations in spawn timing, evidence of genetically based within-system diversity in spawn timing (Smoker et al. 1998), the lack of strong evidence that pink salmon either stray more extensively than other species or rapidly recolonize underutilized habitat suggest that Conservation Units based on the Marine Adaptive Zones alone would underestimate the diversity within the species. Consequently, we used the JAZ rather than MAZ ecotypes to compare with the genetic population structure.

5.5.1 Even-year pink

Genetic samples of even-year pink from 108 sites in British Columbia were first classified (see Section 5.4 and Table 3) and then cross-tabulated with our ecotypic CUs based on the JAZ ecotypes (Table 4). Only the three JAZ from the Queen Charlotte Islands were genetically distinct. The northern and central coastal JAZ were particularly diverse genetically (LNR-P+NSKEST, HecLow+HStr, NC+HStr). Unfortunately, there were no genetic samples for JAZ on Vancouver Island, around the Strait of Georgia or from the northern transboundary rivers.

The genetic evidence supports maintaining the three JAZ on the Queen Charlotte Islands as Conservation Units but there is considerable genetic diversity in the remaining areas of British Columbia that appears to have little or no geographic structure.

5.5.2 Odd-year pink

Genetic samples of even-year pink from 116 sites in British Columbia were first classified (see Section 5.4 and Table 3) and then cross-tabulated with our ecotypic CUs (Table 5). There was more genetic population structure in the odd-year pink than in the even-year race. In the south genetic structure was generally concordant with the ecotypic classification. Within cluster P, sites in the Fraser River fell into a different genetic class (2.6) from those in Puget Sound (class 2.7) and those in Howe Sound and Burrard Inlet (class 2.5)(Table 5, Figure 9). Consequently, Burrard Inlet and the eastern shore of Howe Sound were recognized as a distinct CU.

Members of cluster O were found on both sides of the Strait of Georgia (Table 5, Figure 10) suggesting that, in the absence of life history or ecological differences, those two JAZ could be combined into a single CU. Members of cluster M were found in the from Tribune Channel south in SC+SFj JAZ while members of clusters L and N were found at the same latitudes in the EVI+SFj JAZ (Table 5, Figure 10). The three sites in the EVI+SFj JAZ ecotype could be separated into two groups using the provincial eco-sections and separated from other sites on the east coast of Vancouver Island. Consequently, the two areas on Vancouver Island defined by the eco-sections were recognized as CUs. The northern boundary of the SC+SFj JAZ ecotype was moved into Tribune Channel to align it with the genetic population structure. That alignment is also roughly consistent with the groups identified by Olsen et al. (1998). The remaining genetic samples in clusters A and C to K were distributed broadly among the JAZ ecotypes on the north and central coasts (Table 5, Figure 10). Only two sites were sampled on the Queen Charlotte Islands and both were in cluster B. However, with a small sample and no samples from the other JAZ on the Queen Charlotte Islands it was not possible to determine if those JAZ are genetically distinctive. The HecLow+HStr and NC+HStr JAZ were particularly diverse genetically.

5.6 Spawning time

The mean day of spawning in British Columbia falls between mid-August and mid-November, which is a range of about 100 days (Table 6). There is a definite tendency for the mean day of spawning to become later with decreasing latitude and with proximity to the ocean (Figure 11). A General Linear Model for both races of pink salmon explains about 57% of the variance in mean spawning time (Table 7). The best predictors of spawning time are MAX_P_MAG, a measure of hydrological stability [more stable ≡ later], November air temperatures [warmer ≡ later], latitude [southerly ≡ later] and valley width [wider ≡ later] (Table 7).

There is considerable geographic structure in the variation of spawning timing across the region (Table 6). For example, there are three geographically based run timing components within the Fraser River. The mean spawning date of the earliest group of populations (Lillooet) is Sept. 27th (EFALL). The mean spawning date of the latest group of populations (Lower Fraser) is Oct. 22nd (MFALL). The remaining populations within the Fraser spawn on average around Oct. 11th (EFALL). Neave (1966) identified the same middle and late group but didn't explicitly deal with the Lillooet group. Similar variations in spawning time over small geographies were observed in SE Alaska and attributed to small-scale patterns in stream temperature Sheridan (1962) and were likely facultative. Such variation would not be sufficient evidence to recognize CUs.

Similar regional differences in spawning time occur throughout the province and most appear to be fully explained by the temperature model. For example populations in the Hecate Lowlands spawn significantly later than those in inland areas of the North Coast (ANOVA $P<0.001$). This difference is largely explained by the temperature components of the spawning time model. Populations in the Bella Coola and Dean Rivers spawn significantly earlier than those in the inland areas to the north and south. This difference is mostly explained by the temperature components of the spawning time model. Finally, populations on the east coast of Vancouver Island spawn significantly later than those opposite on the mainland. The spawn timing model fully explains that difference. The temperature model does not explain spawning times in the Lillooet, the Fraser River above Hell's Gate, the lower Thompson, WVI+WQCI, or the upper Skeena and upper Nass ecotypes (Table 6). However, sample sizes in some of those areas are small.

The regional variation in spawn timing and especially the variation that is not explained by the spawn-timing model may be important in considering Conservation Units for pink salmon. Although the geographical variation in spawn timing could indicate only facultative responses of individuals to temperature, it may also be genetically based and adaptive. There is some limited evidence that spawn timing is not simply a plastic response to the environment. Smoker et al. (1998) have demonstrated the genetic basis of variation in spawn timing within a small coastal population of pink salmon and have hypothesized about its adaptive significance. Tallman and Healey (1991) found a similar situation in chum salmon in a small coastal stream on E Vancouver Island. Nevertheless the success of the spawn timing model in accounting for much of the variation in spawning times suggests (but by no means proves) that individuals moved between even widely distant localities would likely spawn at the appropriate time.

5.6.1 Even-year pink

The spawn timing model suggests that even-year pink salmon spawn slightly over one-half day later than odd-year pink salmon, all else being equal (Table 7). ANOVA was used to compare the residuals from the spawn timing model where genetic structure appeared homogeneous across two or more ecotypic CUs. A significant difference in residuals between ecotypic CUs was interpreted as indicating the presence of two (or more) CUs. The lack of a difference was inconclusive. The comparisons made and the conclusions drawn from them are shown in the following table.

On the North and Central Coasts run-timing differences of approximately two weeks allow for the separate management of "outside" versus "inside" runs comprised of sites that correspond to the HecLow+HStr and NC+HStr ecotypic CUs, respectively. Comparison of the spawning times of pink salmon within those ecotypic CUs indicated a highly significant difference of approximately 10 days (following table), confirming the ecotypic CUs as full CUs.

ecotypic CU	number of sites	mean spawn time (DOY)	mean residual (d)
HecLow+HStr	144	260.4	-0.21
NC+HStr	99	250.1	-0.20
HecLow+NSKEst	55	256.3	-0.006
F-statistic and *P*	298	$F_{2,295}$ =35.3; P<<0.0001	$F_{2,295}$=0.024; P>0.95

Comparisons of residuals from the spawn timing model supported decisions to recognized two CUs on the west coast of Vancouver Island and two CUs in the interiors of the Nass and Skeena Rivers (one CU each). No other timing differences were detected, which suggested that, all else equal, multiple JAZ could be merged into CUs.

comparison	*F*-statistic	Probability	Conclusion
WVI+WVI vs. WVI+WQCI	$F_{1,105}$=6.58	0.012	two separate CUs
all JAZ with MAZ=GStr (included both sites in MFR)	$F_{2,48}$=0.54	0.59	inconclusive
SC+GStr vs. SC+SFj	$F_{1,95}$=0.49	0.49	inconclusive
EVI+GStr vs. EVI+SFj	$F_{1,40}$=0.79	0.38	inconclusive
WVI+WQCI vs. EVI+SFj	$F_{1,43}$=4.53	0.039	WVI+WQCI is a separate CU
all JAZ with MAZ=SFj	$F_{2,90}$=0.096	0.91	inconclusive
MAZ SFj vs. MAZ HStr (excluded sites on EQCI)	$F_{1,378}$=0.24	0.62	inconclusive
LSK vs. MSK & USK	$F_{1,89}$=7.53	0.0073	M&USK recognized as separate CU
UNASS vs. LSK, LNR-P and HecStr+NSKEst	$F_{1,165}$=9.83	0.002	UNASS recognized as separate CU
EQCI vs. NQCI & WQCI	$F_{1,164}$=12.0	<0.001	partial confirmation of decision based on genetics to separate into 3 CUs

5.6.2 Odd-year pink

Geographical patterns in spawn timing of odd-year pink were very similar to those in even-year pink salmon. In particular, two temporal groups are recognized in the management of odd-year pink salmon on the North and Central Coasts. Comparison of the spawning times of odd-year pink salmon within HecLow+HStr and NC+HStr ecotypic CUs indicated a highly significant difference of approximately 9 days (following table), confirming the ecotypic CUs as full CUs.

ecotypic CU	number of sites	mean spawn time (DOY)	mean residual (d)
HecLow+HStr	145	259.3	-0.18
NC+HStr	96	250.1	0.77
HecLow+NSKEst	52	255.9	1.09
F-statistic and *P*	293	$F_{2,290}$ =35.3; P<<0.0001	$F_{2,290}$=0.78; P>0.45

In general, the spawn timing model accounted for most of the coast-wide variation in spawn timing, as shown in the following table.

comparison	*F*-statistic	Probability	Conclusion
all FAZ within Fraser River	$F_{6,58}$=2.33	0.044	Tukey multiple-means comparison found no significant differences and we concluded that one CU was sufficient.

comparison	F-statistic	Probability	Conclusion
all JAZ within GStr excluding Fraser	$F_{2,67}$=1.61	0.21	inconclusive
WVI_WVI vs. Nahwitti	$F_{1,66}$=1.26	0.27	inconclusive
EVI+GStr, EVI-JStr, SCS2T, SC+SFj	$F_{3,98}$=2.15	0.098	Tukey multiple means comparison found no significant differences, result inconclusive
HecLow+HStr, NC+HStr, HK+SFj, BCD, RSI, SC+SFj	$F_{5,289}$=0.37	0.87	inconclusive
all JAZ on QCI	$F_{2,116}$=0.302	0.74	inconclusive
LSK vs. MSK & USK	$F_{1,95}$=12.2	<0.001	two CUs in Skeena River
HecLow+NSKEst vs. LNR-P	$F_{1,90}$=4.57	<0.05	HecLow+NSKEst is CU
LNR-P vs. UNR	$F_{1,58}$=5.33	0.025	two CUs in Nass River

Geographic variations in residuals were used to establish two CUs in each of the Skeena and Nass Rivers, which is the same result as obtained for even-year pink salmon.

5.7 Habitat, Environment and Ecology

As described in the methods (see Section 4.5.1), habitat and environmental information was considered when there was evidence of substantial genetic diversity within an ecotypic CU. Such consideration was to be used sparingly. The genetic structure of pink salmon and especially the even-year race presents a dilemma. In even-year pink, seven of the 15 ecotypic CUs are heterogeneous and three of them have five or six of the eight genetic groups). In odd-year pink, 11 of the 20 ecotypic CUs represented in the genetic sampling are heterogeneous, five of the 11 have 3 or more of the 16 genetic groups and one ecotypic CU (NC+HStr) has 10 of the 16 genetic groups (Table 5). With so much heterogeneity and such small samples, there is little scope for attempting to discriminate between the genetic groups within an ecotypic CU using habitat. A quick analysis of the most complex ecotypic CU suggested no geographic pattern to the genetic diversity. Other than the large regional groupings (two in even-year pink: QCI & the rest; two in odd-year pink: southern BC and the rest), it is possible that the genetic population structure is not well defined. If that were so, then the details of the structure would be prone to change with every new sample added and further descriptions of the population structure would be difficult. If the genetic structure actually were a mosaic, then it would not be practicable to pursue population structure using genetics. The full description of diversity in such a situation would entail the genetic characterization of all of the sites within all of the genetically heterogeneous CUs. Furthermore, the genetically homogeneous ecotypic CUs would also have to be examined in detail to insure that diversity was not missed due to small initial sample sizes.

In general, discriminant analysis using habitat variables cannot be used to resolve this dilemma. A habitat-based analysis would only confirm that all of the adaptive zones are distinctive, hardly a surprising result because that distinctiveness was used to define them (see Section 4.2).

To proceed with the definition of CUs for pink salmon we recognized ecotypic CUs based on their Marine Adaptive Zone where there was either no information at all or where neither the genetic nor the timing information that was available was consistent with a practicable, geographically based scheme.

5.7.1 Even-year pink

Ecotypic CUs were grouped by MAZ in two areas with high genetic heterogeneity (Table 8). That grouping led to formation of a North and Central Coast CU that included all of the mainland JAZ draining into Hecate Strait. All of the coastal JAZ ecotypic CUs draining into the Nass-Skeena Estuary MAZ were similarly grouped into the DFO Statistical Area 3/4/5 Coastal CU (Table 8). The Homathko-Klinaklini FAZ was separated from the North and Central Coast CU, to which it is otherwise similar because of its different MAZ (Sothern Fjords vs. Hecate Strait). Finally, all of the ecotypic CUs in the northern transboundary, for which there is no information other than the probable presence of even-year pink, were grouped into two CUs based on their Marine Adaptive Zones (Table 8).

Even-year pink salmon in the upper Nass and upper Skeena are genetically similar and have similar spawn timing deviations from the spawn timing model. The two regions are in different hydrological zones. The sites in the upper Nass are all in the transitional zone between coastal and interior hydrology, while the sole site in the upper Skeena is in the interior zone. We considered this habitat difference sufficient to separate the two ecotypic CUs into two CUs (Table 8).

5.7.2 Odd-year pink

Although there is no genetic or spawn-timing evidence of diversity in the interior Fraser River, we would expect that the environments there are sufficiently different from those on the coast that the pink salmon there are adaptively different from coastal fish, as they appear to be in both the Skeena and Nass Rivers. The Queen Charlotte Islands were not represented well in the genetic sampling (Table 3) and timing information did not differentiate between the ecotypic CUs. Hydrologically and physiographically, the lowlands around Masset Inlet are very distinct from the mountainous terrain to the south and west. The three ecotypic CUs were genetically distinct in even-year pink (Table 4) leading us to expect similar differences in the odd-year race. The three ecotypic CUs on the Islands are characterized by their different Marine Adaptive Zones and we considered that sufficient to form three CUs.

No genetic or timing information was available for the northern transboundary ecotypic CUs so they were grouped by their Marine Adaptive Zones, creating two CUs (Table 9).

5.8 CU summary

There are 13 Conservation Units for even-year pink salmon (Table 8) and 19 for odd-year pink salmon (Table 9). For both races of pink salmon, the CUs in the northern transboundary rivers is speculative because there was very little information available to us for pink salmon in those areas.

6. Chum salmon

6.1 Distribution

Chum salmon are the most widely distributed and most abundant (in terms of biomass) of all the Pacific salmon (Salo 1991). In North America, chum salmon was found from Monterey California to the Mackenzie River in the Canadian Arctic. In Asia, chum salmon was found from Korea to the Lena River in northern Russia. Mature adult chum salmon have two distinctive characteristics. The sides of both sexes but particularly males have a distinctive calico or mottled band of dark red, light green and black. As they mature, both sexes develop prominent canine-like teeth that give the species its common name of dog salmon. Salo (1991) reports that in Japan and the Russian federation there are a large number of local names for chum salmon, an interesting observation in light of recent genetic studies that have demonstrated high levels of genetic diversity in those areas (Sato et al. 2004).

6.2 Life History

Chum salmon, like pink, generally spawn in the lower reaches of coastal streams and their fry spend little time in freshwater. Chum salmon are reputed to be poor or unwilling jumpers. For example, chum salmon in Carnation Creek, BC, did not enter the trap on a fish weir that involved a very modest jump (<30cm; LBH pers. obs.). Chum salmon are seldom observed above Hell's Gate on the Fraser River. However, chum salmon are also capable of among the longest river migrations of any salmon, migrating more than 2,500 km up the Yukon and Amur Rivers.

Unlike pink salmon, which move quickly into and through near-shore waters, chum salmon remain in estuaries and the near-shore during their first summer before moving offshore. One of the most interesting aspects of the early life history of chum salmon is their dependence on harpacticoid copepods and gammarid amphipods during their residence in estuaries (Healey 1980, 1982, Sibert et al. 1977). Much of the detritus that fuels the estuarine food web is discharged from fresh water (Naiman and Sibert 1978). Consequently, the belief that chum salmon are not dependent on fresh water is only superficially correct.

6.3 Ecotypic CUs

With the exception of the Yukon and Mackenzie Rivers, where chum accomplish among the longest salmon migrations known in fresh water, the species is absent or nearly so from the interior regions of the Columbia, Fraser, Skeena, Nass, Stikine and Taku Rivers. Chum like pink salmon is absent from the Alsek River and its tributaries. Chum salmon is the only species of Pacific salmon known to be present in the lower Liard River in the Mackenzie River drainage. There are 29 ecotypic CUs of chum in British Columbia (Table 10).

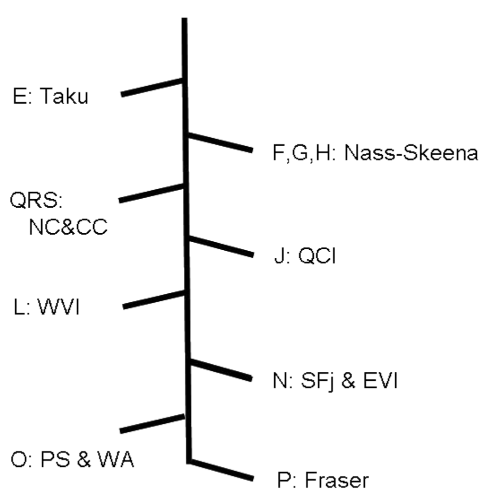
6.4 Lineage

Several studies have considered the broad population structure of chum salmon. Sato et al. (2004) inferred the existence of three groups of chum salmon in Asia and Alaska using mitochondrial DNA. The Japanese group was the most diverse and most distinctive of the three. The Russian and NW Alaskan were more strongly related to each other than to the Japanese group. Nevertheless, Alaskan and Russian chum salmon are reported to be genetically distinct (Wilmot et al. 1994). Two studies have reported the genetic distinctiveness of chum from the lower and upper Yukon River ((Beacham et al. 1988a, Wilmot et al. 1994). In SE Alaska and northern British Columbia Kondzela et al. (1994) used allozymes to characterize four genetic groups in this area: the Queen Charlotte Islands, the southern Alaskan Panhandle, northern and central British Columbia, the northern Alaskan Panhandle and the SW Alaskan Panhandle (Prince of Wales Island). In British Columbia, Beacham et al (1987) concluded that there were five distinct groups of chum salmon based on 9 allozyme loci: Queen Charlotte Islands, north and central coast, coastal populations around Georgia Strait, the Fraser River and the west coast of Vancouver Island. Phelps et al. (1994) concluded that there were eight distinct population groups in southern BC, Washington and Oregon: the Columbia River, the WA and OR outer coast, the summer-run populations of Hood Canal and the Strait of Juan de Fuca, Southern Puget Sound and Hood Canal (fall-run), North Puget Sound, coastal BC populations around the Strait of Georgia, the Fraser River and lastly those on the west coast of Vancouver Island.

A comprehensive study using microsatellite DNA (Beacham et al. unpublished data) largely supports the conclusions of Johnson et al. (1997) that were based on allozymes. Chum salmon of the Pacific Rim are divided into two groups. One group includes Japan, the Russian Federation, mainland Alaska, the Yukon River, the north slope and the Mackenzie River. The second group includes the Alaskan panhandle, Canadian northern transboundary rivers (except the Yukon), and the remainder of North America. Within that group, genetic relatedness appears to correspond roughly to distance between the spawning sites. Chum salmon appear to be structured much as pink salmon are and the general conclusions about the paleo-zoogeography of the two species are very similar (pink: Olsen et al. 1998, chum: Sato et al. 2004).

There are 18 genetic clusters within Canada (Figure 19). Four of the clusters (A to D) include sites in the Mackenzie River drainage (cluster A) or in the Yukon River (B to D). These sites cannot be fully dealt with in this document because ecological information about those areas is lacking. The remaining 14 clusters can be grouped into four super clusters that extend southward down the coast as the following diagram shows.

A five-level genetic and ecotypic classification of over 335 chum populations around the Pacific Rim, of which 174 are in Canada, is shown in Table 11.



A further simplification of the diagrammatic dendrogram of showing the geographic relationships of each genetic cluster.

In the diagram, NC &CC are the north and central coasts, respectively, QCI are the Queen Charlotte Islands, WVI is W Vancouver Island, SFj & EVI are the southern fjords and E Vancouver Island respectively, PS & WA are Puget Sound and coastal Washington State, respectively.

6.5 Ecotypic X Genetic Classifications

Table 12 summarizes the crosswalk of the ecotypic CU and genetic class of 174 sites within Canada. All of the sites in 16 of the 26 JAZ were represented by genetic classes from only one genetic cluster (see following table and Table 11). Five of the JAZ had sites from three different clusters (Yuk, Taku, NC+HStr, RSI, and SC+SFj)[22], and one JAZ (LNR-P) had sites from four clusters. We concluded that, for the most part, there was strong concordance between the ecotypic classification and the genetic classification and proceeded to determine the nature of the within-JAZ genetic diversity.

In three of the JAZ where there were three genetic clusters represented, one of the clusters was represented by a single site that was geographically distant from other members of its cluster. The three sites in question are shown in the table below. In the absence of additional genetic samples from surrounding sites, we have no way of determining how broadly these sites represent genetic diversity within the areas where they are located. However, these sites are found in areas where much larger numbers of sites were classified into other genetic clusters. Consequently, we have treated them as outliers that were not subsequently considered in the description of chum salmon CUs.

Count of number of clusters per ecotypic CU

number of clusters	number of JAZ
1	16
2	4
3	5
4	1
total	26

		outlier		
JAZ	clusters	site & GFE_ID	cluster	predominant geography of outlier's cluster
SC+SFj	K,N	Ahnuati #852	R	NC
HecLow+HStr	Q,S	Cold Creek #958	N	SC
NC+HStr	R,S	Bish #1080	H	LNR-P

Much of the within-JAZ genetic diversity was addressed by some combination of boundary changes to the ecotypic zones, or either subdivision or grouping of JAZ ecotypes. The changes are summarized in the following table. All of the changes were made to reduce the levels of within-JAZ genetic diversity as indicated in a second crosswalk between the revised ecotypic/genetic CUs and the genetic classification (Table 13). After the changes described in the table significant diversity remained in the NC+HStr and LNR-P+NSKEst JAZ ecotypic CUs (Table 13).

[22] For brevity, the MAZ portion of the JAZ name has been dropped where there is no ambiguity.

Type of change	Description	number of sites	JAZ affected
boundary change & pooled CU	Genetic similarity of sites around the Strait of Georgia and in portions of the southern fjords recognized by adjusting boundary of SC+GStr northward into the southern fjords and then pooling it with EVI+GStr. to form GStr+GStr.	163	EVI+GStr, SC+GStr & SC+SFj
boundary change	boundary of GStr+GStr shifted west along Juan de Fuca Strait on Vancouver Island.	13	GStr+GStr & WVI+WVI
new CU	Skidegate Inlet recognized as genetically distinct (SKID)with sites taken from east and west QCI	42	QCI+HStr & QCI+WQCI
new CU	Howe Sound-Burrard Inlet recognized as genetically distinct (HOWE) with sites taken from SC+GStr	64	SC+GStr
boundary change	NC+HStr was moved west in southern portions of HecLow+HStr,	47	NC+HStr, HecLow+HStr
new CUs	The RSI+HecStr JAZ was split into the Rivers Inlet (RI)and Smith Inlet (SI) CUs. Both RI and SI were expanded west by transferring sites from HecLow	14	HecLow+HStr, RSI+HecStr
boundary change	Boundary of NC+HStr adjusted in vicinity of BCD+HStr	17	HecLow+HStr, BCD+HStr, NC+HStr
new CUs	The HK+SFj JAZ was split and each portion expanded along Bute and Knight Inlet incorporating sites from SC+SFj	10	HK+SFj & SC+SFj
new CU	A new CU was formed in and around Loughborough Inlet (LOUGH) from SC+SFj	42	SC+SFj
new CU	A new CU (PCOb) was formed by separating Portland Canal and Observatory Inlet from LNR-P+NSKEst	25	LNR-P+NSKEst

The genetic diversity that is apparent in NC and LNR-P ecotypic CUs was difficult to pursue because there were few genetic samples relative to the total number of sites in those areas. Consequently, consideration of those two JAZ ecotypes was deferred to steps 3 and 4, which follow.

6.6 Spawning time

There is considerable regional variation in the mean day of peak spawning across British Columbia (Table 14). The earliest spawning population in our dataset is that of Brohm River (GFE_ID=720; JAZ=SC+GStr), which has a mean spawning date of May 15th (MSPR). The latest spawning population is that of Liumchen Creek (GFE_ID=71; JAZ=LFR+GStr), which has a mean spawning date of Jan. 29th (MWIN). These are extreme outliers however and most chum populations have a peak spawning date in the late summer or early fall.

The peak spawning date is generally later in the year in southern populations (Table 14) but the relationship is not a simple cline. Exclusive of the populations on the Queen Charlotte Islands the populations to the north of and including those of Smith Inlet spawn significantly earlier than all those to the south including Vancouver Island (ANOVA, P<<0.0001). The populations of the Queen Charlottes, as a whole, are intermediate to the northern and southern groups. This pattern can be seen in the contour plot of Figure 21 and more clearly in Figure 22 (top panel).

A linear, multiple regression model “explains” 79% of the regional variation in mean peak spawning timing (Table 15). Much of the variation is accounted for by latitude as spawning time becomes earlier as one moves up the coast and by longitude as spawning time is generally later on the coast compared to inland (Figure 21). There is considerable geographic patterning to the residuals of the timing model (Figure 23, Figure 24). In general, spawning is later than model predictions in the southern fjords (HOWE, LOUGH and BUTE), north QCI and the Nass-Portland areas. Spawning is earlier than model predictions on W Vancouver Island, in the Bella Coola-Dean (Figure 24). The rapid change in mean spawning date that occurs in the Central Coast (Figure 22 top panel) is largely explained by the model since there is no latitudinal effect in the model residuals (Figure 22 bottom panel).

Spawn timing was used to examine instances where single genetic classes or closely related genetic classes occurred in multiple ecotypic CUs. Significant differences between ecotypic CUs in the residuals of the timing model would support the ecotypic CU structure, while lack of a difference would be inconclusive. However, in the absence of other ecological or habitat differences, merging the ecotypic CUs could be justified. The comparisons are summarized in the following table. Of the five cases considered, the ecotypic CUs were at least partially confirmed as full CUs in two cases and the status of a single site as a CU was suggested in a third case (shown in the second following table). The results were inconclusive in the remaining two cases.

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case	genetic class(es)	CU comparison(s)	significance	conclusions
1.	2.12-2	WVI+WVI< WVI+WQCI	$F_{1,238}$=25.6, P<0.001	ecotypic CUs were confirmed
2.	2.15-2 to 2.15-5	LFr=LILL= FrCany	$F_{3,10}$=0.4, P>0.7	inconclusive
3	2.09.2-2.1	BCD<UKNIGHT=RI	$F_{1,45}$=10.9, P=0.002	BCD has distinctive timing, the relationship between UKNIGHT and RI is unresolved
4	2.08-3	LSK=MSK	$F_{1,38}$=0.18, P>0.5	inconclusive

The fifth case involves a comparison between genetic classes 2.10-1, present only in the QCIN ecotypic CU and class 2.10-2, present only in the QCIE ecotypic CU with the sole exception of Stanley Creek (GFE_ID=1557), which is in Naden Harbour in the QCIN ecotypic CU. As can be seen from the following table, Stanley Creek has a uniquely early spawn timing, which is not explained by the timing model. Recognizing a single stream as a CU is unusual but seems warranted in this instance. We were alerted by Area assessment biologist (B. Spilsted, DFO North Coast, Prince Rupert) to the special status of this population to the local First Nation because of its unusual run timing. Although the population is not large (mean escapement 1950-2004 is 1044, N=40), its unique timing has persisted in very close proximity (≈8 km) to the much larger Naden River population (GFE_ID=1559) for the over 50 years on record (mean escapement to Naden River is 11949, N=47). Stanley Creek is also somewhat out of place genetically, belonging to a genetic class (2.10-2) that is otherwise confined to the areas of the Queen Charlotte Islands bordering Hecate Strait.

case	ecotypic CU or site	genetic class	N sites	DOY peak spawn	residual (d)
5	QCI-N	2.10-1	11	288.4	18.4
	QCI-E	2.10-2	125	283.8	2.8
	Stanley Creek	2.10-1	1	253.0	-17.2
		Stanley Creek is in QCI-N ecotypic CU but has QCI-E genetic type		$F_{2,134}$=16.3 P<0.0001 all pairwise comparisons significant with P<0.05	$F_{2,134}$=18.4 P<<0.0001 all pairwise comparisons significant with P<0.005

Spawn timing was also used to further examine genetic diversity within ecotypic CUs in the NC+HStr (Figure 25) and LNR-P (Figure 26) ecotypic CUs. Although the various genetic classes within these ecotypic CUs are geographically separate, there are too few samples to partition the CUs. Instead, a variety of geographically based partitioning schemes was considered within each ecotypic CU to examine systematically whether there was geographic structure to timing variations that was consistent with the genetic structure. In the NC+HStr ecotypic CU, three partitions consistent with the genetic structure were found and recognized as CUs (Figure 25): Douglas-Gardner in the north, Mussel-Kynoch in the center and Spiller-Fitz Hugh-Burke in the south (Figure 25). No timing differences were found among the site configurations examined in the LNR-P ecotypic CU (Figure 26).

Two other instances of marked diversity in run-timing were brought to our attention by local biologists. In the Bella-Coola River there is “late” run that appears in the river in late September (EFALL). The predominant run-timing in the Bella Coola River and Dean Rivers and the other smaller systems in the BCD JAZ is mid-to late-August (LSUM). The EFALL component in the Bella Coola is represented by a single site (#358, the Atnarko spawning channel). The mean spawning date at this site is significantly later than the other sites in the JAZ as are the residuals for the spawn-timing model (following table). We concluded that the EFALL component is a separate CU. We do not know if there are other distinguishing phenotypic characteristics. Such differences would be of interest, in part because the spawn-timing model does not predict spawn timing well in either group.

ecotypic CU or sites	sites	genetic class	N sites	DOY peak spawn	residual (d)
BCD	Atnarko spawning channel	no data	1	277.0	15.0
	all other	2.9.2-2.1	29	240.6	-24.1
	ANOVA comparisons of group means			$F_{1,28}$=6.4 P<0.05	$F_{1,28}$=9.3 P=0.005

A similar situation was reported in Rivers Inlet. There the chum spawn in the Wannock River much later than in the tributaries to Owikeno Lake and the other headwater streams in the Inlet. Both the mean spawning date and the mean residuals from the spawn-timing model were significantly different (see following table).

ecotypic CU or sites	sites	genetic class	N sites	DOY peak spawn	residual (d)
River Inlet	Wannock River	no data	1	307.0	30.8
	all other	2.9.3-2	10	263.3	-9.2
	ANOVA comparisons of group means			$F_{1,9}$=12.9 P<0.01	$F_{1,9}$=12.4 P<0.01

The lateness of spawning in the Wannock River is likely attributable to the lake influence although it is poorly predicted by the model. We concluded that the Wannock River chum population was a separate CU.

6.7 Habitat and ecological considerations

Genetic variation within the LNR-P+NSKEst ecotypic CU was not resolved by examining spawn timing so habitat was considered. No habitat model could be found that reliably separated all of the genetic classes present in the ecotypic CU. However, the habitat of the lower Nass River was readily distinguishable from the habitats of coastal tributaries to Portland Inlet and Work Channel on most of the variables considered, and a simple discriminant function perfectly classified all of the sites (Table 16). We concluded that there were two CUs in the area. However, the Portland Inlet CU remains genetically diverse.

A habitat discriminant function was also considered in the lower Fraser River where the LFr, LILL and FRCany ecotypic CUs show overlapping genetic diversity. There were no timing differences between the CUs although the FRCany sites tended to have negative residuals compared to surrounding ecotypic CUs (Table 14, Figure 24). No discriminant model was found that could reliably classify the three ecotypic CUs present but a simple model incorporating average annual rainfall (PPT_ANN), the proportion of high elevation tundra (TUNDRA_PC) and an index of hydrological stability (KFAC_LOG) successfully classified 97% of the sites when the LFR and LILL CUs were pooled (Table 17). We concluded that there were two CUs of chum salmon in the Fraser River and its tributaries.

6.8 Chum salmon summary

There are 39 Conservation Units of chum salmon in British Columbia (Table 18, Figure 27). That total includes the LIARD CU for which there is no information beyond the probable presence of chum salmon. It is highly probable that the chum salmon in the headwaters of the Mackenzie River, thousands of kilometers from the Arctic Ocean, will prove to be genetically and adaptively distinct. There is at least one other CU in the Mackenzie drainage consisting of sites in the Peel River but its nature and extent are unknown. The TESLIN CU, which is partially in BC, is likely a part of a larger CU that occupies the tributaries of the upper Yukon River. Based on genetic evidence there are likely at least three CUs of chum in the Canadian portions of the Yukon River but without ecological information further resolution of the population structure there would be speculative.

7. Coho salmon

7.1 Distribution

Coho salmon are the sister species of chinook to which they are physically similar especially as juveniles and in early sea life (McKay et al. 1996, Utter and Allendorf 1994). Coho salmon are found from northern Japan to the Anadyr River region in Asia and in North America from Kotzebue Sound in NW Alaska to Monterey Bay in California (Sandercock 1991). In British Columbia, coho salmon can be found in nearly every accessible coastal stream. Coho also migrate upstream in the larger rivers and are found in the headwaters of the Skeena River (e.g. Kluatantan River GFE_ID 501, 560 km from mouth) and in the middle tributaries of the Fraser River, (e.g. McKinley Creek GFE_ID 2401, 840 km from mouth).

7.2 Life History

Other than pink salmon, coho salmon has the least variable life history of the Pacific salmon species found in Canada. Adult coho typically return to spawn in the fall and early winter. Although there are populations where river entry can be much earlier (e.g. Docee River, GFE_ID 914, Smith Inlet, where coho enter freshwater as early as late June), the existence of discrete seasonal runs is not generally recognized. Juvenile coho salmon typically spend about one year in freshwater after emergence in the south of their North American range (Georgia Strait southward). To the north of Georgia Strait, the age composition of smolts is site dependent and probably related to the growth potential of their natal stream. For example, in Carnation Creek in Barkley Sound on WVI (GFE_ID) there were roughly equal numbers of one- and two-year old smolts (Andersen 1983) while neighboring streams produced mostly one-year old smolts. Stream temperatures warmed after the watershed was logged and two-year old smolts became rare (Holtby 1988). Babine Lake and its tributaries (GFE_ID 2107) produce almost entirely one-year old smolts but at the same latitude and on the coast, the Lachmach River at the head of Work Channel (GFE_ID 1748) produces mostly two-year old smolts (Finnegan 1991, Finnegan et al. 1990). Geographical patterns in smolt age (Bradford 1999) could be the result of factors other than growth potential in freshwater. For example, one and two-year old smolts in the Lachmach River have been differently coded-wire tagged and the survival rates of the younger (and smaller) smolts are significantly lower, which is indicative of strong selection against early smolting. All females and variable proportions of the males return to spawn after two summers in the ocean making most spawners either three or four years old. The other males, which are known as jacks, return to spawn after only one summer in the ocean. In some populations the majority of male spawners are jacks (Holtby and Healey 1990).

While coho might have a relatively simple life history, their use of freshwater habitats is highly variable and opportunistic. Coho are typically found in small and low-elevation streams with shallow or moderate gradients (<5-8%). However, coho make extensive use of lakes (Swain and Holtby 1989), estuaries (Crone and Bond 1976, Miller and Sadro 2003, Ryall and Levings 1987, Tschaplinski 1987) and large rivers (Beechie et al. 2005). Most coho juveniles live in freshwater for about half their lives and due to this dependence, their ubiquitous presence in small streams and their tolerance of experimental manipulation, there has been an extensive examination of habitat use and population dynamics. Several generalities from this work are pertinent to the description of Conservation Units. First, coho populations are numerous but are generally small, typically comprising less than 500 spawners and often many fewer. Second, in most populations smolt production is strongly density-dependent (Chapman 1965, Mason and Chapman 1965, Nickelson and Lawson 1998) and limited by a complex interaction of habitat space, stream productivity and size-dependent survival processes (Holtby and Scrivener 1989). A corollary of this density limitation to survival is that population size is generally related to the available rearing habitat rather than to spawning habitat (Bradford et al. 1997). Over-winter survival has been identified as the key process in determining smolt production in small streams, with the limiting mechanism being related either to the availability of some essential habitat (Nickelson and Lawson 1998, Nickelson et al. 1992b) or to the size of the fish entering the winter (Holtby 1988, Quinn and Peterson 1996). Coho have several strategies for winter survival. Over-wintering coho are commonly described in association with large woody debris in the mainstem of streams . Over-wintering coho undertake a variety of migrations. In large river systems, coho juveniles have been observed moving downstream to enter valley bottom ponds during the winter (Cederholm and Scarlett 1981). In smaller, coastal streams, coho juveniles have been observed to move laterally into side-channels and sloughs (Brown and Hartman 1988, Hartman and Brown 1987, Swales et al. 1986). Where such habitats are lacking, coho have been observed to move to deep and protected mainstem pools (Nickelson et al. 1992a) or to move upstream into ponds (pers. obs. B. Finnegan and LBH on Lachmach River GFE_ID 1748). In systems with complex networks of streams and lakes it is possible to observe coho that utilized different rearing habitats in the summer move in opposite directions through the same weir at the beginning of winter (pers. obs. LBH at Mesachie Lake GFE_ID 2627). It is possible that these behaviors are opportunistic responses by individuals to their particular circumstances. However, such opportunism has not been demonstrated and it is possible that this diversity of behaviors is genetically programmed. This is relevant to the description of Conservation Units for coho because the matrix of habitats that make up a stream watershed systematically changes across the landscape due to geology (e.g. compare the physiography of the Hecate Lowlands to the coastal fjords they abut) and climate (e.g. streams in the northern areas of the Hecate Lowlands are significantly colder than those in the south). Much of this variation is not captured by the JAZ ecotypes. To the extent that such variation is associated with systematic variation in the habitat conditions to which coho are adapted, we would expect the significant diversity exists at finer geographic scales than the scale of our ecotypic zones.

7.3 Lineage

The genetic population structure of coho salmon proved recalcitrant using both allozymes (various studies cited in Weitkamp et al. 1995) and mini-satellites (Miller et al. 1996) leading to the early conclusion that there was relatively little geographic structure (e.g. Wehrhahn and Powell 1987). However, subsequent use of micro-satellite DNA has shown considerable geographic structure. Small et al. (1998a) demonstrated the distinctiveness of Thompson River coho and suggested that it resulted from two patterns of recolonization after the last glaciation. The distinctiveness of coho above and below Hell's Gate on the Fraser River has been a consistent finding in all subsequent studies. Small et al. (1998b) demonstrated three major groups of British Columbia coho:

Thompson River, southern coastal and northern coastal. In their study of the glacial biogeography of coho salmon in North America, Smith et al. (2001) used both mitochondrial and microsatellite DNA to study the glacial biogeography of coho in North America. They inferred five biographic groups using the microsatellite data that supported the persistence of coho in at least three refugia during the last glaciation (Alaska, the Queen Charlotte Islands, and the southern USA). The recolonization of Canada after that glaciation led to distinct groups in northern British Columbia (and presumably the Yukon), the Queen Charlotte Islands, the southern and central coasts including Vancouver Island, Georgia Strait and the lower Fraser, and the Thompson River. The mitochondrial DNA suggested one lineage with diversity decreasing from south to north, suggesting that coho were eliminated from all but southern areas during some previous glacial period.

The population structure found by Smith et al. (2001) can be refined with microsatellite data (Beacham et al. unpublished data; Table 20, Figure 29, summarized in Figure 30 and Figure 31) as indicated in the following table.

In the Skeena River, Wood and Holtby (1998) found coho populations were related by distance and that gene flow was sufficiently restricted between major tributaries of that large river to allow local adaptations to persist. However Olsen et al. (2003) found that relatedness by distance was apparent only within river drainages in Alaska but that there was considerable regional differentiation elsewhere, even at a fine scale. They argued that, in general, coho populations were small and isolated, that genetic drift and not gene flow was the primary force in determining population structure, and that coho are probably locally adapted at a fine spatial scale.

groups from Smith et al. (2001)	groups from Beacham et al. (unpublished data)	genetic clusters (Table 20 &Figure 30)
northern BC	Alsek	C
	transboundary fjords, Nass, Skeena	T to Z
	Oona, Brim, Wahoo	A
Queen Charlotte Islands	Graham Island lowlands	B
	remainder of QC Islands	G, H
	Barkley and Nootka Sound	G
south and central coasts	Hecate Strait	D, E
	Smith Inlet	F
	Georgia Strait including eastern Vancouver Island and lower Fraser	I to M
	Nahwitti Lowlands and portions of western Vancouver Island	Q to S
Thompson	Fraser River interior	N to P

7.4 Life History Variants

Little morphological or life-history variation has been reported at a regional level. There are differences in body morphology and swimming performance between coastal and interior populations in the Fraser River (Taylor and McPhail 1985a, b) that are genetically based and very probably adaptive. Similar differences have been observed in other species (Crossin et al. 2004). Morphological and behavioral differences, also genetically based and likely adaptive, have also been demonstrated within single watersheds (Swain and Holtby 1989) and between neighboring streams (Rosenau 1984, Rosenau and McPhail 1987). Weitkamp and Neely (2002)·found that the geographic patterns in the ocean recoveries of coded-wire tags from 126 wild and hatchery populations on the west coast of North America were very similar within geographic areas similar to our MAZ ecotypic zones. There were two exceptions, however, both within the Georgia Strait MAZ. Unlike other populations around the Strait those of the Thompson River (and presumably all of the Fraser River above Hell's Gate) and Mesachie Creek (GFE_ID 2627, a tributary of Cowichan Lake on E Vancouver Island) had "outside" distributions, meaning that recoveries were predominantly on the outer west coast. The genetic distinctiveness of the interior Fraser River coho has been well established and is recognized in our ecotypic zonation as well. The distinctive distribution of Cowichan Lake coho is likely a result of the post-glacial history of the Cowichan Lake drainage that involved a shift in drainage from the west coast (through the Nitinat River) to the east coast of Vancouver Island. Understandably, no ecotypic classification could capture diversity at the fine spatial level that appears typical of coho salmon.

Coastal coho typically enter their natal streams with the first fall freshets but striking exceptions to this generality are known in most regions of British Columbia. For example, coho enter the Gold and Tsitika Rivers (GFE_ID 1358 and 1117, respectively) in mid-summer. Similar timing in the Capilano River (GFE_ID 697) has been exploited by the local hatchery to produce a summer sport fishery in Burrard Inlet. The most distinctive run timing pattern might be in the Docee River (GFE_ID 914), which drains Long Lake in Smith Inlet. Coho are moving up the river into the lake from late June to at least October, when the counting weir is closed. The adaptive basis of such a prolonged run into a single lake is unknown.

7.5 Ecotypic X Genetic Classifications

A hierarchical classification of a synoptic survey of 277 British Columbian coho populations (Beacham et al. unpublished data; Table 20, Figure 29, summarized in Figure 30 and Figure 31) indicates considerable population structure. There are 26 distinctive genetic clusters within British Columbia alone (Figure 30), which can be grouped into 10 larger clusters (Figure 31). Some aspects of the population structure, such as the distinctiveness of the Fraser River populations above Hell's Gate and the grouping of populations around the Strait of Georgia including the lower Fraser, were anticipated, while other were not.. Notably, there is no indication of the distinctiveness the Queen Charlotte Islands as a whole. Instead, there are two groups on the Charlottes corresponding to the northern lowlands of Graham Island (cluster B) and the mountainous remainder of the islands (clusters G & H). Cluster G contains sites in Nootka Sound and Barkley Sound on the west coast of Vancouver Island. The diversity on the west coast of Vancouver Island where there are representatives of two distinct clusters (G and Q+R+S) was also not anticipated.

We first compared the JAZ ecotypic classification to the genetic clusters, which correspond to level-3 of a five level hierarchical classification (Figure 32, Table 21). Although there was some correspondence between the genetic and ecotypic structure we found that some small boundary changes made that correspondence considerably more general. Those changes are summarized in the following table.

Type of change	Description	*N* sites	JAZ affected
border change	EVI was expanded west in the Juan de Fuca Strait to the Jordan River	11	EVI+GStr, WVI+WVI
border change	The boundaries of JAZ bordering Hecate Strait JAZ were changed to reflect apparent genetic structure	32	HecLow+HStr, HecLow+NSKEst, and NC+HStr

Some of the differences between the genetic and ecotypic classification probably reflect the greater dependence of coho salmon on fresh water than marine habitats. In two instances, new CUs were created to accommodate those differences by combining sites with different MAZ but common FAZ or other terrestrial ecotypes into CUs. Two such changes are summarized in the following table.

Type of change	Description	*N* sites	JAZ affected
border change/new CU	The northern QCI JAZ was redefined to correspond to the Graham Island Lowlands provincial eco-section. This redefinition reassigned sites from the portions of Graham Island that border Hecate Strait	10	QCI+HStr, QCI+NQCI
border change/new CU	The sites in genetic cluster R are in a distinct geographic group that corresponds closely to the Nahwitti Lowlands provincial eco-section. All sites in the WVI+WQCI JAZ and 10 sites in the northern portion of the EVI+SFj JAZ were assigned to this CU	10	EVI+SFj, WVI+WQCI

Seven new CUs were defined based on their genetic distinctiveness as summarized in the following table.

Type of change	Description	*N* sites	JAZ affected
new CU	The sites in Howe Sound-Burrard Inlet form a distinctive group (cluster I). Coastal sites in the SC+GStr JAZ are in cluster K. The coastward boundary of the CU is arbitrary.	50	SC+GStr
new CUs	The WVI+WVI JAZ was broken into three new CUs based on genetic structure: Jan de Fuca-Pachena corresponds to cluster S, Barkley and Nootka Sounds (WVI+WVI) correspond to cluster G and Clayoquot Sound corresponds to cluster Q. The boundaries correspond to major coastal features.	179	WVI+WVI
new CUs	The RSI+HStr JAZ was split into two CUs: Rivers and Smith based on their genetic distinctiveness (clusters U and F respectively)..	34	RSI+HStr
new CU	Mussel-Kynoch was split from the NC+HStr based on the genetic distinctiveness of Kainet Creek. This recognition is debatable because of the limited genetic sampling. However, we note that the distinctiveness of this area was also seen in chum salmon	12	NC+HStr

In addition, the genetic distinctiveness of two other areas, Douglass Channel-Kitimat Arm and the Brim River was noted. These two areas were considered in step 4 (habitat).

A re-examination of the genetic×ecotypic cross walk (Table 22) shows close correspondence between the putative CUs and genetic structure.

7.6 Spawning time

The only life history trait that we could examine in detail is spawn timing. The mean date of peak spawning in 1532 SEDS populations in British Columbia is DOY 301 or Oct. 28th in MFALL (Table 23). The earliest spawning populations are Crab River (GFE_ID 1038, JAZ NC+HStr) and Dogfish Bay Creek (GFE_ID 1768, JAZ LNR-P+NSKEst) both of which spawn on DOY 227 in mid-August. The latest spawning populations are all in the lower Fraser and spawn in late January (Liumchen Creek GFE_ID 71, Mountain Slough GFE_ID 101, and Hopedale Slough GFE_ID 67). Liumchen Creek is of some interest because the chum salmon there also spawn very late in the year (see Section 5.5). The range in mean spawning dates is particularly broad in the populations of the LFR+GStr, SC+GStr (including Howe-Burrard), NC+HStr and LNR-P+NSKEst JAZ ecotypes Table 23). Those ecotypes are also areas of particularly high genetic diversity.

Although there is a general latitudinal cline in mean spawning time spawning (Figure 33, Figure 34) and latitude is by far the most important independent variable in the spawning time model (Table 24), separation of the sites into those draining into Georgia Strait and all of the others reveals a clear dichotomy in mean spawning times (Figure 35). Sites draining into the Strait of Georgia comprise sites in genetic clusters I to P, which, in turn, comprise, one of the major groupings in the genetic population structure (Figure 31).

The predictive model for spawn timing explains 61% of the total variation and includes variables for fall temperatures and precipitation, stream stability and the mean gradient of tributaries in addition to a categorical variable describing genetic cluster membership (Table 24). There are numerous regional grouping in the residuals from the overall model (Figure 36, Figure 37). The only pattern that we were able to discern from the residuals is that there is a tendency for inland populations (e.g. FRCany, LTh, STh, UNR, USK) to spawn significantly earlier than the model predictions (negative residuals) and vice-versa for coastal populations (e.g. BCD, CLAY, LNR-P, LSK, SC+GStr). However, migration distance did not explain a significant amount of variance.

The apparent dichotomy in mean spawning times that was observed for sites draining into Georgia Strait versus elsewhere (Figure 35a), which have a genetic component (all sites are in the related clusters I through P inclusive), are not seen in the model residuals (Figure 35b).

Geographic variations in residuals were used to examine situations where genetic clusters were found in more than one putative CU after step 2 with the following results.

case	genetic cluster(s)	CUs comparison	significance	conclusion
1	P	MFR>STHOM=LTHOM	$F_{1,53}=8.15$, $P<0.01$	MFR is a CU, differences between the two Thompson River JAZ inconclusive
2	L, M	in LFR, cluster L=M	$F_{1,37}=0.02$, $P>0.8$	deferred to step 4
3	J	EVI+GStr>EVI+SFj	$F_{1,109}=43.9$, $P<<0.01$	EVI+SFj confirmed as CU
4	V	DOUG>neighboring NC+HStr	$F_{1,49}=23.1$, $P<0.01$	Douglas Channel-Kitimat Arm recognized as new CU
5	Z	MSK=USK=UNR	$P>0.5$	inconclusive
6	Y	LSK=LNR-P	$P>0.9$	inconclusive
7	U, Y	PORT=NASS	$F_{1,44}=1.9$, $P=0.18$	suggestive, deferred to step 4

Timing differences supported the recognition of a new CU in Douglass Channel-Kitimat Arm. Timing differences confirmed the CU status of the MFR as distinct from the lower and south Thompson ecotypic CUs and the CU status of EVI+SFj as distinct from EVI+GStr.

7.7 Habitat and ecological considerations

Consideration of habitat differences among sites with the same genetic classification and no known life history differences is step 4 of our procedure. From step 3, five cases emerged where habitat considerations could be useful (see immediately previous table). Of those, three cases involved two or three ecotypic CUs (cases 1, 5, & 6). Since, there are multiple habitat differences between the ecotypic CUs, by definition all of the JAZ concerned were assumed CUs. Case 7, which involves a contrast between the lower Nass River and coastal sites in Portland Sound, Portland Canal and Observatory Inlet, has been considered previously in the analysis of chum salmon (see Section 6.7), where we demonstrated sufficient differences between a large river and coastal streams to warrant the recognition of two CUs. Consequently, the LNR-P+NSKEst ecotypic CU was split into two coho CUs.

Case 2 (see immediately previous table) involves two genetic clusters in the lower Fraser ecotypic CU. The habitat associated with the two genetic clusters was significantly different (Table 25). Sites in Cluster M had lower gradients, were at lower elevations, were more hydrologically stable, were warmer, and had lower precipitation than those in cluster L. Those in cluster M also tended to be in the lower reaches of the Fraser River and on the south side of the river (Figure 38). Consequently, cluster M was recognized as a coho Conservation Unit.

7.8 Summary

There are 43 Conservation Units of coho in British Columbia (Figure 39, Table 26). Several of those CUs should be regarded as provisional. The Brim-Wahoo CU comprises only a few small systems but its genetic distinctiveness would seem sufficient to justify its status. What is remarkable is that such distinctiveness has been maintained presumably for thousands of generations. The Brim River and Wahoo Creek populations are most closely related to the Oona River population, which was the only genetic sample from the ecotypic HecLow+NSKEst ecotypic CU. Without additional genetic samples, we cannot determine if the other systems in the CU are related to the Oona River. If not, then it is plausible that the Oona River is another distinctive CU in that genetically diverse area. The boundaries of other small CUs established at step 2, such as the Mussel-Kynoch, Douglas Channel-Kitimat Arm, and Clayoquot, are provisional pending the acquisition of additional genetic samples. Finally, ecotypic CUs in the northern transboundary rivers where there are few data are provisional on the acquisition of basic biological information.

8. Chinook salmon

8.1 Distribution

In North America, chinook are distributed from central California (Yoshiyama et al. 1996) to Kotzebue Sound, Alaska (McPhail and Lindsey 1970). Chinook might also occur in the Mackenzie River, NWT, but the single observation was considered a rare stray (McLeod and O'Neil 1983). The distribution in Asia, from northern Hokkaido, Japan, to the Anadyr River in the Russian Federation, is similar in latitudinal extent (Healey 1991). Chinook were successfully transplanted to New Zealand in the early 1900's, one of the very few successful transplants of any Pacific salmon species (McDowall 1994)

8.2 Life History

Chinook salmon are the largest of the Pacific salmon with some individuals weighing over 50 kg. Sub-adult chinook are piscivorous, readily take trolled lures, and consequently are highly sought after by commercial and recreational fishers. Their large size also makes them the preferred food of piscivorous killer whales (Ford et al. 1998), an iconic and at-risk species. Chinook salmon have a highly diverse life history with variations in age of seaward migration, variations in the duration of estuarine and ocean residence, migration patterns in the ocean, and timing of spawning migrations and spawning (Healey 1991). This complexity has been studied extensively and can be conceptually summarized succinctly (Healey 2001). Much of the variation in life history is associated with the length of time juveniles spend in freshwater before smolting. In one form, called the stream-type, juveniles spend at least one winter (after emergence) in freshwater. In the other form, called the ocean-type, juveniles smolt sometime during the spring or summer after emergence. Stream-type populations are usually situated distant from the ocean whereas ocean-type populations are usually coastal. Stream-type adults usually return to freshwater during the spring and summer, months before spawning while ocean-type return in the fall, shortly before spawning. Stream-type individuals typically undertake long ocean migrations that are far offshore whereas oceanic migrations in ocean-type fish are often shorter and are mostly in coastal waters.

The two forms appear to have arisen multiple times and are only genetically distinct, i.e., strongly reproductively isolated, in the interior Columbia (Waples et al. 2004). Nevertheless, there is no evidence to suggest that facultative switching between the two life history types occurs (Healey 2001).

8.3 Lineage

The post-glacial zoogeography of chinook salmon in Canada is unclear. Teel et al. (2000) demonstrated two major lineages in British Columbia using allozyme data. A coastal lineage comprised populations in the lower Fraser River, W Vancouver Island, around Georgia Strait and the Central Coast. The second "interior" lineage comprised populations in the Fraser River above Hell's Gate and the Nass and Skeena Rivers. This study did not include any samples from the Queen Charlotte Islands, the northern transboundary rivers or the Yukon River.

Beacham et al. (2006b) undertook a comprehensive survey of the population structure of chinook around the Pacific Rim using microsatellite DNA with substantially the same results as Teel et al. (2000) at least in terms of population structure if not the association of genetic lineage and life-history type. Beacham et al. (2006b) concluded that there were at least two lineages of chinook in Canada: a Yukon River-Alsek River lineage closely associated with populations in the Russian Federation and a southern lineage with separate colonization routes into the lower and interior Fraser. The provenance of populations on the Central and North Coasts was uncertain. At a smaller spatial scale the population structure (dendrogram: Figure 41, schematic: Figure 42) is consistent with there being approximately 12 major sub-groups of chinook salmon in Canada as summarized in the following table.

group	sub-group	genetic cluster(s)	example major systems	description
1	A	V, W	Yukon River	Yukon River
	B	U	Klukshu River	Alsek River
	C	S, T	Unuk River, Ecstall River	isolated sites in the two named rivers
2	A	N-R	Yakoun River, Stikine River, Taku River, Nass River, Babine River	The major transboundary rivers in the Alaskan Panhandle, the Nass and Skeena Rivers and the Queen Charlotte Islands
	B	L	Bella Coola River	North and Central Coast streams from south of the Skeena to Rivers Inlet
3	A	K	Wannock River	isolated ocean-type population in Rivers Inlet
	B	H-J	S Thompson River	sites above Hell's Gate in the Fraser River
	C	G	Harrison River	chinook in the Fraser River below Hell's Gate and the mainland bordering the Strait of Georgia
	D	F	Robertson Creek	the West Coast of Vancouver Island
	E	A-C	Quinsam River	East Coast of Vancouver Island and Boundary Bay (Puget Sound)
	F	D	Okanagan	sole Canadian site in the upper Columbia River
	G	E	Docee River	a very isolated single site in Smith Inlet

These groupings represent an alternative starting point to the ecotypic zones for the description of chinook Conservation Units.

8.4 Life History Variants

The division of chinook salmon populations into either "stream-type" or "ocean-type" is the most important generalization made from the extensive study of the species' highly varied life-history (Healey 2001). Most of the coastal populations in southern BC including Vancouver Island are predominantly ocean-type, while most on the central and northern coasts are stream-type. Most of the populations in the headwaters of the large river systems are stream-type regardless of where they are located. There are some prominent exceptions to these generalities that are important components of diversity in the species and are, therefore, important to the description of CUs for chinook salmon. For example, the summer-run populations in the southern Thompson River are predominantly ocean-type, which is unusual for chinook far removed from the ocean.

8.5 Ecotypic Conservation Units

Chinook salmon are known to be present in 34 of the 39 JAZ ecotypes and are probably present in two others (Table 27). Chinook salmon are not thought to be present in streams on the west coast of the Queen Charlotte Islands or in the upper Mackenzie River drainage, although a range extension into the Arctic is certainly anticipated as the northern climate warms. Chinook are known to be present in at least six streams of the QCI+HStr JAZ but the records are scant and it is possible that chinook is not persistent in this JAZ. One population (Pallant Creek) is a naturalized transplant from the Quinsam River and was excluded from the analysis. Although chinook salmon are widespread, the species is present in only 584 of the 2277 sites (26%) in our database that have one or more species of Pacific salmon, making it (by far) the rarest of the 5 species we considered[23]. Chinook salmon are noticeably absent from some JAZ ecotypes where the other species are ubiquitous. For example, chinook populations are rare on the Queen Charlotte Islands (3% of 243 sites) compared to chum and coho salmon, which are present in 87% and 83% of those same sites, respectively. In the HecLow FAZ chinook are present in only 4% of the 241 sites while the other species (sockeye excluded) are present in between 77% and 83% of the sites. Such differences have been explained by differences in habitat requirements and the general absence of large rivers from some regions (Healey 1991). That reasoning seems suspect in some areas such as streams of the NC and LNR-P FAZ, where chinook are found in about 25% of the streams while chum and coho are often present in more than 80% of them, many of which appear to be of a suitable size for chinook.

8.6 Ecotypic X Genetic Classifications

Genetic samples were available from 312 sites in Canada (Table 28). Twenty-three of those sites are in the Yukon River drainage. The neighbor-joining dendrogram (Figure 41) was summarized into 21 genetic clusters (Figure 42) that were then compared to the ecotypic CUs (Table 29, Figure 43).

Nineteen of 29 ecotypic CUs were genetically monotypic, six had two genetic clusters and the remaining four CUs had three clusters (Table 29). Four of the genetic clusters (G, H, L & R) had sites from four ecotypic CUs, two clusters (C & J) had sites from three ecotypic CUs and four (F, I, P & Q) had sites from two CUs (Table 29, summarized in the following table).

number of JAZ in cluster	cluster	JAZ present in cluster†
4	G	LFR, LILL, SC+GStr, HK
	H	LFR, MFR, LTH, STH
	L	RSI, BCD, NC, LNR-P
	R	MSK, USK, LNR-P, UNR
3	C	SC+SFj, EVI+GStr, EVI+SFj
	J	LFR, MRF, UFR
2	F	WVI+WVI, WVI+WQCI
	I	LTh, NTh
	P	LStk, TAKU
	Q	LNR-P, LSK

† Only the FAZ part of the JAZ name is given where there is no ambiguity.

Most of this apparent lack of agreement between the genetic and ecotypic population structure was resolved by removing transplanted and hatchery stocks, minor border adjustments or by considering the genetic structure at the "class" rather than the "cluster" level. Those considerations are summarized in Table 30.

The Fraser River chinook populations are the most ecologically and genetically diverse in Canada. Fortunately, due to their economic and cultural value their genetics and biology have been extensively studied (e.g. Beacham et al. 2003, Murray and Rosenau 1989, Nelson et al. 2001, Rieman and Dunham 2000, Schubert et al. 2007, Teel et al. 2000, Withler et al. 1997) and Conservation Units for Fraser River chinook have

[23] However, river-type sockeye are found in only 10% of the sites we considered.

been proposed (Candy et al. 2002). Sites in the Fraser River and its tributaries fell into four genetic clusters, G to J (Table 28, Table 29). Within cluster G, two genetic classes, 03.01.01 and 03.01.02, separate the distinctive ocean-type, fall run-timing Harrison River (GFE_ID #179) population from stream-type summer run-timing populations in the LFR and LILL FAZs. The Harrison population has been transplanted by means of hatcheries to the Chehalis (#181), Stave (#34) and the Chilliwack/Vedder (#62) and as it is now the dominant form in those systems they must be considered non-wild. The non-Harrison group encompasses considerable diversity. The remaining sites in the lower Fraser are similar genetically based on limited information and their treatment has been deferred to the following section on spawn timing.

Cluster H comprises five CUs that, for the most part, can be distinguished at the third or fourth genetic class and by a combination of life history, spawn and run timing and habitat characteristics. Two of the CUs are monotypic. The Maria Slough population (#104) is an ocean-type (age 0.3) MSUM run-timing population in the lower Fraser, which is genetically related to the summer chinook in the South Thompson. It is sufficiently distinctive to warrant CU status. The Portage population (#129) is also related to the summer populations in the South Thompson but is suspected of being stream-type and having, atypically for this life-history type, a fall run timing. Biologists in the Fraser Area have suggested that it is also a CU (pers. comm.. R. Bailey, DFO Kamloops). The distinctiveness of this population could be due to the tumultuous geological and hydrological history of the area[24]. Four sites in this cluster (class 04.01.02) are ocean-type (age 0.3) chinook that spawn at the outlets of large lakes and are together a CU. Five sites, which are tributaries of the South Thompson or of Shuswap Lake, are not lake-influenced, and have stream-type, age 1.3 chinook with an ESUM run-timing. Together these sites are a second CU in the STh JAZ. A third CU in the STh JAZ is comprised of the two large populations in the lower (#241) and middle (#240) Shuswap Rivers. Like the populations around the outlet of Shuswap Lake, these two populations are ocean-type with a MSUM run-timing and Candy et al. (2002) placed all of the ocean-type fish in the same CU. However, the two groups are of different third-level genetic classes (Table 28) and appear to be sufficiently distinctive (Figure 41) to be a separate CU. Although the Shuswap populations have a slightly earlier run timing (by ≈12 d), their mean spawning times are indistinguishable. Three sites in the headwaters of Bessette Creek (#252), which is a tributary of the middle Shuswap River (#241) comprise what might be a fourth CU in STh JAZ. Unlike the very closely related populations in the lower and middle Shuswap River these chinook are stream-type but unlike the other stream-type chinook they are aged 1.2 rather than 1.3. A younger age would indicate a smaller size at maturity, which is quite possibly an adaptation to the relatively small hydraulic size of the streams these fish are found in. The possibility that the difference in life history compared to the Shuswap River populations might be facultative cannot be discounted, but we have tentatively placed these sites into a novel CU.

Cluster I comprises two genetic classes that correspond, with one exception, to the NTH and LTH ecotypic CUs (Table 28). There are also age and timing differences between the populations of the two CUs (Table 30). Fraser River biologists have indicated that the boundary between the LTh and NTh ecotypes should be at Fishtrap Canyon and Louis Creek (#257) (pers. comm. Bailey, DFO Kamloops). The

[24] See http://www.cayoosh.net/portage.html for a short history of the area.

complexities of population structure in this area probably reflect the immediate post-glacial patterns of ice-damming and discharge (Johnsen and Brennand 2004).

Cluster J comprises the most of the sites in the MFR ecotypic CU and all of the sites in the UFR ecotypic CU. The genetic relatedness of these sites suggests relationship by distance but an exploration of the geographic relationships among the sites does not reveal much evidence for that explanation. For example, The Stuart River (#305) in the NW of the MFR JAZ is genetically closer to the Bridge River (#133) near the southern boundary of the MFR JAZ than to many of its geographic neighbors. The patterns of genetic relationships probably arose because of drainage patterns during deglaciation. Regardless, this large cluster can be partitioned into the MFR and UFR ecotypic CUs at class 04-09 (MFR) and 04-10 (UFR) with only two exceptions (Table 28, Figure 41, Figure 42).

In addition to three CUs in the lower Fraser River, cluster G comprises sites in the SC+GStr and HK+SFj ecotypic CUs. Sites in the Homathko River (#819) and the Klinaklini River (#850) can be separated at the third level of the genetic hierarchy (Table 28) suggestion a partition of the ecotypic CU would be warranted. The remaining sites in cluster G are from Howe Sound (principally the Squamish River #708). There are no other genetic sample from the SC+GStr ecotypic CU. Howe Sound and Burrard Inlet have been split of the SC+GStr CU in both coho and chum but there is insufficient genetic evidence to warrant such a split in chinook. However, such a split can be examined using the spawn timing and habitat data.

Cluster L comprises sites in three third-level genetic classes that conform to the three ecotypic CUs involved (Table 28). These are all stream-type populations. The Wannock population (#935) is ocean-type and defines a distinctive monotypic cluster (K; Figure 41, Figure 42). There were no genetic samples from the small number of chinook populations in the HecLow+HStr ecotypic CU.

Cluster R comprises four third-level genetic classes with sites in the Nass River and Skeena Rivers (Table 29). The two river basins can be distinguished at that level of the genetic hierarchy (Table 30) but no simple separation scheme is apparent within the two river basins (Table 28).

Cluster P included sites from the Taku and the lower Stikine Rivers. Cluster Q included sites from the LNR-P and LSK ecotypic CUs. In both cases, the two ecotypic CUs in each cluster could be distinguished at the fourth level of the genetic classification. Decisions on CU-status were deferred to steps 3 or 4.

The Okanagan population is the only extant population of Columbia River chinook in Canada. It is closely related genetically to chinook populations in the Okanagan River drainage in the USA, which are part of the Upper-Columbia River Summer-and Fall-Run ESU (Myers et al. 1998). The remaining Canadian populations to consider are in the Boundary Bay FAZ and are closely related genetically to chinook populations in eastern Puget Sound with which they likely share life-history and ecological characteristics (Myers et al. 1998).

There were four single-site clusters in Canada (Table 29, Table 30). In only one of those cases did the single site represent the only genetic sample from an ecotypic CU (N, (Table 28, Table 29). In the other three cases, the genetic distinctiveness of the site warranted CU status.

8.7 Spawn timing

Run timing, the period during which adults enter freshwater, is commonly used to describe chinook populations and to identify significant population groups. Run-time is certainly important to fisheries management in guiding terminal fisheries and has been used to describe Conservation Units of chinook in the Fraser River (Candy et al. 2002). Waples et al. (2004) found that geographical and ecological zones (ecotypes in this paper) were more useful in describing population structure. We do not have a comprehensive database of run timing but instead use spawning time, for which we have a detailed record for most SEDS populations (Table 32). However, run-timing information through the Albion test-fishery at the mouth of the Fraser River is available for 53 chinook populations in the Fraser River and we did use that information in describing Fraser River chinook CUs. Mean spawn timing was also available for 50 of those populations, and there was a highly significant correlation between migration timing and spawn timing:

mean DOY spawning=161.4 + 0.482median DOY migration	$r^2_{adj} = 0.595$ $SE_{est} = 20.75$ $F_{1,49} = 74.4; P < 0.0001$

The time of spawning would appear to be a reasonable surrogate of migration timing, at least for Fraser River chinook, but there is no compelling evidence indicating that run timing and spawn timing are more generally related (Healey 1991). Because run timing is so frequently used to describe chinook populations, we use both spawn timing and the residuals from our spawn timing model to describe population structure at a level finer than our ecotypic zones allow.

Although local knowledge suggests that many rivers have more than one run of chinook, the SEDS database lists only 12 populations with more than one spawn-timing categorization (Table 31). Only four of them have a sufficient number of observations in more than one category to evaluate. In the Chilcotin River (GFE_ID 285) there is a four day difference in the mean spawning times of the two recorded runs (timing categorizations are not specified), which is not a statistically significant difference. The differences in spawning time between the run time components in the Puntledge (GFE 1156) and Nanaimo (GFE_ID 1194) Rivers are small and not statistically significant (Table 31). Healey (1991) observed that chinook of different run timing components have similar spawning times and often spawn on the same riffles. However, in the single instance where a natural and a transplanted population can be compared, the natural population in the Chilliwack River (GFE_ID 62) spawned in late summer, 53 days before the transplanted population (from Harrison River GFE_ID 179). The transplanted population has a similar mean date of spawning (DOY 307.2) to the source population (DOY 313.6).

The geographical pattern of spawn timing in chinook salmon (Figure 45) is somewhat atypical in that there appears to very little variation over a broad latitudinal range (approximately 51°N to 56°N) and longitudinal range (-117°W to -131°W at its broadest). When spawn timing is plotted against latitude (Figure 46), a discontinuity in the relationship can be seen in the Central Coast around 51°N to 53°N. Similar discontinuities were seen in both chum and coho salmon. Like those species, the spawn timing model fully accounted for the discontinuity (Figure 46, inset).

A linear regression model for spawn timing accounts for 53% of the variation in the 502 populations considered (Table 33). Chinook spawn earlier with increasing latitude, as the proportion of the upstream watersheds that are either glaciers or tundra increase, in watersheds without lakes and in colder temperature regimes. The latitudinal cline in spawning time can be seen in Figure 45. The following table shows some comparisons of mean spawning time with populations grouped by the JAZ ecotype. In general the spawning times of populations in the same FAZ but different MAZ ecotypes are significantly different as are the spawning times of populations in different FAZ that have the same MAZ. Of particular interest are the comparisons within the FAZ surrounding the Strait of Georgia and Hecate Strait. Within the Fraser River, the spawning times vary between the FAZ but the only significant difference is that populations in the Upper Fraser River spawn, on average, earlier than in any of the other FAZ. Spawning times within the Skeena and Nass Rivers FAZs are not significantly different.

Same FAZ different MAZ	*P*
EVI+GStr>EVI+SFj	<0.005
SC+GStr>SC+SFj	0.053
WVI+WVI>WVI+WQCI	<0.05
HecLow+HStr=HecLow+NSKEst	~0.6
QCI+HStr>QCI+NQCI	<0.05
Same MAZ different FAZ	
EVI+GStr>SC+GStr	<0.001
LFR+GStr=SC+GStr	~0.4
LFR+GStr<EVI+GStr	<0.001
EVI+SFj>(SC+SFj=HK+SFj)	<0.01
HecLow+HStr>NC+HStr	<0.05
QCI+HStr>HecLow+HStr	<0.001
Fraser River FAZ	
UFR<MFR	<0.001
All other FAZ equal	>0.5
Skeena/Nass River FAZ	
All Skeena FAZ equal	~0.9
Both Nass FAZ equal	~0.2

The early timed (MSPR) Birkenhead population (#198) has been recommended as a CU (Schubert et al. 2007). Based on limited records of spawn timing, the pre-enhancement populations in the Stave River (#34) and the Chehalis River (#181) likely would have been included in that CU. The remaining sites in the lower Fraser River (including the Lillooet River (#177 & #178), Big Silver (#192), and the upper Pitt River (#13) share a similar life history and are genetically similar but vary in spawn-timing and presumably run-timing as shown in the following table.

population group	number of sites	number of observations	mean spawn time=§ (DOY)
spring run (Birkenhead, Chehalis	4	63	177.0
Upper Pitt River	1	34	237.9
summer run (Big Silver, Lillooet River)	9	87	271.9
ANOVA			$F_{2,219}$=164.2 P<<0.0001

§ All pairwise comparisons were significant P<0.0001.

The chinook of the upper Pitt River spawn, on average, on Aug. 27th (LSUM) or two months after the spring run into the Birkenhead (June 26th or ESUM) and one month before those in the summer runs in the Lillooet River and elsewhere in the lower Fraser River (Sept. 28th or EFALL). Consequently, we consider the upper Pitt River chinook to be a separate CU.

The disposition of the Nahatlatch River (#125), the only chinook site in the Fraser Canyon ecotypic CU was problematic. The Nahatlatch chinook are thought to be stream-type and are known to be predominantly age 1.3, so they resemble summer chinook populations in the Lillooet ecotypic CU rather than those in the lower Thompson River (Candy et al. 2002). The spawn timing, and presumably the run timing, of the Nahatlatch chinook are more similar to the lower Fraser summer chinook than to the lower Thompson chinook, as the following table shows.

population group	number of sites	mean spawn time (DOY)	mean residual (d)
Lillooet	4	272.8	10.5
Nahatlatch	1	264.4	4.53
LTh	6	243.2	-13.7
F-statistic and P	11	$F_{2,8}$=2.81; P=0.12	$F_{2,8}$=1.93P=0.21

We had no genetic information for the Nahatlatch site but more recent information indicates that the site is more closely related to Middle Fraser springs than to the sites in the Lillooet (pers. comm.. R. Bailey, DFO, Kamloops). In the absence of definitive evidence, we maintained the Nahatlatch as an ecotypic CU.

Although all the sites in the middle Fraser are very similar genetically, there are two spawn timing groups. The earlier spawning group is associated with headwater streams while the later spawning group is generally associated with large lakes. The spawning time difference is approximately 20 days as shown in the following table. We concluded that the two groups are separate CUs.

population group	number of sites	mean spawn time (DOY)	mean residual (d)
early timing, headwater streams	21	238.0	-8.21
later timing, lake headed	14	258.3	4.53
F-statistic and P	35	$F_{1,33}$=60.3; P<0.0001	$F_{1,33}$=11.0; P<0.005

Within the SC+GStr JAZ, no genetic samples were available outside of Howe Sound. For both coho and chum salmon, Howe Sound-Burrard Inlet was deemed a CU, raising the possibility that such would be the case for chinook as well. Although there were differences in the both the mean spawning date and the timing model residuals, the differences were not statistically significant (see following table). Consequently, the ecotypic CU was not altered. However, further investigation of the genetic affinities of the populations in the SC+GStr CU would appear warranted.

population group	mean spawn time (DOY)	mean residual (d)
Howe Sound-Burrard Inlet	261.4	-18.2
SC+GStr (remaining sites)	248.6	+9.9
F-statistic and *P*	$F_{1,30}$=1.42; *P*=0.24	$F_{1,30}$=0.80; *P*=0.38

Genetic cluster C (genetic class 01.02.03) includes sites from the EVI+SFj ecotypic CU and one site from the SC+SFj CU (Table 28, Table 30). On average, populations on Vancouver Island spawned significantly later than populations on the mainland but there were no significant differences in the residuals from the spawn timing model

population group	mean spawn time (DOY)	mean residual (d)
EVI+SFj	272.8	-3.5
SC+SFj	250.6	-7.5
F-statistic and *P*	$F_{1,32}$=5.45; *P*=0.026	$F_{1,32}$=0.27; *P*=0.60

The mean spawning dates are both in September and the populations in both ecotypic CUs would likely be considered summer-run. The spawn timing model accounts fully for the differences in spawn timing. The differences in mean spawning time are also fully explained by the percentage of high elevation terrain within the watersheds of the various populations, leading us to conclude that there were sufficient habitat (i.e., ecological) differences between the systems occupied by chinook in the two areas to maintain the two ecotypic CUs.

Only one genetic sample was available from the eight populations on the Queen Charlotte Islands (Table 28). Pallant Creek population (#1584) was excluded because it is a naturalized population from a Quinsam River hatchery transplant. There were significant timing differences between the two ecotypic CUs represented and near-significant differences in the timing model residuals. Consequently, two chinook CUs, defined by the ecotypic CUs, were recognized on the Queen Charlotte Islands.

population group	mean spawn time (DOY)	mean residual (d)
QCI+NQCI	255.9	-7.6
QCI+HStr	289.6	21.9
F-statistic and *P*	$F_{1,5}$=9.90; *P*=0.025	$F_{1,5}$=5.36 *P*=0.068

There are only six chinook populations in the HecLow+HStr ecotypic CU compared to 34 in the adjoining NC+HStr CU. There are no genetic samples available for the ecotypic CU. Ten of the 40 sites are associated with a large (>100 ha) lake and five of those sites are in the HecLow+HStr CU. There are significant differences in the spawn timing and in the model residuals when the comparison is made between those with and without a large lake.

population group within HecLow+HStr and NC+HStr	mean spawn time (DOY)	mean residual (d)
with large lake†	250.3	-12.5
no large lake	232.1	0.24
F-statistic and *P*	$F_{1,39}$=13.3; *P*<0.001	$F_{1,39}$=6.81 *P*=0.013

† in HecLow+HStr: Kiskosh (#1087), Kumealon (#1097), Bloomfield (#1844), Little (#1840), Koeye (#957); in NC+HStr: Mussel (#1015), Carter (#1017), Kitkiata (#1085), Quaal (#1086), Kitlope (#7990614)

In the absence of genetic samples for sites in the HecLow+HStr JAZ and since the spawn timing model does not fully account for the differences in spawn timing between sites with and without lakes, we decided to combine the ecotypic CUs and then to designate two new CUs based on the presence of a large lake.

The WVI+WVI ecotypic CU (the west coast of Vancouver Island south of the Brooks Peninsula) has two population groups defined at the fourth level of the genetic hierarchy (genetic classes 02.02-01, 02.02-02; Table 28). A third population group in the ecotypic CU (genetic class 02.03) comprises the Robertson Creek hatchery population, which is one of the largest chinook hatchery populations and is not considered here. The two wild population groupings are approximately separated geographically by Barkley Sound. The Toquart River (#1288) on the north shore of Barkley Sound has been recently stocked with Nitinat River (#1242) fish so it is possible that the genetic samples did not come from native the Toquart population. We examined the spawn timing of 101 populations in the WVI+WVI ecotypic CU to determine the two apparent genetic groups also had different timing. A plot of the mean date of peak spawning against site latitude Figure 50) suggests that there are three distinctive population groups. First, there is an abrupt shift in the date of peak spawning from late September (EFALL) to late October (MFALL) that occurs to the immediate south of Kyuquot Sound at latitude 49.58°N. A third group is apparent in the early spawning populations in the San Juan (#1231) and Gordon Rivers (#1238). The differences between mean spawning dates within the three groups are highly significant as are the residuals for the timing model.

population group	mean spawn time (DOY)	mean residual (d)
Nootka & Kyuquot Sounds	275.8	-0.90
south of Nootka Sound†	299.8	9.31
San Juan & Gordon Rivers	270.9	-23.5
F-statistic and *P*	$F_{2,99}$=71.2; *P*<<0.0001	$F_{2,99}$=16.8 *P*<0.0001

†excluding sites in the Somass River drainage and Thorton Creek, all of which are Robertson Creek hatchery populations and hence not wild.

This division of populations is concordant with the genetic structure with the exception of the Nahmint River (#1270), which has southern timing but northern genetics Figure 41, Table 28). The Robertson Creek group has southern timing (DOY of peak spawning=298.3), which is consistent with its derivation from a wild population in the southern group. It would be interesting to examine whether the southern timing has been maintained in the hatchery population apparent colonization of the Gold and Muchalat Rivers (these errant fish appear to have been sampled, see Figure 41). Timing thus helps interpret the genetic structure and leads us to the conclusion that there are three chinook CUs in the WVI+WVI JAZ.

There are three genetic clusters present in the LNR-P ecotypic CU. One of the clusters (L) is represented by a single site (Kateen River #2001754) that is geographically distant from other members of the cluster (Figure 43). There are no spawn timing data available for the Kateen River, but timing in its parent stream, the Khutzeymateen River (#1754), is similar to other coastal sites in the ecotypic CU. Its timing is also similar to other sites in cluster L, so it is possible that genetic affinity of the Kateen population is not an anomaly but is indicative of additional genetic diversity in the ecotypic CU. Spawn timing data, which are summarized in the following table, indicates that the four sites in the LNR-P CU that are in proximity or upstream of the two sites in LNR-P in cluster R are similar to UNR sites in cluster R and significantly different than those in cluster Q. We conclude that the timing data supports the genetic data and that there are (at least) two CUs in the Nass River.

population group	mean spawn time (DOY)	mean residual (d)
LNR-P – cluster Q	226.3	-6.4
LNR-P – cluster R (Tseax and upstream)	256.2	8.3
UNR – cluster R	243.1	2.8
F-statistic and *P*	$F_{2,25}$=9.3; P<0.001	$F_{2,25}$=1.59; P=0.22

The Skeena River like the Nass River is genetically diverse with representatives of four genetic clusters (Table 28, Table 30, Figure 42, Figure 52). Two of the clusters (O and S, Table 28) are not closely related genetically to each other or to the prevalent clusters of the Skeena River watershed (Q & R, Table 28). The single site in cluster O is the Gitnadoix River (#460), which appears to be more closely related to sites in the Stikine and Taku Rivers than to sites in the Skeena River (Figure 41). The other cluster (S) also has only one site (Ecstall River #447), which most closely related to the Unuk River (#2002118) and the Chickamin River in SE Alaska (Figure 41). We consider both the Ecstall and the Gitnadoix to be two CUs.

There are only two genetic samples in the remainder of the LSK ecotypic CU. Both of the sampled sites are in the Kitsumkalum River system but are in different level-4 classes in cluster Q (Table 28). The sample from the Cedar River (#531, a tributary to the Kitsumkalum River above Kitsumkalum Lake) is notably distinctive within the cluster (Figure 41). In terms of life history and timing the chinook of the mainstem Kitsumkalum are distinctive. These fish are predominantly aged 1.4 (six years old) compared to the typical age of other chinook in the area (predominantly 1.2) and consequently, are much larger (McNicol 1999, Roni and Quinn 1995). Mainstem Kalum chinook spawn about three weeks after the headwater tributaries of the Kitsumkalum River and other neighboring systems (see following tables). The Kitsumkalum populations are also the largest chinook populations in the lower Skeena (see following tables).

GFE_ID	site	mean escapement	N obs	mean DOY peak spawn	N obs	timing model residual
456	Khyex River	134	26	256.4	20	20.3
459	Kasiks River	145	41	241.9	37	10.5
469	Exstew River	71	24	238.8	19	2.4
473	Zymagotitz River	57	31	237.3	28	-7.9
477	Kleanza Creek	14	9	248.6	16	8.2
482	Fiddler Creek	113	15	239.7	15	-0.46

GFE_ID	site	mean escapement	N obs	mean DOY peak spawn	N obs	timing model residual
504	Exchamsiks Rivers	106	37	239.1	35	12.7
505	Lakelse River	190	44	247.3	38	-24.3
520	Kitsumkalum River-upper	4002	20	257.2	12	9.1
521	Kitsumkalum River-lower	9935	43	258.3	27	10.2
530	Clear Creek	166	48	244.0	38	7.0
531	Cedar River	764	48	238.4	44	-7.2
533	Zymoetz River (Copper)	401	30	241.3	27	-7.1

In terms of mean DOY of peak spawning, the sites in the lower Skeena ecotypic CU can be divided into three groups : Kitsumkalum mainstem (latest); Lakelse (intermediate); and the upper Kalum tributaries plus the other sites except the Khyex (see following table).

site(s)	N	mean DOY peak spawn
lower Skeena tributaries	183	239.8
Kalum headwater tributaries (early timing)	82	241.0
Lakelse River and tributaries	53	246.1
Kalum mainstem (late timing)	39	257.9
ANOVA	357	$F_{3,353}$=29.4; P<<0.0001

Based on timing and the genetic distinctiveness of the two Kalum timing groups we recognized four CUs in the lower Skeena in addition to the Ecstall and Gitnadoix CUs previously recognized because of their distinctive genetics. The four CUs are Kitsumkalum-late timing (or mainstem), Kitsumkalum-early timing (or headwater tributaries), Lakelse River and tributaries, and the remaining Skeena tributaries collectively referred to as the Lower Skeena CU. The Khyex River, the lowest tributary (i.e., closest to the ocean) in the group is late timed like the Kalum mainstem sites. Interestingly, like the other late-timed sites, there is a large lake in the system, Arden Lake of 201 ha surface area. The lake appears to be inaccessible but probably moderates stream temperatures in the fall. We were unable to discover detailed information about Khyex chinook and without genetic information we cannot determining to which group they belong. We assigned this site to the Lower Skeena CU recognizing that with additional information it may be reassigned or recognized as an additional CU.

There are six sites with genetic samples in the MSK ecotypic CU and three sites in the USK ecotypic CU (Table 28). All of the sites are in cluster F (Table 28) and are closely related (Figure 41). The most distinctive site in the group is the upper Bulkley River (GFE_ID=541; Figure 42), a large population (mean escapement 822, N=52) that has undergone extensive supplementation[25]. The genetic structure in the USK and MSK ecotypic CUs suggests three groups corresponding to the second-level genetic classes 8.7, 8.8 and 8.9 (Figure 42). The genetic distance of the Sustut River from other members of its genetic class suggest that it represents a fourth genetic group in the USK ecotypic CU (Figure 41). We assumed that there are four genetic groups in the two ecotypic CUs and then examined variation in spawn timing within and between those groups.

[25] 27 annual releases between 1987 and 2005 with 18 releases of 1^+ smolts (average release 34,073); 4 releases of 0^+ smolts (average release 15151) and 5 releases of fall fry (average release 18143).

Table 34 summarizes the available information on genetic classification, time of peak spawning, mean escapement, and the residuals from the spawn timing models for all chinook sites within the MSK and USK ecotypic CUs. When we examined the DOY of peak spawning within each of the four genetic groups, we found that there was a marked bimodality within group 2. The two groups corresponded to an early spawning group that comprised mainstem tributaries to the Skeena River (Kitseguecla River-#537 and Shegunia River #496) and several lower tributaries to the Kispiox Rivers (Date-#567, Hevenor-#568, McCully-#569 and Cullon-#571 Creeks), and a later spawning group comprised of sites in proximity to the small lakes of the Kitwanga, Kispiox and Slamgeesh watersheds (Table 34). When separated into two groups (2 and 2a, Table 34), the order of spawning times in the five groups (Figure 53) indicates the influence of lakes and altitude and corresponds to the genetic classification of the sites (see following table).

genetic classification		DOY peak spawning				
MSK-USK group	class	mean	N_{obs}	statistical comparison of mean DOY	residual from timing model	site characteristics
gg1	08.09-2	252.1	158	gg1>gg2 *P*<0.001	7.61	large lakes
gg2	08.08	244.1	132	gg2>gg2 *P*<0.01	-1.13	small lakes
gg3	08.07	237.1	24	gg3=gg2a=gg4 *P*>0.05	-10.8	upper Bulkley
gg2a	no data-	230.6	49		-9.74	mainstem headwater tributaries
gg4	08.09-1	224.6	5		-4.5	high elevation in USK

We concluded that the five groups in the middle and upper Skeena River drainage are Conservation Units. The assignment of the sites in that area to the five CUs is shown in Table 34

In collaboration with CDFO, the Alaskan Dept. of Fish and Game has made extensive studies of Canadian chinook populations in the transboundary rivers of northern British Columbia that provide useful data about run timing and age composition. The studies in most of the rivers consisted of river-mouth test fisheries and trapping to obtain overall run timing and biological information and the application of radio frequency internal tags. Radio telemetric surveys of river junctions and selected spawning areas provided the destinations of the tagged fish (Pahlke 1995, Pahlke and Bernard 1996, Pahlke and Etherton 1999, Pahlke et al. 1999).

In the Stikine drainage there appear to be two run-timing groups. Chinook destined for the Little Tahltan and Chutine Rivers () enter the Stikine around June 9th, while chinook destined for the Iskut River and its tributaries (Craig and Verrett Rivers) enter around June 30th (Pahlke and Etherton 1999). Chinook in the Stikine River drainage are a mix of age 1.3 (preponderance of males) and age 1.4 (preponderance of females) fish, with an overall preponderance of age 1.4 fish. The differences in run timing are likely sufficient to recognize two CUs but a final decision was deferred to habitat considerations.

There are three distinct run timing groups of chinook in the Taku River drainage. The first group enters the river around May 12th destined for the Nahlin River in the headwaters of the Inklin River () (Pahlke and Bernard 1996). The second group, which enters about one month later in mid-June spawns in the Nakina River drainage. The third group enters in the first week of July and spawns in the Kowatua River and Tatsatua Creek, which are associated with the Little Trapper and Tatsamenie Lakes, respectively (). Taku drainage chinook are mostly age 1.3 or 1.4 with a preponderance of age 1.3 in both sexes. There are likely three chinook CUs in the Taku River drainage but a final decision was deferred to habitat considerations.

There was less information available for the minor transboundary rivers. In the Alsek River there appears to be only one run of chinook, which enters the river around the middle of June (Pahlke et al. 1999). The radio telemetry study indicated no differences in run timing among fish destined for different areas of this large river system. Alsek River chinook were predominantly aged 1.3. We were unable to find timing information for chinook in the Unuk River other than the dates for operation of a counting weir in the river, which were mid-July to late August. This suggests that Unuk River chinook have the latest timing in the transboundary area. The fish were predominantly age 1.4. We could find no information for Whiting River chinook other than a confirmation of their presence in the system (Committee 2005).

There are 15 river systems with chinook salmon on the east coast of Vancouver Island bordering the Strait of Georgia (Figure 55) but only one very small population (Simms Creek #1145) has not been augmented with hatchery-reared chinook between 1968 and 2005 (Table 38). Some of these interventions have been small or of limited duration but all of the major chinook populations (Puntledge, Qualicum, Nanaimo, & Cowichan) have been heavily augmented for many years (Table 38). Consequently, their status as wild populations is uncertain.

The Nanaimo and Puntledge Rivers have three and two run-timing groups, respectively, and two timing groups might exist in the Chemainus River. The genetic relationships among the EVI+GStr populations suggest that there are five to seven distinctive groups (Table 28, Figure 41). To the extent that we could examine their relationship, spawn timing data mirrors the genetic structure (Figure 56 and following table).

spawn timing group	population	mean date of spawning	genetic class
early	Nanaimo (fall)	275.9	01.02.02-04
	Chemainus	280.9	
mid	Qualicum	286.6	01.02.02-02
	Little Qualicum	286.6	
	Puntledge (fall)	286.3	
	Cowichan	289.3	01.02.02-03
	Koksilah	292.8	
late	Goldstream	306.9	01.02.02-01

The differences between the mean timing within groups are highly significant and the differences among the model residuals are near significance.

population group	mean spawn time (DOY)	mean residual (d)
early	278.4	-10.9
mid	289.2	-3.04
late	306.9	15.0
F-statistic and *P*	$F_{2,5}$=30.8; *P*=0.0015	$F_{2,5}$=4.42; *P*=0.08

The Cowichan and Koksilah Rivers, unlike the Qualicum and Puntledge Rivers have not been dammed and the Cowichan River watershed has not been impacted by human activities to the same extent as either the Puntledge-Campbell-Tsolum or Qualicum River watersheds. Although the Big Qualicum and Cowichan chinook are similar in many ways, the Big Qualicum population has been under intensive hatchery supplementation for over 40 years. We doubt that it would prove acceptable as a source of wild fish with which to rescue the Cowichan population, should such rescue be required in the future. Consequently, we propose that the Cowichan-Koksilah population be considered a CU, resulting in four CUs of fall chinook in the EVI+GStr ecotypic zone.

There are three remaining populations of significance in the ecotypic CU that warrant CU status. The summer-run Puntledge chinook is a de facto CU. This population is genetically distinctive from the fall run in the Puntledge and from other populations in the EVI+GStr JAZ (Figure 41). The viability of the population in the wild has been seriously compromised by the consequences of hydro development on the river and rescue efforts are underway using a captive breeding program[26]. The genetic and morphometric distinctiveness of summer and spring runs in the Nanaimo River has been previously established (Carl and Healey 1984). Although the morphometric component of that study has recently been questioned (Swain and Foote 1999), the genetic distinctiveness of the three timing groups has been confirmed (e.g. Figure 41) as have there are consistent differences in both life history and spawning and rearing habitats (Carl and Healey 1984, Healey 1991).

8.8 Habitat and ecological considerations

The distinctiveness of Dean River chinook was brought to our attention by local biologists (pers. comm. M. Mortimer, DFO, Port Hardy). Dean River chinook are stream-type in contrast to the chinook of the Bella Coola River and other chinook sites of South Bentinck Arm. Dean River were also reported to spawn later than other chinook in the ecotypic CU. We were unable to confirm differences in spawning date (see following table) but the habitats of the Dean River are markedly different from those of the other sites in the ecotypic CU.

site(s)	N	mean DOY peak spawn	mean residual (d)
Bella Coola River and South Bentinck Arm	4	250.3	0.33
Dean River and tributaries	1	242.0	-9.83
ANOVA	5	$F_{1,3}$=0.86 *P* =0.42	$F_{1,3}$=0.42 *P* =0.56

The habitat of the Dean River and its tributaries compared to the other sites in the ecotypic CU is lower gradient (e.g. mean mainstem gradient is 0.5% vs. 2.4%), with less high altitude terrain (e.g. mean % of watershed as tundra is 9.2% vs. 26%) and less lake influence (e.g. mean % of watershed as lakes is 1.2% vs. 3.4%). The climate of the Dean

[26] bchydro.com/bcrp/projects/docs/vancouver_island/99VI03.pdf

River watershed is transitional (coastal-interior) compared to the coastal climate of the other sites in the ecotypic CU (e.g., about half the rainfall, distinctly warmer summers but colder winters). Such differences might explain the differences in life history but certainly counter-examples are readily found (e.g. South Thompson River ocean-type chinook). Finally, there are small differences in the genetics classification of the Dean Rivers at the fourth level (group 7.1-2) vs. 7.1-1 respectively. The difference in life-history type and the significant habitat differences led us to conclude that the Dean River chinook are a separate CU.

Chinook salmon populations in the Taku and Stikine Rivers appear comprised of three and two run timing groups, respectively and the populations in the two rivers () appear to be closely related genetically (Figure 41, Table 28). We used discriminant analysis to first determine if the tributaries used by chinook in each of the two watersheds could be distinguished and then to determine if the sites used by the run timing groups within the Stikine and the Taku could be distinguished.

Overall, the sites utilized by chinook in the Stikine River drainage have steeper terrain and higher elevation with higher percentages of tundra and less lake influences than sites in the Taku River drainage (Table 35). The discriminant function correctly classified 13 of the 16 sites (81%), confirming the validity of the ecotypic CUs.

A discriminant model for the two run timing groups of chinook in the Stikine River drainage correctly classified seven or eight sites (88%, Table 36). Chinook in the second or later run utilize sites that are more heavily influenced by lakes and glaciers and have higher fall rainfall than those used by the earlier run. The Christina Creek site was misclassified. The site is in the coastal mountains with terrain and climate closer to the late run sites in the Iskut River drainage (). There was very little run-timing data available for this site (Pahlke and Etherton 1999) and it may have been misclassified. Nevertheless, the differences in habitats used by the two run timing groups are sufficient to confirm their status as CUs.

A discriminant model for the three run timing groups of chinook in the Taku River drainage correctly classified all of the eight sites (Table 37). Temperature was the most important distinguishing characteristic with run timing positively correlated with fall (and mean annual) temperatures. We concluded that there are three chinook CUs in the Taku River drainage.

8.9 Summary

There are 63 CUs of chinook salmon in British Columbia, including the partial CU located in the Teslin River drainage that is part of one of the CUs in the Yukon River (Table 39, Figure 57, Figure 58). Eleven of the CUs comprise only one site and an additional 27 CUs comprise between two and five sites (Table 39). The large number of CUs and their generally small extent and size (number of sites but not necessarily abundance) are indicative of the diversity found within the species in British Columbia.

9. Sockeye salmon

9.1 Distribution

In North America, spawning populations of sockeye salmon, *O. nerka,* have been reported from the Sacramento River in the south to the shores of the Chukchi Sea in NW

Alaska (Burgner 1991, McPhail and Lindsey 1970) and possibly far into the Canadian Arctic (Babaluk et al. 2000). The most numerous spawning populations are found in areas with an abundance of large lakes such as the Bristol Bay complex in SW Alaska, the Skeena River in north coastal British Columbia and the Fraser River in SW British Columbia. Sockeye salmon are found throughout British Columbia (Figure 59) including a population that has persisted in Okanagan Lake in the Columbia River drainage. Interestingly, sockeye salmon are largely absent from the Yukon River and are not present in the Canadian portions of that river (Burgner 1991). Sockeye occur in a third of all sites in our database (Table 40). There is a slight tendency for sockeye to be more prevalent in southern and northern areas of the Province (Figure 60), a pattern largely due to the relative absence of sockeye in the coastal streams around the Strait of Georgia and much of the Queen Charlotte Islands (Table 40).

9.2 Life History

Sockeye salmon has three distinct life history types, the largest number of any of the Pacific salmon. The lake-type form is anadromous and the juveniles rear for a year or more in freshwater lakes. The ocean-, stream- or river-type is also anadromous but the juveniles of this type rear in flowing water and may smolt soon after emergence. The third form, kokanee, is not anadromous and spends its entire life in fresh water. Taylor et al. (1996) compared the molecular genetics of sympatric anadromous sockeye and kokanee and found that the kokanee were much more similar to sympatric and geographically proximate sockeye than to each other and concluded that the kokanee form has arisen multiple times throughout the range of the species. Kokanee and sockeye have diverged ecologically (Foote et al. 1999, Wood 1995, Wood et al. 1999) and genetically (Craig and Foote 2001, Foote et al. 1999, Taylor et al. 1996, Taylor et al. 1997) and are effectively sympatric species (Taylor et al. 1996, Wood and Foote 1996).

Lake- and river-type sockeye are found throughout BC, although there is a preponderance of the river-type in northern glacial rivers (Figure 61) and a preponderance of the lake-type in the large rivers such as the Fraser, Skeena and Nass (Figure 61). A simple discriminant function emphasizing characteristics such as the prevalence of large lakes, stream stability, high-elevation influence and both latitude and longitude, performs well at distinguishing the characteristics associated with the two life-history types (Table 41).

Wood (1995) has persuasively argued that sockeye salmon are locally specialized forms of the ocean-type sockeye and that the population of a single lake is a useful “unit” of diversity for human-centric conservation. Local adaptation has proceeded within individual lakes so that for both sockeye and kokanee there often are ecotypes that are substantively reproductively isolated (Blair et al. 1993, Burger et al. 1995, Fillatre et al. 2003, Hendry 2001, Hendry et al. 1996, Quinn et al. 1999, Ramstad et al. 2003, Taylor et al. 1997, Varnavskaya et al. 1994, Winans et al. 2003). Thus, from a long-term evolutionary perspective, conservation of the ocean-type sockeye throughout its range is paramount because it is unlikely that the specialized lake-type forms could colonize vacant habitats outside their natal lake. However, from a human-centric perspective only, conservation of individual lake-type forms and possibly within-lake ecotypes is more important. While the lake is the significant unit of population structure in lake-type sockeye, the river of origin is the corresponding unit of structure for river-type sockeye at least in the transboundary rivers of northern British Columbia (Beacham et al. 2004). That finding suggests that the ecotypic approach will be applicable to river-type sockeye since the rivers considered by Beacham et al. correspond to our FAZ or JAZ ecotypes.

In Canada, kokanee is considered a freshwater “species”, and is under provincial jurisdiction and not covered by the Wild Salmon Policy. To describe Conservation Units for kokanee would require the extension of our ecotypic approach by developing an ecotypology that specifically dealt with lake-stream ecosystems.

To describe Conservation Units for the two anadromous life history types we have considered them separately. Consideration of the river-type follows the approach used for the other species. For lake-type sockeye, we have begun with the assumption that the population of an individual lake is a single Conservation Unit. In some cases the populations of small lakes (<~100 ha) that are close together and hydrologically tightly coupled are combined into single Conservation Units unless there is evidence of distinctiveness. For example, the series of lakes on the S Atnarko River (Elbow, Rainbow, Tenas, and Lonesome) have been combined into one Conservation Unit. Different run-timing groups in single lakes were generally considered distinct Conservation Units and were always considered so when there were demonstrable differences in spawning locations and/or spawning times (Varnavskaya et al. 1994). In two locations and on the advice of CDFO biologists geographically based Conservation Units were recognized. In Harrison Lake, outlet and inlet spawners were explicitly recognized as separate Conservation Units. Such a distinction could likely be made in other lakes (e.g. Babine) but generally has not been, usually because of a lack of detailed information. Two Conservation Units of lake-type sockeye were recognized in Chilko Lake based on geographic and temporal separation of run and spawning times. Doubtless there is similar structure within other lakes and, possibly, within most other large lakes in British Columbia. Managers should be mindful of the importance of conserving such structure even when it is not explicitly recognized as a unit of conservation (Hilborn et al. 2003, Ramstad et al. 2003)

9.3 Lineage

Wood (1995) concluded that there were three sockeye lineages in North America based on allozyme data. That conclusion has subsequently been confirmed by an analysis of variation in microsatellite DNA (Beacham et al. 2006a). We have used the neighbor-joining dendrogram from Beacham et al. (2006a) (Figure 63) to develop a five-level hierarchical genetic classification for British Columbian sockeye (Table 42). Figure 64 shows a diagrammatic summary of the dendrogram of Figure 63. The three lineages are described by level-1 of the hierarchy. One lineage (classes 01.n) consists of a small number of populations in SE Alaska and does not include any Canadian populations. The second lineage (classes 02.n) is primarily Asian and Alaskan with two genetic clusters in Canada (clusters A and B). The third lineage (classes 03.n) is found throughout British Columbia (Table 42). Sites within the lineage have been divided into 12 genetic clusters (C – N; Figure 64, Figure 76). The overall population structure has suggested recolonization from at least three glacial refugia (Beacham et al. 2006a) The overall population structure shows both relatedness by distance, particularly within the Fraser River (Withler et al. 2000), but also instances of a mosaic where geographical proximity does not entail genetic similarity (Winans et al. 1996). For example, Owikeno Lake sockeye (GFE_ID 935-943, genetic group 2.1.2) and Sustut River sockeye (GFE_ID 620, genetic group 2.1.6) are genetically distant from their geographical neighbors.

9.4 Ecotypic Conservation Units

River-type sockeye are found in at least 30 of the 39 JAZ ecotypic CUs (Figure 62, Table 43) and are probably present in an additional two JAZ CUs. Although the life-history type is ubiquitous, it is found in only 10% of the sites in our database (Table 43), and in many areas, especially in southern British Columbia, its populations are small and seldom enumerated. Consequently, in comparison with lake-type sockeye, little information is available for many of the sites, and our description of its CUs is necessarily limited.

9.5 Ecotypic X Genetic Classifications

River type sockeye are found in 31.9% of the sites in our database where sockeye is present and in 21.1% of the sites with genetic samples (Table 44). The incidence of the river-type is the same in both lineages in Canada (20.8% of sites in classes 2.n, 17.4% in classes 3.n; Table 44), but its incidence in the genetic clusters is not uniform. Most of the river-type sites are found in genetic clusters A, C, and D. Interestingly, all 14 sites in the class 1.n lineage, which are most closely related to Canadian sites in clusters A, C and D (Figure 64), are lake-type, although that may be a sampling artifact. There are relatively few river-type sites in genetic clusters E through N (Table 44) but few of the river-type sites in southern BC, where sites in those clusters are located, were sampled.

Thirty-six river-type populations were sampled genetically (Table 42). At the cluster level of the hierarchical classification (levels 2 and 3 of the classification), samples were obtained from 12 of the 30 JAZ ecotypic CUs with river-type populations (Table 45). Only two of the JAZ CUs had more than one cluster present (Table 45) and the life history type of one of those populations is uncertain[27]. The presence of the Widgeon population in the lower Fraser is one of several very distinctive representatives of a northern coastal lineage in the south. Another member of the group is found in Ozette Lake on the Olympic Peninsula in WA. There is considerable genetic diversity at levels 3 and 4 of the genetic classification within the northern Transboundary Rivers, as was concluded by Beacham et al. (2004). The populations in the Alsek and Stikine Rivers are particularly diverse with seven and thirteen genetic classes respectively present in the two systems (Table 42).

9.6 Spawn timing

Run timing and spawn timing are considered important attributes of population adaptation in sockeye as in other species of Pacific salmon. For example, four run-timing groups are recognized in the Fraser River watershed and, until recently, the temporal consistency of passage through ocean fishing areas, river entry and spawning have been the basis for managing fisheries on the assemblage. When compared within the same JAZ ecotype, river-type sockeye spawned later than lake-type sockeye in 12 of 17 instances with sufficient data for the comparison, and in five instances significantly so (Table 48).

Regression models predicting spawning time for the two life-history types are very different. The model for river-type sockeye (Table 46) explains 55% of the variance

[27] The spawning location of the “Harrison” population sampled by Beacham et al. (2006a) is unclear. It could be part of the Harrison (U/S) lake-type CU or it could be river-type population. We have assumed the latter.

in the DOY of peak spawning and indicates that spawning occurs later in the year in the south, at lower elevations and where the late fall is wetter. The regression model for lake-type sockeye (Table 47) explains relatively little of the variance (34%). Spawning is later in the south and in low gradient, high order watersheds with relatively narrow floodplains (i.e., non-glacial). Although we did not explore the model in detail, most of the relatively low amount of variance explained by the model is contributed by latitude. The poor performance of the model suggests that spawning time in lake-type sockeye is very dependent on local conditions at a geographic scale that was not captured well by our variable set.

9.6.1 River-type sockeye

Comparisons of mean spawn timing and the residuals of the spawn timing model among the JAZ ecotypic CUs were useful in characterizing about one-third of the eventual CUs of river-type sockeye. Spawn timing data for the ecotypic CUs of the Fraser River upstream of the Fraser River canyon suggest that there are at least two CUs (see following table). There is no information available for the single site in the UFR JAZZ and that status of that site is unknown. We have recognized a CU in the UFR JAZZ, while recognizing that it might not be extant.

population group	number of sites	mean spawn time (DOY)	mean residual (d)
LFR	3	294.2	31.5
MFR	5	257.4	14.9
LTh	2	285.0	19.8
F-statistic and *P*		$F_{2,7}$=7.9 P=0.016	$F_{2,7}$=0.91 P=0.45

The difference in mean spawn timing for the two JAZ on the west coast of Vancouver Island was highly significant and the difference in the mean residual was close to significance (following table). We conclude that there are two CUs of river-type sockeye corresponding to the ecotypic CUs.

population group	number of sites	mean spawn time (DOY)	mean residual (d)
WVI+WVI	55	292.4	0.43
WVI+WQCI	6	266.0	-10.5
F-statistic and *P*		$F_{1,59}$=21.9 P<<0.001	$F_{1,59}$=3.24 P=0.077

There were no differences in mean spawning times or in the model residuals among the two ecotypic CUs on the east coast of Vancouver Island and the two CUs on the mainland (SC, see following table). The many river-type sockeye populations in

population group	number of sites	mean spawn time (DOY)	mean residual (d)
EVI+GStr	9	268.9	-2.9
EVI+SFj	5	265.5	6.4
SC+GStr	10	257.2	-9.7
SC+SFj	8	255.3	-4.1
F-statistic and *P*		$F_{3,28}$=0.46 P=0.71	$F_{3,28}$=0.43 P=0.73

these four ecotypic CUs are not routinely monitored and there is very little information available for them. For instance, there was only one genetic sample. The lake-type populations in the same ecotypic CUs have been more extensively sampled (Table 42). Assuming that the river-type populations are closely related to the lake-type populations, the genetic information from the area is consistent with two river-type CUs, one comprised of all sites in the EVI FAZ and the SC+GStr JAZ, and the other comprised of the populations in the SC+SFj JAZ.

On the Queen Charlotte Islands there were large differences in mean spawning time and in the mean model residuals among the three ecotypic CUs but also a lot of variability within the CUs and few sites with data (see following table). Spawning was significantly later at sites bordering Hecate Strait than in the other two JAZ. The model residuals follow the same pattern. We interpreted these observations as weak support for the recognition of three CUs on the Islands corresponding to the ecotypic CUs.

population group	number of sites	mean spawn time (DOY)	mean residual (d)
QCI+HStr	4	258.9	25.6
QCI+NQCI	2	209.7	-6.8
QCI+WQCI	2	185.5	-40.3
F-statistic and *P*		$F_{2,5}$=6.4 P=0.04	$F_{2,5}$=3.47 P=0.11

Spawn timing data was useful in resolving population structure around Hecate Strait. In the analysis of spawn timing, we included the four sites in the QCI+HStr JAZ to determine if there were timing differences between that JAZ and those on the mainland.

population group	number of sites	mean spawn time (DOY)	mean residual (d)
RSI	3	258.9	8.9
BCD+HStr	5	256.2	-5.8
NC+HStr	27	258.1	5.85
HecLow+HStr	16	226.0	-7.23
QCI+HStr	4	258.9	25.6
F-statistic and *P*		$F_{4,50}$=6.38 P<0.001	$F_{4,50}$=2.89P=0.03

Spawning was significantly earlier in the HecLow JAZ relative to the other four JAZ, which were indistinguishable. Although the mean spawning time in QCI+HStr was the same as the fjord dominated JAZ on the mainland but not in the physiographically similar HecLow, the mean model residual for that JAZ was significantly larger than in all of the other JAZ. The lake-type populations in this area have been more extensively sampled. The genetic population structure corresponds very well to the division of the HecLow and NC ecotypic CUs (Table 42, Figure 64, Figure 65). There are only two genetic samples from the 55 sites with river-type sockeye on the north and central coasts. Assuming that adjacent river-type and lake-type populations are closely related genetically, one would expect that the river-type populations in the RSI ecotypic CU would be genetically distinctive. Consequently, we conclude that there are three CUs in the area corresponding to the HecLow JAZ, the RSI JAZ, and the combined NC+BCD JAZ.

Spawn timing also proved useful in clarifying population structure in the Skeena and Nass Rivers. Mean spawn timing was significantly earlier in the LNR-P than in any of the other ecotypic CUs, while mean spawn timing was significantly later in the USK and UNR than in the other ecotypic CUs (see following table). Model residuals were

ecotypic CU	number of sites	mean spawn time (DOY)	mean residual (d)
LSK	2	243.4	-3.98
MSK	2	230.9	-10.4
USK	1	254.5	36.1
LNR-P	7	213.1	-19.4
UNR	2	258.8	31.1
F-statistic and *P*		$F_{4,9}$=7.7 P<0.01	$F_{4,9}$=9.1 P<0.005

significantly larger in the two interior CUs than in the others. There were no significant differences between the four sites in the LSK and MSK. We concluded that there were four CUs in the area: LNR-P, UNR, LSK+MSK and USK. There is only one site in the USK CU and there is no recent information for it. Consequently, we do not know if this CU is extant.

9.7 Conservation Units for river-type sockeye

There are 24 CUs of river-type sockeye (Table 49). Genetics and/or timing was the determining factor in 11 of the 24 CUs while the remaining 13 CUs were ecotypic. Two of the CUs consist of single populations of unknown status and it is possible that neither CU is extant. Of all the species and CUs that we have considered, river-type sockeye, particularly in the southern half of the province, are, by far, the least studied.

9.8 Conservation Units for lake-type sockeye

We assumed with few exceptions, that individual lakes were Conservation Units. This assumption is supported by most of the genetic studies that have examined sockeye (Beacham et al. 2006a, Beacham et al. 2005, Beacham et al. 2004, Gustafson and Winans 1999, Nelson et al. 1998, Nelson et al. 2003, Withler et al. 2000, Wood 1995, Wood and Holtby 1998, Wood et al. 1994). Furthermore, reduced gene flow and local adaptation have been shown numerous times within lakes (Burger et al. 2000, Burger and Spearman 1997, Fillatre et al. 2003, Hendry 2001, Hendry et al. 1996, Taylor et al. 1997, Varnavskaya et al. 1994, Wood and Foote 1996), suggesting that, in some cases, there is significant diversity within individual lakes.

In some locations the *a priori* declaration of individual lakes as Conservation Units is likely to be controversial either because there is evidence of substantial gene flow between the putative Conservation Units or because the lakes are small, close together and ecologically similar. In the former situation, it is presumed that substantial gene flow is indicative of sufficient migratory exchange that recolonization of one lake in a group in the event of a chance extirpation would be rapid. The hypothesis has yet to be rigorously tested and the available evidence suggests that natural recolonization might be too slow to warrant combining lakes into single CUs. For example, the extirpation of both Early Summer and Late-run sockeye from Adams Lake through dam construction on the Lower Adams River, has taken over 50 years to reverse even partially despite substantial intervention and the proximity of ecologically and genetically related populations in Shuswap Lake (Williams 1987). Small lakes (<100 ha) may be incapable of supporting large enough populations to be viable over many generations. Where there are several ecologically similar lakes in close proximity, the lakes might be part of a large meta-population that could be considered a single CU. However plausible such a configuration might be, an example has yet to be described. Where it has been examined, lake-type sockeye home to their natal spawning grounds with uncanny precision (Burger et al. 1995, Burger and Spearman 1997, Hendry 2001, Quinn et al. 1999). In the absence of life history, biological and genetic evidence indicating otherwise, we held that an appropriately conservative approach was to characterize each lake or lake cluster as an individual CU.

A high degree of genetic similarity is often observed between lakes that are in close proximity and are hydrologically coupled. Three examples of this are the Stuart, Babine and Shuswap Lake complexes. The Stuart Lake complex consists of three large lakes: Stuart, Trembleur, and Takla. The Babine Lake cluster consists of four lakes: Babine, Nilkitkwa, Morrison, and Tahlo. There are six lakes in the Shuswap Lake complex: Shuswap, Little Shuswap, Mara, Mabel, Adams, and Momich. In all three cases, the lake-type sockeye populations of all of the lakes are closely related genetically (Table 42, Figure 63, Figure 64). In all three cases there are highly significant differences in spawning time that are associated with inlet or outlet spawning locations, or more generally with stream fed versus lake fed spawning locations, which follow the general pattern observed by Brannon (1987)[28].. Such differences in spawning time and the necessary differences in fry behavior associated with inlet versus outlet spawning are important components of adaptive diversity in these lakes and probably in many other sockeye lakes.

In the Babine Lake complex all of the sites that have been examined are very similar genetically (Table 42, Figure 63) (Beacham et al. 2005). Peak spawning is significantly earlier in the Babine Lake tributaries ($F_{1,26}$=7.4, P<0.05) and later in the Babine River ($F_{1,25}$=4.96, P<0.05) but intermediate in the other two systems., which are also predominantly lake outlet spawners. Physiographically, the Babine Lake tributaries, the Nilkitkwa Lake spawning locations (i.e., the Babine River) and the Morrison/Tahlo Lakes spawning locations form three readily distinguishable groups based on topography, hydrology and temperature. We conclude that there are three sockeye Conservation Units in the Babine Lake complex.

The potential exists for six Conservation Units in the Stuart Lake complex since two run-timing groups (Early Stuart or ESTU and Summer or S) are present in all three lakes. The populations appear to be genetically similar suggesting high levels of gene flow among all of the populations (Beacham et al. 2005), although the comparison seems to have been between only the Early-Stuart timing components. The two run-timing groups do not use the three lakes equally as the following table illustrates.

[28] One prominent example of this general rule is Harrison Lake where two CUs are recognized. However, the difference between the Harrison Lake (U/S) and (D/S) Conservation Units is more complex than distinguishing outlet and inlet spawners. The spawning location of the Harrison (U/S) populations is not at the outlet of Harrison Lake but in Weaver Creek, which is a tributary of the Harrison River below the lake. The fry of these populations migrate down Weaver Creek and then up the Harrison River to reach the lake. This is one of the most spectacular of local adaptations observed in sockeye (Burgner, R.L. 1991. Life history of sockeye salmon (*Oncorhynchus nerka*). *In* Pacific Salmon Life Histories. *Edited by* C. Groot and L. Margolis. University of British Columbia Press, Vancouver, BC. pp. 3–117.).

	number of spawning sites			
Lake	ESTU component	S component	common sites	total sites
Stuart	2	6	0	8
Trembleur	10	3	3	10
Takla	32	3	2	33

The Early Stuart timing component predominates in Takla and Trembleur Lakes while the Summer timing component predominates in Stuart Lake tributaries. That pattern of use corresponds to the climates and physiography of the lakes. Stuart Lake and its tributaries have a warmer and drier climate than either Trembleur or Takla Lakes. The tributaries of Stuart Lake also have lower elevations, shallower gradients and less high altitude tundra and glacial influences. However, the tributaries used by sockeye salmon around Takla and Trembleur Lakes were indistinguishable on the variables we used to describe habitat.

Spawn timing of the dominant timing components in each of the three lakes is well characterized but there are few data for the other timing component (see following table). The spawn timing of the two run-timing components is significantly different (or nearly so in Stuart Lake). Within the two timing components, spawn timing differed only between the ESTU component in Stuart Lake and the other two lakes. There were no differences among the lakes in the Summer component. Interestingly, Stuart Lake was the only nursery lake where the spawning tributaries of the two run-timing components were disjunct. In the two colder lakes, sockeye from the Summer timing component spawn only in the outlet streams of large lakes (i.e., Middle River (#2485), Sakeniche Creek (#325) and Kazchek Creek (#316) (Figure 70), apparently in the same locations as the earlier spawning fish from the ESTU run-timing component.

	mean DOY of spawning (number of observations)		
	ESTU	Summer	comparison within lake
Stuart	245.4 (8)	261.8 (90)	$t_{df=7.1}$= -2.3; P=0.054
Trembleur	220.6 (220)	259.8 (6)	$t_{df=6.4}$= -19.9; P<<0.001
Takla	220.7 (561)	259.5 (2)	$t_{df=7.1}$= -25.0; P=0.016
overall	221.0 (789)	261.6 (98)	$t_{df=178}$= -59.0 P<<0.0001
comparison within timing component	$F_{2,794}$=21.9; P<<0.001	$F_{2,95}$=0.44; P=0.64	

We have concluded that there are three lake-type sockeye CUs in the three lakes. Stuart Lake supports two CUs, one of each run-timing component. There is a single CU of the ESTU timing component in the Trembleur and Takla lakes. A fourth CU of Summer timing component populations might exist in the two northern lakes but there are too few data available to us to verify that late spawning fish are persistently present in the few locations where they have been sporadically reported.

There are six lakes in the Shuswap Lake complex, two Fraser run-timing components (early summer [ES] and late[L]) and the potential for eight Conservation Units, four of the lakes having only one of the timing components. Two of the lakes with only one timing component, Little Shuswap Lake [L] and Momich Lake [ES], appear genetically distinct from each other and from the rest of the complex (Figure 63, Figure 64). Although the genetic dendrogram indicates that Little Shuswap sockeye are relatively distant from neighboring sites (e.g. the lower Adams River), the dendrogram also indicates that Little River sockeye are very similar to the lower Adams. Little River is assumed to be the spawning site of sockeye that rear in Little Shuswap Lake. The genetic evidence suggests that that assumption should be re-examined.

In the early 1900's the early summer run of sockeye into Adams Lake was one of the largest runs in the Fraser River. Splash damming of the lower Adams River from 1908 to 1921 severely obstructed sockeye access to Adams Lake. The dam and the impact of the Hell's Gate slide (1913) is thought to have extirpated the ES sockeye of Adams Lake. The reappearance of early summer sockeye in the upper Adams River beginning in 1954 has been attributed to a lengthy hatchery-restocking program that began in 1949 (Williams 1987) using (mostly) fish from the Seymour River (#229) a nearby tributary of the Shuswap Lake. The genetic distinctiveness of the current Adams and Momich Lakes ES populations is likely due to founder effects and/or genetic drift ((Withler et al. 2000). However, because the Adams/Momich Lakes ES populations were likely established through transplants, those populations should be placed in the CU of the source population they most closely resemble, in this case the Shuswap Lake ES CU.

Spawn-timing information is available for many of the populations in the six-lake complex and is summarized in the following table. There is a highly significant difference in the mean spawning DOY of the two run-timing components (57.5 days), confirming the ecological if not the genetic distinctiveness of the two components. The spawn timing of the three lakes supporting the ES timing component are indistinguishable, which is consistent with the origins of the Adams and Momich populations (see above and Williams 1987, Withler et al. 2000). Although there is one observation of ES spawning in the lower Shuswap River (#240) made in 1983 while there are 27 observations of significantly later spawning made in the same river. We think that such early spawning in a lake outlet is either an anomaly or an error and have assumed that Mara Lake supports only a LATE spawning population. We conclude that there is currently one CU of Early Summer sockeye in the six-lake complex.

	mean DOY of spawning (number of observations)		
lake	ES	LATE	comparison within lake
Momich	241.0 (3)	-	$t_{df=7.1}$= -2.3; *P*=0.054
Adams	246.3 (22)	296.9 (7)	$t_{df=26.1}$= -26.8; *P*<<0.001
Little Shuswap	-	293.2 (38)	-
Shuswap	248.1 (92)	294.9 (58)	$t_{df=133}$= -44.1; *P*<<0.0001
Mara	244.0 (1)	291.0 (27)	-
Mabel	-	292.6 (8)	-
overall	247.6 (118)	293.6 (138)	$t_{df=225}$= -57.5; *P*<<0.0001
comparison within timing component	$F_{3,114}$=1.43; *=0.24*	$F_{4,133}$=3.10; *P*=0.02	

Populations of the LATE run-timing component are present in all of the lakes except Momich. The LATE spawning populations of Adams Lake were presumably extirpated by the same splash dam on the Adams River that played a prominent role in the extirpation of the ES run into the lake. Consequently, the populations there now are probably recent colonists with Shuswap Lake the most likely source. This conjecture is supported by the similarly late spawning times of populations in the two lakes. The differences in spawn timing among populations in the late run-timing component are small and the only statistically significant differences are between the populations of Mara Lake (earliest spawning) and those of Adams and Shuswap Lakes (the latest spawning)($P<0.05$, Fisher's Least Significant Difference test).

One of the most interesting aspects of sockeye in the complex and particularly those in Shuswap Lake is that most of the streams have spawners from both of the two run-timing components. Very discrete run-timing variation, such as is found in all of the streams with both timing components, has probably arisen as an adaptation to unfavorable migration conditions in late summer (Hodgson and Quinn 2002) and required concomitant changes in spawn readiness (*ibid.*). However, if spawning of the two groups occurs in exactly the same locations, as it apparently does, and emergence timing is the same, which it apparently is, then there must also be adaptations in temperature-development time relationships in the two timing components as well. Although the lakes in the Shuswap complex appear to be climatically, hydrologically and physiographically quite different (see following table), only the differences in precipitation are statistically significant. Furthermore, we were unable to construct discriminant functions that reliably separated the lakes.

	lake averages over streams used by the LATE run timing component				
variable	Little Shuswap-L	Shuswap-L	Mara-L	Mabel-L	Adams-L
GRAD_MS_MN	0.04	2.35	0.18	5.62	0.50
GRAD_T_MN	9.4	18.2	21.4	20.9	18.5
VFW_MEAN	8.9	0.4	3.4	0.6	2.7
ELEV_MEAN	714.0	908.2	793.0	1287.0	1028.0
GLAC_PERC	1.0	0.8	0.9	0.1	1.6
PERCTUNDRA	3.9	4.2	2.8	4.6	8.6
HIGHLEVEL	4.9	5.0	3.7	4.8	10.2
LAKE_PERC	3.2	14.9	16.2	0.3	9.9
PPT_AUG_M	37.2	62.9	55.5	92.3	70.1
PPT_SEP_M	38.7	67.0	59.4	98.4	70.7
PPT_OCT_M	32.4	67.5	59.3	101.7	77.3
PPT_NOV_M	42.3	87.3	74.0	135.0	94.9
PPT_DEC_M	52.9	101.0	91.0	138.2	111.3
PPT_ANN_M	440.3	844.1	756.6	1254.7	909.7
TEMP_AUG_M	17.1	15.6	15.4	14.2	14.2
TEMP_SEP_M	11.9	10.6	10.6	9.3	9.2
TEMP_OCT_M	6.3	4.8	4.7	3.7	3.6
TEMP_NOV_M	-0.5	-1.8	-2.0	-3.2	-3.2
TEMP_DEC_M	-5.4	-6.5	-6.6	-7.8	-7.7
TEMP_ANN_M	6.0	4.6	4.4	3.2	3.3
ORDER_MAX	6	4.875	6	3.67	5
MELTONS_R	0.06	0.11	0.13	0.20	0.07
LOG_KFACT_	3.396	3.887	3.849	4.001	3.913

Within the lake complex, the only arguably distinctive population is that of the Little Shuswap Lake but only because of its possibly distinctive genetics. Little Shuswap Lake is also the warmest of the lakes and the only one where there is unquestionably no mix of stream and lake-influenced spawners. The populations of the other lakes are indistinguishable genetically and biologically as are their nursery lakes. Notwithstanding the possible distinctiveness of the LATE population of Little Shuswap Lake, we conclude that there is one CU of LATE sockeye in the six lakes.

The sockeye population of North Barriere Lake on the Barriere River (#258), a tributary of the North Thompson River (#256), was likely extirpated by a series of hydropower dams on the Barriere River built around 1914 but removed or decommissioned in the mid-1950's (Evenden 2004). The population was successfully reestablished with transplants from the Raft River, which is upstream of the Barriere-Thompson confluence. The nursery lake of Raft River sockeye is Kamloops Lake, which is downstream of both the Raft and Barriere Rivers, which might partially explain why the transplant was successful. However, because the North Barriere Lake population is a transplant, we consider it part of the Kamloops Lake CU.

Another transplant within the Fraser River drainage took place in 1950 when eyed eggs from the lower Adams River were moved to Portage Creek and juvenile fish from the same source were released into Seton Lake (Aro 1979). The current population of Portage Creek is genetically very similar to the donor population (Withler et al. 2000) and quite dissimilar to the Gates Creek population (#132), whose nursery lake (Anderson Lake) is immediately upstream of Seton Lake[29]. A high degree of genetic similarity of two geographically distinct populations appears to be sufficiently unusual that it probably indicates a high degree of introgression between the original Portage Creek population and the donor population, if not an outright replacement (Withler et al. 2000). In either case, Seton Lake sockeye cannot be considered a CU.

In total, there are 214 lake-type sockeye Conservation Units (Table 51, Figure 71 to Figure 75).

10. Discussion

In a species group as fantastically diverse, as adaptable and as rapidly evolving as *Oncorhynchus,* we think it very unlikely that any one characterization of diversity could ever be accepted for all purposes to which it might be put. We had two objectives in describing an approach to describe Conservation Units for Pacific salmon in Canada. First, we wanted to establish at what level in the biological continuum of diversity the WSP is focusing conservation efforts for Pacific salmon. We concluded that that level appears to lie below the wildlife species of SARA or the ESU of the American ESA. In other words, a CU is not equivalent to a Designatable Unit (DU) of COSEWIC or to an ESU of the American ESA as applied to Pacific salmon. However, Conservation Units are based on the same kinds of criteria as are DUs (Green 2005) and we have used much of the same information. Consequently, CUs will always be nested within a DU. We think that characterizing the CU in this way fully supports the first priority of conservation under the WSP: to safeguard genetic diversity. Defining the CU at a higher level in the continuum would not fully support the objectives of the WSP because the loss of a closed population (i.e., a DU) is not reversible within a reasonable time (Waples et al. 2001). Viewed from the reverse perspective, the loss of a CU might not

[29] The Gates Creek population has an Early Summer timing, while the Portage Creek population is a LATE timing population as is its donor population in the lower Adams River.

appreciably increase the risk of extinction for the DU and so would not necessarily result in invocation of SARA protections.

The methodology that we propose for use in characterizing CUs is closely modeled on the approach of Waples (Waples 1995, Waples et al. 2001). Compared to Waples we emphasize ecotypology more than molecular genetics but we use both in a complimentary way.

In most cases, there was a high level of concordance between the ecotypic characterizations of diversity and the patterns in genetic diversity. The only major disagreements came in areas where there were there were high levels of genetic diversity. In many of those situations, however, additional environmental typology appeared useful in mapping much the apparent genetic diversity. This was particularly the case for coho. The power of molecular techniques to detect diversity at a fine spatial scale and once recognized, the ability to explain the patterns through ecological patterns suggests that both approaches are detecting real and likely adaptive diversity.

Both the ecotypic and molecular genetics approaches for characterizing diversity are indirect in the sense that they both use a proxy of adaptive variation but do not actually measure it. For example, recent theoretical work (Hendry and Day 2005) and numerous examples in salmonids (e.g. Østbye et al. 2006, Tallman and Healey 1991) suggest that there is likely a considerable amount of temporal diversity that would not be easily detected by either an ecotypic or molecular genetics approach.. Such finely scaled adaptive variation cannot be detected except through experimentation, which is unlikely to be widely conducted because of the time and expense involved. Such adaptive variation is however, essential to maintaining viable and productive populations and speaks to the need to protect process as well as pattern (Moritz 2002). We note that one important benefit of an ecotypic approach is that it characterizes the habitats, environments, and ecosystems where diversity exists and on which the processes that maintain diversity rely. By doing so the intent of the WSP to use Conservation Units as more than collections of representative populations but as the basis for comprehensive habitat and ecosystem-based management is made apparent and operational.

One general conclusion from this exercise is that Pacific salmon in Canada are very diverse. This is reflected in the estimated numbers of CUs by species shown in the following table:

species	number of CUs
pink-odd	19
pink-even	13
chum	39†
coho	43
chinook	68†
sockeye-river	24
sockeye-lake	214

† Additional CUs will be described in the Yukon River and possibly in the Mackenzie River.

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We dedicate this paper to the memory of John Allen Livingston (November 10, 1923- January 17, 2006), Canadian naturalist, broadcaster, author, teacher, and founding trustee of the Nature Conservancy of Canada.

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13. Tables and Figures

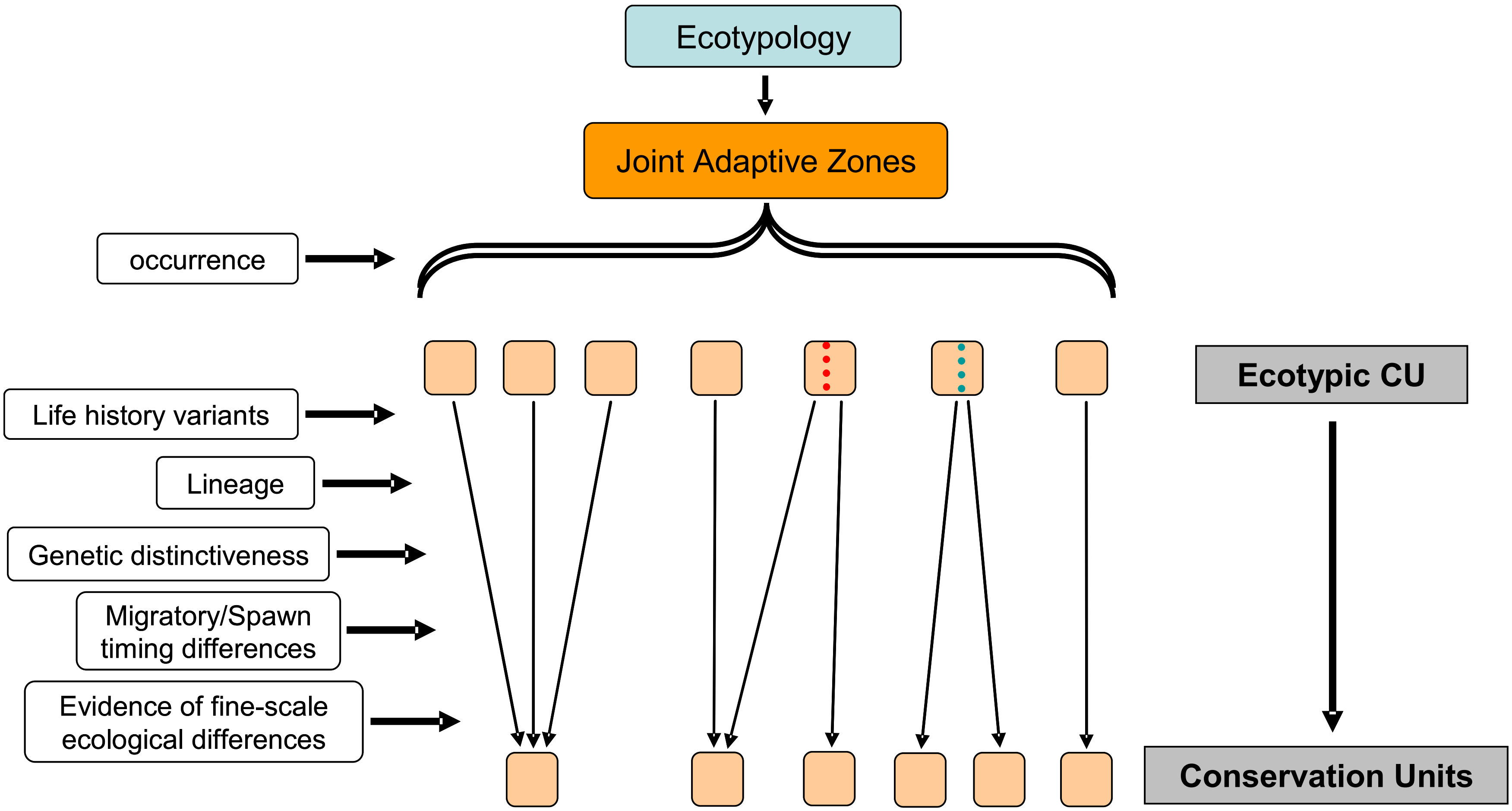


Figure 1. A diagrammatic outline of our methodology.

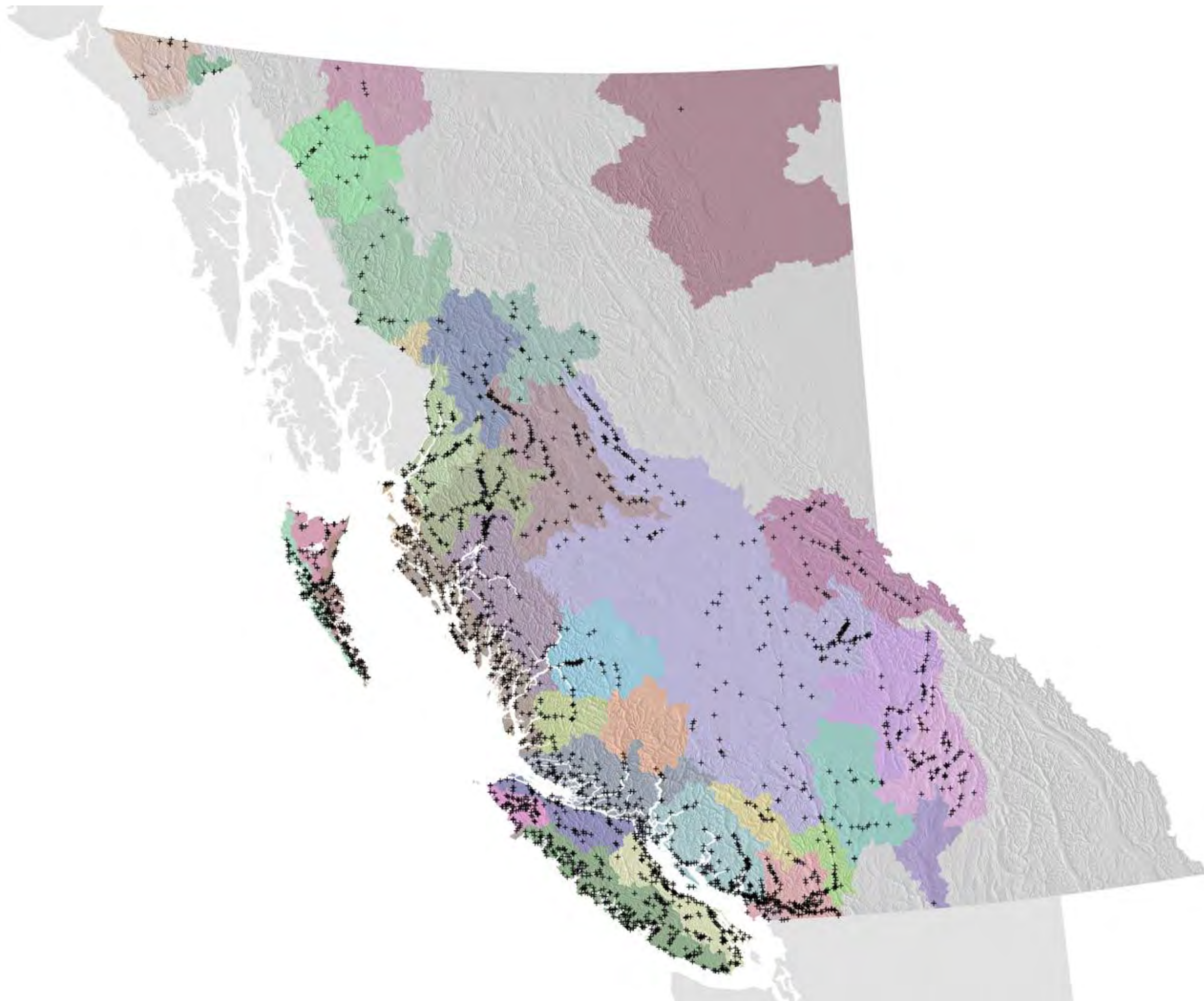
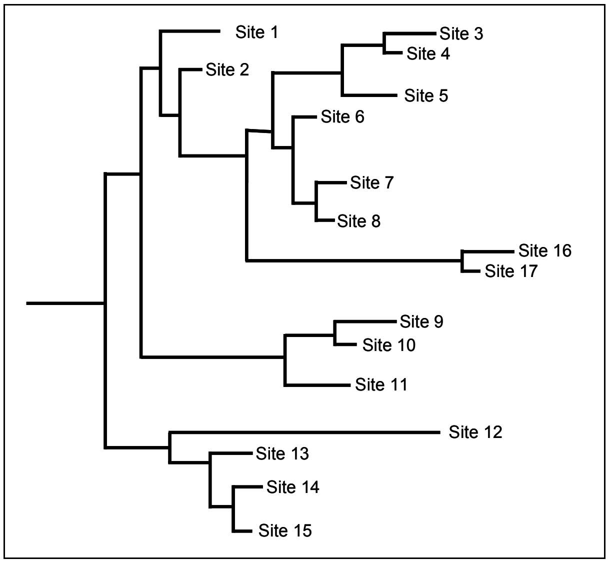


Figure 2. The map shows the locations in British Columbia of the 2662 sites in our database where genetic, timing or abundance information was available for at least one of the seven "species" we considered. The colored polygons are the JAZ ecotypes.



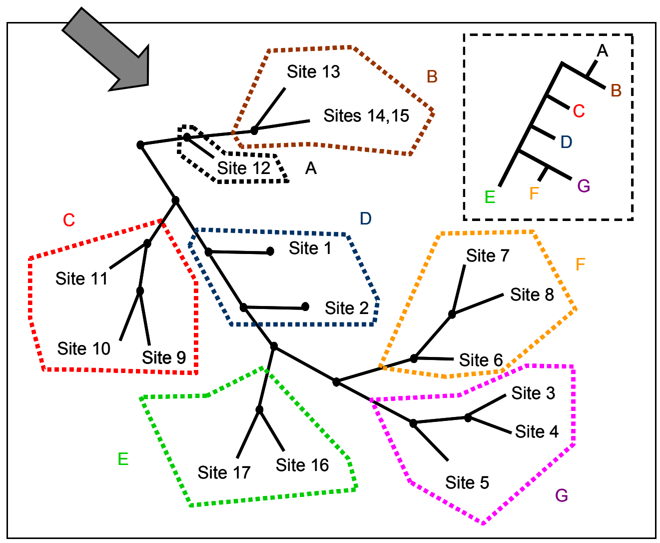
To the left is a hypothetical, neighbor-joining dendrogram. Dendrograms for each species were provided by the PBS Genetics Lab. In this example there are 17 sites, numbered by their GFE_ID. Each would have been associated with a JAZ or ecotypic CU.

To begin the genetic classification the dendrogram was rearranged as shown in the two diagrams below. Major groupings of sites or "clusters" were recognized and assigned a letter code. There are seven clusters in our example. The relationship of the clusters is shown by the small, inset diagram.

The code of the genetic class is divided into two parts. The first part (to the left of the '–' indicates the placement of the cluster in the inset diagram below. The branch containing cluster A and B is branch 1 and the other is branch two. The clusters are numbered in sequence down a branch. Thus 'D' is '2.2'.

Branching within a node is coded at the third level in the hierarchy so cluster F is coded '2.3.1'. Cluster 'E' is the terminus of the branch because the sites within it are the furthest away from the node where the two branches separate.

In the dendrogram, genetic distance is represented by the total horizontal distance between two sites. We attempted to preserve the distance information in our grouping into clusters. For example, the three sites within clusters F are closer to each other than to the three sites in cluster G but all six sites are on the same branch of the dendrogram.



site (GFE_ID)	class	cluster
12	1.1-1	A
13	1.2-1	B
14	1.2-2	B
15	1.2-2	B
11	2.1-1	C
9	2.1-2	C
10	2.1-2	C
1	2.2-1	D
2	2.2-2	D
6	2.3.1-1	F
7	2.3.1-2	F
8	2.3.1-2	F
5	2.3.2-1	G
3	2.3.2-2	G
4	2.3.2-2	G
16	2.4-1	E
17	2.4-1	E

The sites within clusters A and B are similarly arranged.

The part of the genetic classification to the right of the '–' describes the branching within a cluster following the same principle. The code in the example has four levels, three to the left of the '–' and one to the right. In coding most species a five or six level code was used with the first (leftmost) two or three levels defining the clusters.

Figure 3. A three-part illustration of the procedure followed for genetic classification.

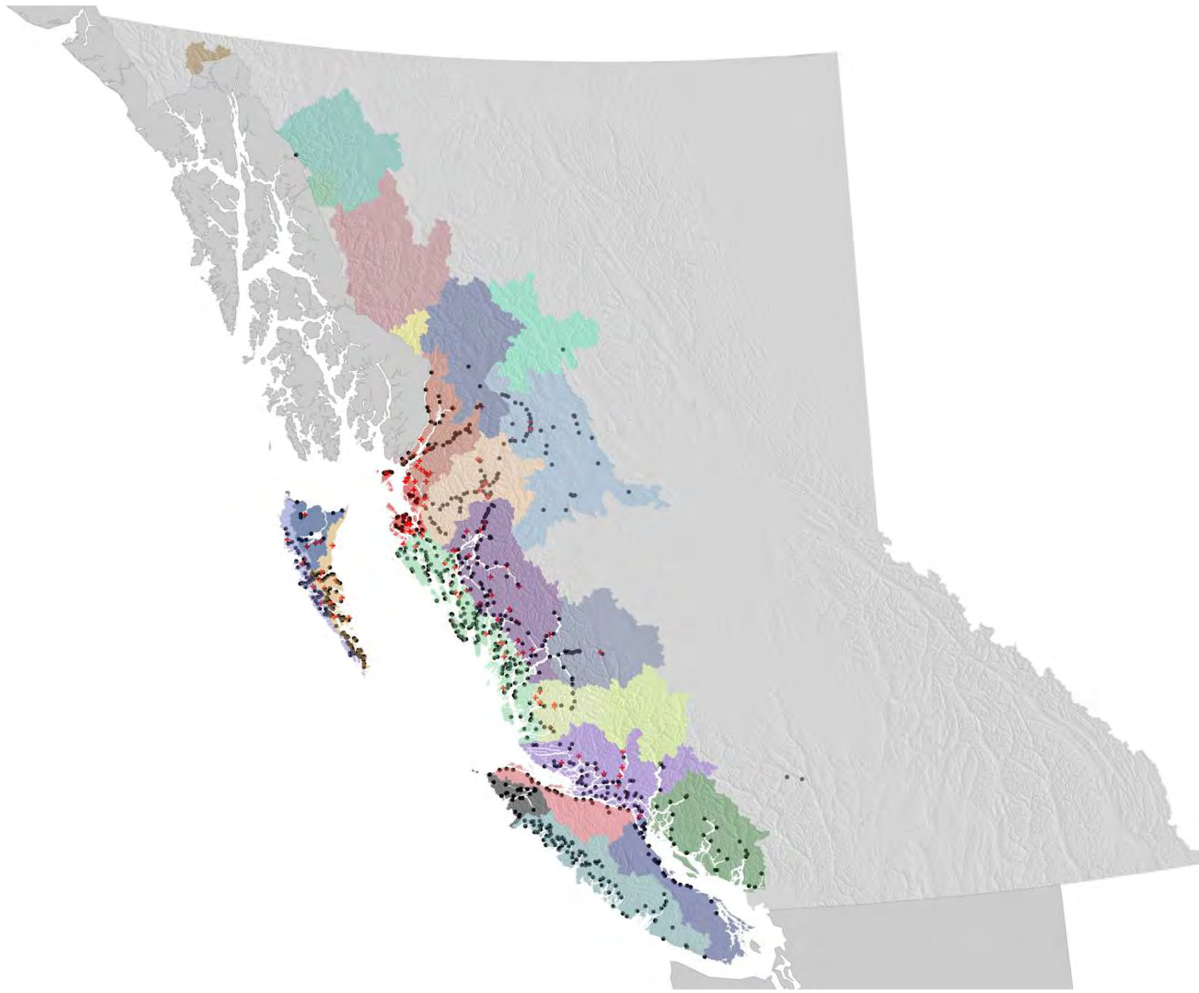


Figure 4. The map shows the locations in British Columbia with records of even-year pink salmon. The presence of the race in the Fraser River is uncertain. There are limited observational and timing records suggesting that the race is persistent at low abundance. Even-year pink salmon are present in the northern transboundary rivers but we have no information beyond a single site in the Taku River. The red crosses indicate where genetic samples were available. Note the absence of genetic samples from Vancouver Island, sites around Georgia Strait, the Queen Charlotte Islands and the northern transboundary rivers.

Table 1 Ecotypic Conservation Units for even-year pink salmon. The name, acronym, and number of sites for each JAZ within with British Columbia are listed. The number of sites includes all AEW with escapement records of any duration for any species, all sites where genetic samples of any species were obtained and all sites with a record of spawn timing for any species. The number of known sites is the count of AEW where at least 3 escapement records are available plus AEW where genetic samples or spawn-timing records are available. Interpreted presence is a categorical determination of the confidence in our assertion that the species is currently self-sustaining within a JAZ. The categories are described in the text. The number of sites where the species is documented as a percentage of the total number of sites in the JAZ is also tabulated.

JAZ			even-year pink salmon			
name	acronym	index	number of sites	known sites	interpreted presence	% documented of total sites
Okanagan|OR-WA Coastal	OK+ORWA	1	1	0	unlikely	-
Boundary Bay|Georgia Strait	BB+GStr	2	8	0	possible	-
Lower Fraser|Georgia Strait	LFR+GStr	3	133	0	possible	-
Lillooet|Georgia Strait	LILL+GStr	4	16	0	possible	-
Fraser Canyon|Georgia Strait	FRCany+GStr	5	20	0	possible	-
Middle Fraser|Georgia Strait	MFR+GStr	6	176	2	possible	1%
Upper Fraser|Georgia Strait	UFR+GStr	7	45	0	unlikely	-
Lower Thompson|Georgia Strait	LTh+GStr	8	20	0	possible	-
South Thompson|Georgia Strait	STh+GStr	9	66	0	possible	-
North Thompson|Georgia Strait	NTh+GStr	10	47	0	possible	-
S Coastal Streams|Georgia Strait	SC+GStr	11	131	29	documented	22%
S Coastal Streams|QCStr-JStr-SFjords	SC+SFj	12	109	69	documented	63%
E Vancouver Island|Georgia Strait	EVI+GStr	13	90	22	documented	24%
E Vancouver Island|QCStr-JStr-SFjords	EVI+SFj	14	33	21	documented	64%
W Vancouver Island|Vancouver Island Coastal Current	WVI+WVI	15	249	84	documented	34%
W Vancouver Island|Outer Graham Island	WVI+WQCI	16	64	24	documented	38%
Homathko - Klinaklini Rivers|QCStr-JStr-SFjords	HK+SFj	17	4	3	documented	75%
Rivers-Smith Inlets|Hecate Strait - Q.C. Sound	RSI+HStr	18	30	23	documented	77%
Bella Coola - Dean Rivers|Hecate Strait - Q.C. Sound	BCD+HStr	19	40	22	documented	55%
Queen Charlottes|Hecate Strait - Q.C. Sound	QCI+HStr	20	142	95	documented	67%
Queen Charlottes|Outer Graham Island	QCI+WQCI	21	83	59	documented	71%
Queen Charlottes|North Graham Island	QCI+NQCI	22	18	15	documented	83%
Hecate Lowlands|Hecate Strait - Q.C. Sound	HecLow+HStr	23	174	144	documented	83%
N Coastal Streams|Hecate Strait - Q.C. Sound	NC+HStr	24	118	100	documented	85%
Hecate Lowlands|Nass - Skeena Estuary	HecLow+NSKEst	25	67	55	documented	82%

JAZ		even-year pink salmon				
name	acronym	index	number of sites	known sites	interpreted presence	% documented of total sites
Lower Skeena|Nass - Skeena Estuary	LSK+NSKEst	26	107	54	documented	50%
Middle Skeena|Nass - Skeena Estuary	MSK+NSKEst	27	113	44	documented	39%
Upper Skeena|Nass - Skeena Estuary	USK+NSKEst	28	19	1	documented	5%
Lower Nass - Portland|Nass - Skeena Estuary	LNR-P+NSKEst	29	75	60	documented	80%
Upper Nass|Nass - Skeena Estuary	UNR+NSKEst	30	23	5	documented	22%
Unuk River|Transboundary Fjords	UNUK+TBFj	31	2	0	probable	-
Lower Stikine|Transboundary Fjords	LStk+TBFj	32	18	0	probable	-
Whiting River|Transboundary Fjords	Whtng+TBFj	33	1	0	probable	-
Taku|Transboundary Fjords	Taku+TBFj	34	19	1	documented	5%
Lynn Canal|Transboundary Fjords	LYNN+TBFj	35	4	0	probable	-
Alsek|Alaska Coastal Downwelling	Alsek+AKCst	36	6	0	possible	-
Teslin Headwaters|Bering Sea	TesHW+Ber	37	4	0	unlikely	-
Lower Liard|Arctic Ocean	Liard+AO	38	1	0	unlikely	-

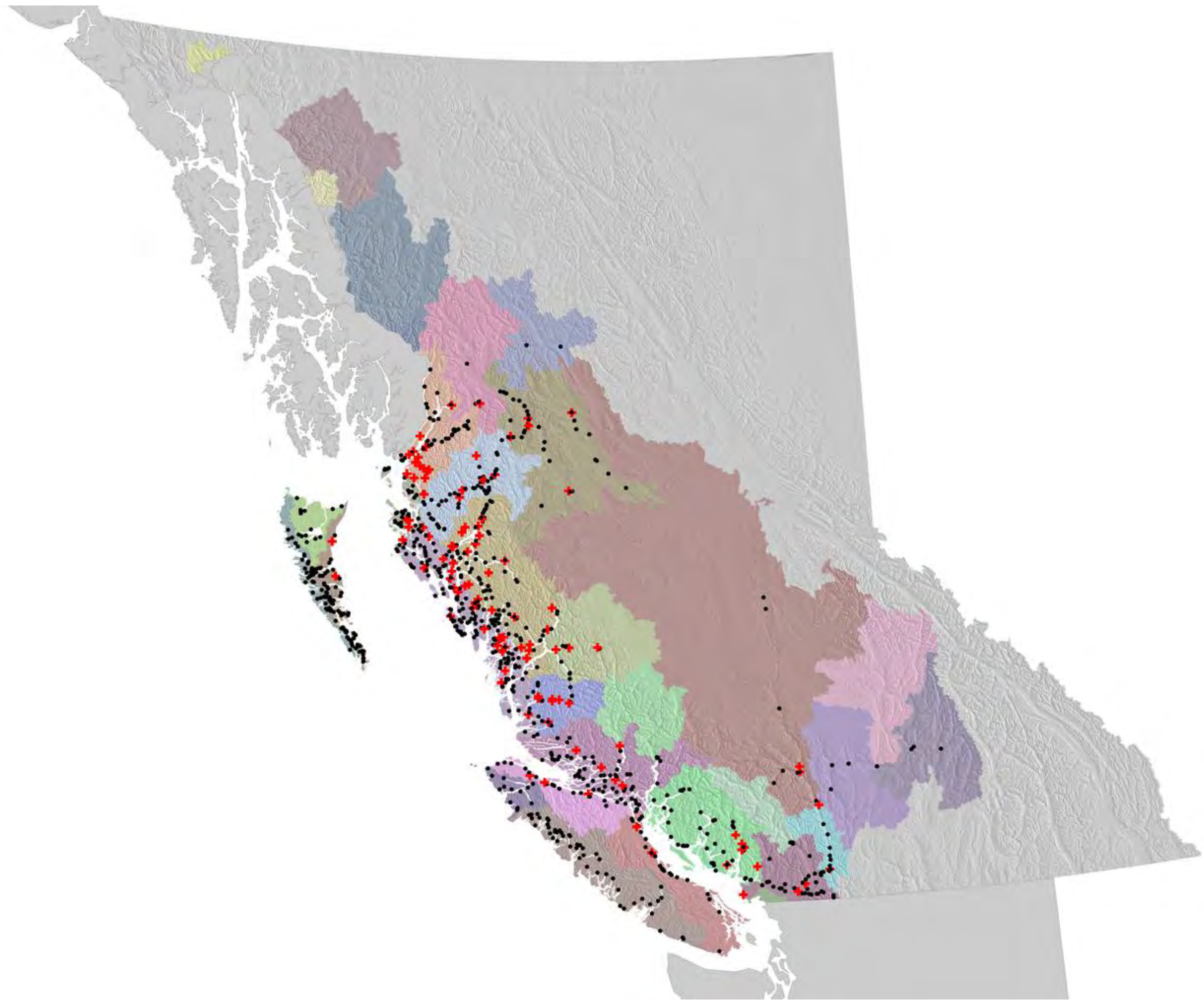


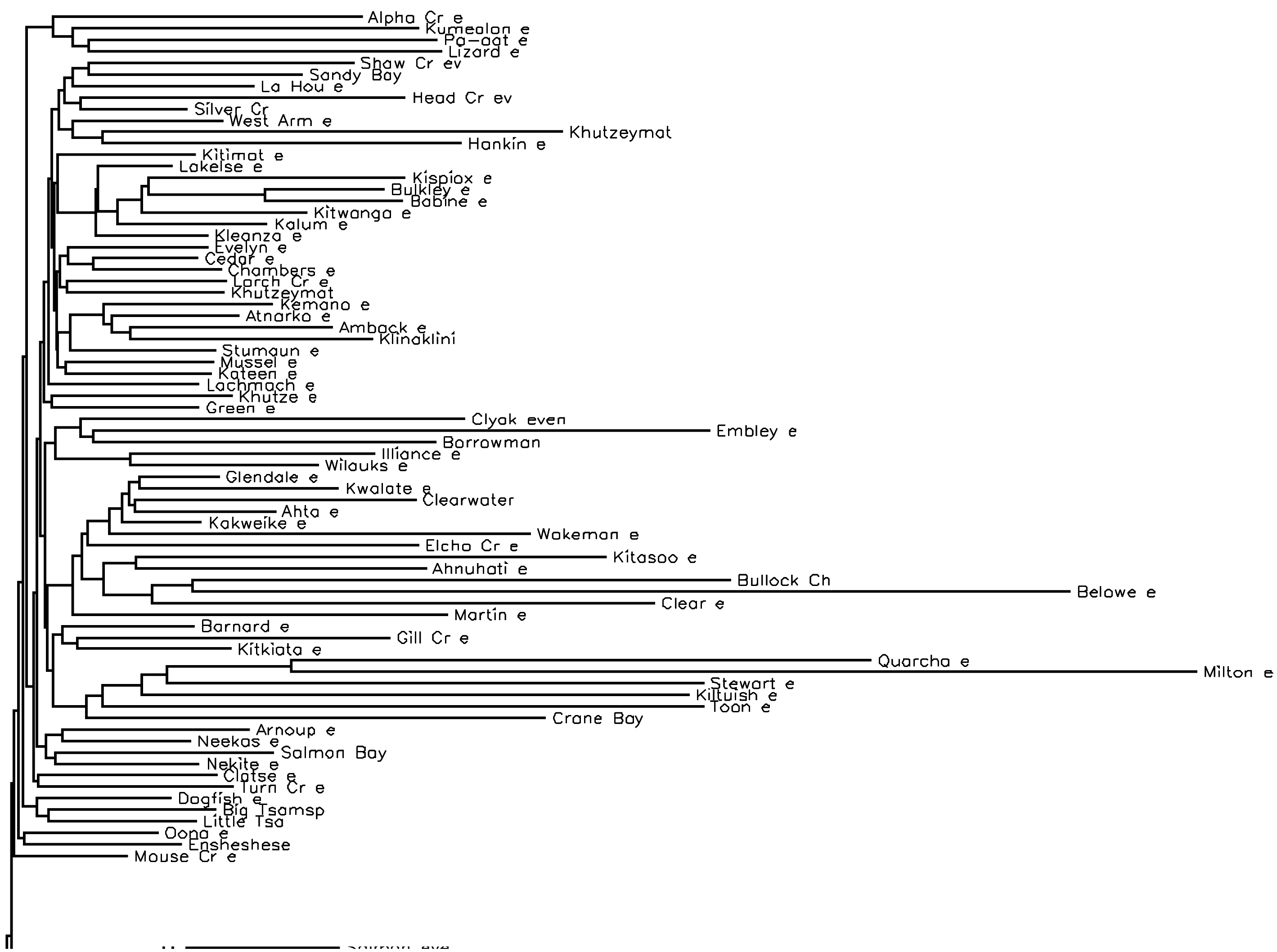
Figure 5. The map shows the locations in British Columbia with records of odd-year pink salmon. The red crosses indicate where genetic samples were available. Odd-year pink salmon are present in the northern transboundary rivers but we have no information. Note the absence of genetic samples from much of Vancouver Island and their lack from sites around Georgia Strait, the Queen Charlotte Islands.

Table 2 Ecotypic Conservation Units for odd-year pink salmon. The name, acronym, and number of sites for each JAZ within with British Columbia are listed. The number of sites includes all AEW with escapement records of any duration for any species, all sites where genetic samples of any species were obtained and all sites with a record of spawn timing for any species. The number of known sites is the count of AEW where at least 3 escapement records are available plus AEW where genetic samples or spawn-timing records are available. Interpreted presence is a categorical determination of the confidence in our assertion that the species is currently self-sustaining within a JAZ. The categories are described in the text. The number of sites where the species is documented as a percentage of the total number of sites in the JAZ is also tabulated.

JAZ			odd-year pink salmon			
name	acronym	code	number sites	known sites	interpreted presence	% documented of total sites
Okanagan|OR-WA Coastal	OK+ORWA	1	1	0	unlikely	-
Boundary Bay|Georgia Strait	BB+GStr	2	8	0	possible	-
Lower Fraser|Georgia Strait	LFR+GStr	3	133	35	documented	26%
Lillooet|Georgia Strait	LILL+GStr	4	16	3	documented	19%
Fraser Canyon|Georgia Strait	FRCany+GStr	5	20	11	documented	55%
Middle Fraser|Georgia Strait	MFR+GStr	6	176	11	documented	6%
Upper Fraser|Georgia Strait	UFR+GStr	7	45	0	unlikely	-
Lower Thompson|Georgia Strait	LTh+GStr	8	20	4	documented	20%
South Thompson|Georgia Strait	STh+GStr	9	66	4	documented	6%
North Thompson|Georgia Strait	NTh+GStr	10	47	1	documented	2%
S Coastal Streams|Georgia Strait	SC+GStr	11	131	49	documented	37%
S Coastal Streams|QCStr-JStr-SFjords	SC+SFj	12	109	65	documented	60%
E Vancouver Island|Georgia Strait	EVI+GStr	13	90	23	documented	26%
E Vancouver Island|QCStr-JStr-SFjords	EVI+SFj	14	33	20	documented	61%
W Vancouver Island|Vancouver Island Coastal Current	WVI+WVI	15	249	50	documented	20%
W Vancouver Island|Outer Graham Island	WVI+WQCI	16	64	13	documented	20%
Homathko - Klinaklini Rivers|QCStr-JStr-SFjords	HK+SFj	17	4	3	documented	75%
Rivers-Smith Inlets|Hecate Strait - Q.C. Sound	RSI+HStr	18	30	23	documented	77%
Bella Coola - Dean Rivers|Hecate Strait - Q.C. Sound	BCD+HStr	19	40	13	documented	33%
Queen Charlottes|Hecate Strait - Q.C. Sound	QCI+HStr	20	142	80	documented	56%
Queen Charlottes|Outer Graham Island	QCI+WQCI	21	83	30	documented	36%
Queen Charlottes|North Graham Island	QCI+NQCI	22	18	14	documented	78%
Hecate Lowlands|Hecate Strait - Q.C. Sound	HecLow+HStr	23	174	146	documented	84%
N Coastal Streams|Hecate Strait - Q.C. Sound	NC+HStr	24	118	97	documented	82%
Hecate Lowlands|Nass - Skeena Estuary	HecLow+NSKEst	25	67	52	documented	78%

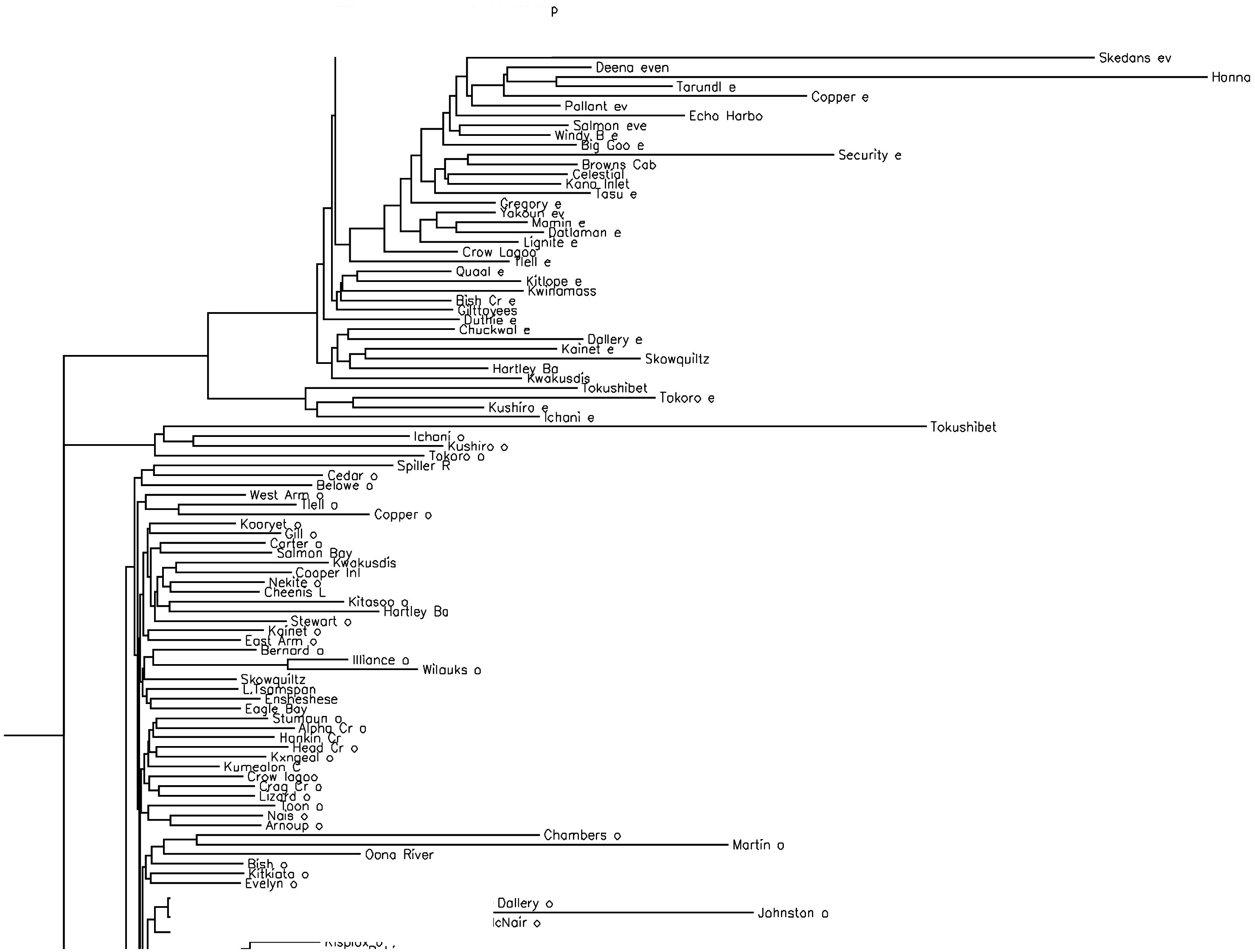
Lower Skeena|Nass - Skeena Estuary	LSK+NSKEst	26	107	54	documented	50%
Middle Skeena|Nass - Skeena Estuary	MSK+NSKEst	27	113	47	documented	42%
Upper Skeena|Nass - Skeena Estuary	USK+NSKEst	28	19	2	documented	11%
Lower Nass - Portland|Nass - Skeena Estuary	LNR-P+NSKEst	29	75	57	documented	76%
Nass|Nass - Skeena Estuary	UNR+NSKEst	30	23	4	documented	17%
Unuk River|Transboundary Fjords	Unuk+TBFj	31	2	0	probable	-
Lower Stikine|Transboundary Fjords	LStk+TBFj	32	18	0	probable	-
Whiting River|Transboundary Fjords	Whtng+TBFj	33	1	0	probable	-
Taku|Transboundary Fjords	Taku+TBFj	34	19	0	probable	-
Lynn Canal|Transboundary Fjords	LYNN+TBFj	35	4	0	probable	-
Alsek|Alaska Coastal Downwelling	Alsek+AKCst	36	6	0	possible	-
Teslin Headwaters|Bering Sea	TesHW+Ber	37	4	0	unlikely	-
Lower Liard|Arctic Ocean	Liard+AO	38	1	0	unlikely	-

Figure 6…



Alpha Cr e
Kumealon e
Pa-aat e
Lizard e
Shaw Cr ev
Sandy Bay
La Hou e
Head Cr ev
Silver Cr
West Arm e
Khutzeymat
Hankin e
Kitimat e
Lakelse e
Kispiox e
Bulkley e
Babine e
Kitwanga e
Kalum e
Kleanza e
Evelyn e
Cedar e
Chambers e
Larch Cr e
Khutzeymat
Kemano e
Atnarko e
Amback e
Klinaklini
Stumaun e
Mussel e
Kateen e
Lachmach e
Khutze e
Green e
Clyak even
Embley e
Borrowman
Illiance e
Wilauks e
Glendale e
Kwalate e
Clearwater
Ahta e
Kakweike e
Wakeman e
Elcho Cr e
Kitasoo e
Ahnuhati e
Bullock Ch
Belowe e
Clear e
Martin e
Barnard e
Gill Cr e
Kitkiata e
Quarcha e
Milton e
Stewart e
Kiltuish e
Toon e
Crane Bay
Arnoup e
Neekas e
Salmon Bay
Nekite e
Clatse e
Turn Cr e
Dogfish e
Big Tsamsp
Little Tsa
Oona e
Ensheshese
Mouse Cr e

Figure 6…


Skedans ev
Deena even
Honna e
Tarundl e
Copper e
Pallant ev
Echo Harbo
Salmon eve
Windy B e
Big Goo e
Security e
Browns Cab
Celestial
Kana Inlet
Tasu e
Gregory e
Yakoun ev
Mamin e
Datlaman e
Lignite e
Crow Lagoo
Tlell e
Quaal e
Kitlope e
Kwinamass
Bish Cr e
Gittoyees
Duthie e
Chuckwal e
Dallery e
Kainet e
Skowquiltz
Hartley Ba
Kwakusdis
Tokushibet
Tokoro e
Kushiro e
Ichani e
Tokushibet
Ichani o
Kushiro o
Tokoro o
Spiller R
Cedar o
Belowe o
West Arm o
Tlell o
Copper o
Kooryet o
Gill o
Carter o
Salmon Bay
Kwakusdis
Cooper Inl
Nekite o
Cheenis L
Kitasoo o
Hartley Ba
Stewart o
Kainet o
East Arm o
Bernard o
Illiance o
Wilauks o
Skowquiltz
L.Tsamspan
Ensheshese
Eagle Bay
Stumaun o
Alpha Cr o
Hankin Cr
Head Cr o
Kxngeal o
Kumealon C
Crow lagoo
Crag Cr o
Lizard o
Toon o
Nais o
Arnoup o
Chambers o
Martin o
Oona River
Bish o
Kitkiata o
Evelyn o
Dallery o
Johnston o
lcNair o

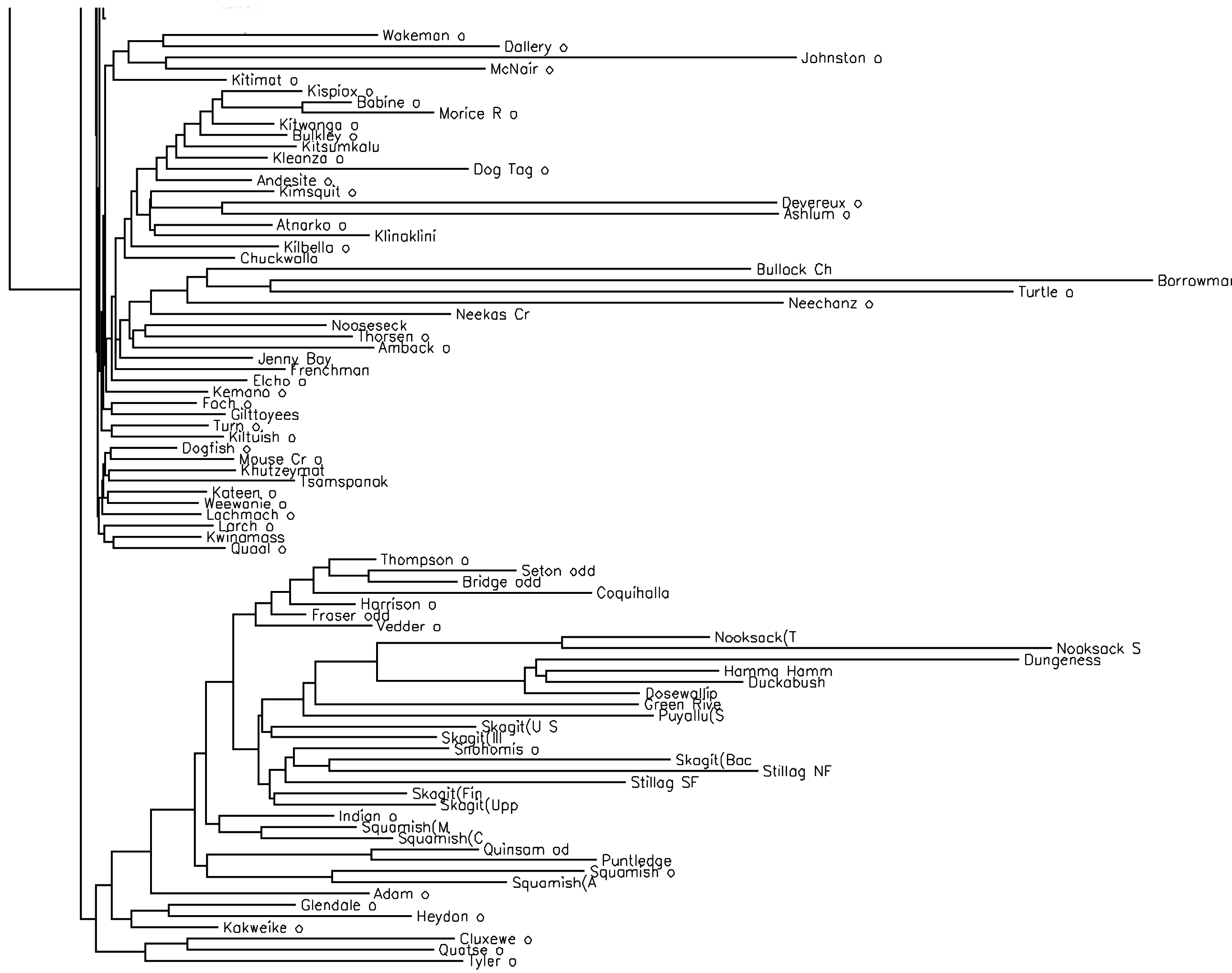


Figure 6. Neighbor-joining tree of Cavalli-Sforza and Edwards (1967) chord distance for populations of pink salmon.

Table 3. Pink salmon populations with a genetic classification available for comparison with the three ecotypic classifications. The "race" is either Odd-year or Even-year. The GFE_ID is the SEDS AEW site identifier. A five level hierarchical genetic classification was used but all levels are shown only where necessary. The horizontal lines in the table divide sites into genetic clusters.

Race	GFE_ID	Sites	genetic cluster	genetic class	FAZ	MAZ	JAZ
Odd-year	Asia	Tokoro		01			
Odd-year	Asia	Kushiro		01			
Odd-year	Asia	Ichani		01			
Odd-year	Asia	Takushibet		01			
Odd-year	1854	Tyler	L	02.01-01	HecLow	HStr	HecLow+HStr
Odd-year	1106	Quatse	L	02.01-02	EVI	SFj	EVI+SFj
Odd-year	1109	Cluxewe	L	02.01-02	EVI	SFj	EVI+SFj
Odd-year	860	Kakweiken	M	02.02-01	SC	SFj	SC+SFj
Odd-year	831	Heydon	M	02.02-02	SC	SFj	SC+SFj
Odd-year	847	Glendale	M	02.02-02	SC	SFj	SC+SFj
Odd-year	1119	Adam	N	02.03	EVI	SFj	EVI+SFj
Odd-year	708	Squamish	O	02.04-01	SC	GStr	SC+GStr
Odd-year	715	Squamish (A)	O	02.04-01	SC	GStr	SC+GStr
Odd-year	1144	Quinsam	O	02.04-02	EVI	GStr	EVI+GStr
Odd-year	1156	Puntledge	O	02.04-02	EVI	GStr	EVI+GStr
Odd-year	688	Indian	P	02.05-01	SC	GStr	SC+GStr
Odd-year	711	Squamish (M)	P	02.05-02	SC	GStr	SC+GStr
Odd-year	724	Squamish (C)	P	02.05-02	SC	GStr	SC+GStr
Odd-year	62	Vedder	P	02.06-01	LFR	GStr	LFR+GStr
Odd-year	1	Fraser	P	02.06-02	LFR	GStr	LFR+GStr
Odd-year	179	Harrison	P	02.06-03	LFR	GStr	LFR+GStr
Odd-year	112	Coquihalla	P	02.06-04	FRCany	GStr	FRCany+GStr
Odd-year	211	Thompson	P	02.06-05	LTh	GStr	LTh+GStr
Odd-year	133	Bridge	P	02.06-06	MFR	GStr	MFR+GStr
Odd-year	2476	Seton	P	02.06-06	MFR	GStr	MFR+GStr
Odd-year	WA	Skagit_upper	P	02.07.01-01			
Odd-year	WA	Skagit_Fin	P	02.07.01-01			
Odd-year	WA	Stillaguamish_SF	P	02.07.01-02			
Odd-year	WA	Snohomish	P	02.07.01-03			
Odd-year	WA	Stillaguamish_NF	P	02.07.01-04			
Odd-year	WA	Skagit_Bac	P	02.07.01-04			
Odd-year	WA	Skagit_US	P	02.07.02-01			
Odd-year	WA	Skagit_ill	P	02.07.02-01			
Odd-year	WA	Puyallup	P	02.07.02-02			
Odd-year	WA	Green	P	02.07.02-03			
Odd-year	WA	Dosewallip	P	02.07.02-04			
Odd-year	WA	Duckabush	P	02.07.02-04			
Odd-year	WA	Hamma Hamm	P	02.07.02-04			
Odd-year	WA	Dungeness	P	02.07.02-04			
Odd-year	WA	Nooksack_S	P	02.07.02-05			
Odd-year	WA	Nooksack_T	P	02.07.02-05			
Odd-year	531	Cedar	A	03	LSK	NSKEst	LSK+NSKEst

Race	GFE_ID	Sites	genetic cluster	genetic class	FAZ	MAZ	JAZ
Odd-year	1000	Spiller	A	03	HecLow	HStr	HecLow+HStr
Odd-year	1091	Belowe	A	03	HecLow	HStr	HecLow+HStr
Odd-year	1497	Tlell	B	04	QCI	HStr	QCI+HStr
Odd-year	1579	Copper	B	04	QCI	HStr	QCI+HStr
Odd-year	1870	West Arm	B	04	NC	HStr	NC+HStr
Odd-year	1010	Kainet	C	05.01	NC	HStr	NC+HStr
Odd-year	1871	East Arm	C	05.01	NC	HStr	NC+HStr
Odd-year	918	Nekite	D	05.02	RSI	HStr	RSI+HStr
Odd-year	998	Cheenis	D	05.02	HecLow	HStr	HecLow+HStr
Odd-year	1007	Salmon Bay	D	05.02	HecLow	HStr	HecLow+HStr
Odd-year	1017	Carter	D	05.02	NC	HStr	NC+HStr
Odd-year	1090	Hartley Bay	D	05.02	HecLow	HStr	HecLow+HStr
Odd-year	1789	Stewart	D	05.02	HecLow	HStr	HecLow+HStr
Odd-year	1813	Kwakusdis	D	05.02	HecLow	HStr	HecLow+HStr
Odd-year	1820	Kitasoo	D	05.02	HecLow	HStr	HecLow+HStr
Odd-year	1897	Gill	D	05.02	HecLow	HStr	HecLow+HStr
Odd-year	1936	Kooryet	D	05.02	HecLow	HStr	HecLow+HStr
Odd-year	2683	Cooper Inlet	D	05.02	HecLow	HStr	HecLow+HStr
Odd-year	1750	Toon	D	05.03-01	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	1850	Arnoup	D	05.03-01	NC	HStr	NC+HStr
Odd-year	1852	Nias	D	05.03-01	NC	HStr	NC+HStr
Odd-year	1094	Kxngeal	D	05.03-02	HecLow	NSKEst	HecLow+NSKEst
Odd-year	1097	Kumealon	D	05.03-02	HecLow	NSKEst	HecLow+NSKEst
Odd-year	1744	Stumaun	D	05.03-02	HecLow	NSKEst	HecLow+NSKEst
Odd-year	1769	Lizard	D	05.03-02	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	1932	Alpha	D	05.03-02	HecLow	NSKEst	HecLow+NSKEst
Odd-year	1951	Hankin	D	05.03-02	HecLow	NSKEst	HecLow+NSKEst
Odd-year	1959	Head	D	05.03-02	HecLow	NSKEst	HecLow+NSKEst
Odd-year	2307	Crow Lagoon	D	05.03-02	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	2312	Crag	D	05.03-02	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	978	Skowquiltz	D	05.04-01	NC	HStr	NC+HStr
Odd-year	1760	Illiance	D	05.04-01	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	1761	Wilauks	D	05.04-01	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	1869	Bernard	D	05.04-01	HecLow	HStr	HecLow+HStr
Odd-year	1042	Eagle Bay	D	05.04-02	NC	HStr	NC+HStr
Odd-year	1751	Ensheshese	D	05.04-02	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	1752	Tsamspanaknok	D	05.04-02	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	664	Kateen	E	06	UNR	NSKEst	UNR+NSKEst
Odd-year	1040	Weewanie	E	06	NC	HStr	NC+HStr
Odd-year	1086	Quaal	E	06	NC	HStr	NC+HStr
Odd-year	1748	Lachmach	E	06	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	1752	Tsamspanaknok	E	06	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	1753	Larch	E	06	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	1754	Khutzeymateen	E	06	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	1755	Mouse	E	06	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	1756	Kwinamass	E	06	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	1768	Dogfish	E	06	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	1085	Kitkiata	F	07-01	NC	HStr	NC+HStr

Race	GFE_ID	Sites	genetic cluster	genetic class	FAZ	MAZ	JAZ
Odd-year	1906	Evelyn	F	07-01	NC	HStr	NC+HStr
Odd-year	1080	Bish	F	07-02	NC	HStr	NC+HStr
Odd-year	1955	Oona	F	07-03	HecLow	NSKEst	HecLow+NSKEst
Odd-year	631	Chambers	F	07-04	LNR-P	NSKEst	LNR-P+NSKEst
Odd-year	986	Martin	F	07-05	NC	HStr	NC+HStr
Odd-year	1030	Kiltuish	G	08	NC	HStr	NC+HStr
Odd-year	1901	Turn	G	08	HecLow	HStr	HecLow+HStr
Odd-year	1082	Gilttoyees	G	09	NC	HStr	NC+HStr
Odd-year	1083	Foch	G	09	NC	HStr	NC+HStr
Odd-year	1050	Kitimat	H	10.01	NC	HStr	NC+HStr
Odd-year	744	McNair	H	10.02-01	SC	GStr	SC+GStr
Odd-year	931	Johnston	H	10.02-02	HecLow	HStr	HecLow+HStr
Odd-year	874	Wakeman	H	10.03-01	SC	SFj	SC+SFj
Odd-year	938	Dallery	H	10.03-02	RSI	HStr	RSI+HStr
Odd-year	1034	Kemano	I	11.01	NC	HStr	NC+HStr
Odd-year	984	Elcho	I	11.02	NC	HStr	NC+HStr
Odd-year	985	Frenchman	I	11.03	NC	HStr	NC+HStr
Odd-year	1798	Jenny Bay	K	11.04-01	NC	HStr	NC+HStr
Odd-year	937	Amback	K	11.04-02.01	RSI	HStr	RSI+HStr
Odd-year	973	Nooseseck	K	11.04-02.02	BCD	HStr	BCD+HStr
Odd-year	2242	Thorsen	K	11.04-02.02	BCD	HStr	BCD+HStr
Odd-year	999	Neekas	K	11.04-03.01	HecLow	HStr	HecLow+HStr
Odd-year	941	Neechanze	K	11.04-03.02	RSI	HStr	RSI+HStr
Odd-year	995	Bullock	K	11.04-03.03	HecLow	HStr	HecLow+HStr
Odd-year	1903	Turtle	K	11.04-03.04	HecLow	HStr	HecLow+HStr
Odd-year	1890	Borrowman	K	11.04-03.05	HecLow	HStr	HecLow+HStr
Odd-year	948	Chuckwalla	J	11.05-01	RSI	HStr	RSI+HStr
Odd-year	947	Kilbella	J	11.05-02	RSI	HStr	RSI+HStr
Odd-year	850	Klinaklini	J	11.05-03.01	HK	SFj	HK+SFj
Odd-year	970	Atnarko	J	11.05-03.01	BCD	HStr	BCD+HStr
Odd-year	977	Kimsquit	J	11.05-03.02	NC	HStr	NC+HStr
Odd-year	850	Devereux	J	11.05-03.03	HK	SFj	HK+SFj
Odd-year	939	Ashlum	J	11.05-03.03	RSI	HStr	RSI+HStr
Odd-year	468	Andesite	J	11.05-04.01	LSK	NSKEst	LSK+NSKEst
Odd-year	463	Dog Tag	J	11.05-04.02	LSK	NSKEst	LSK+NSKEst
Odd-year	477	Kleanza	J	11.05-04.03	LSK	NSKEst	LSK+NSKEst
Odd-year	521	Kitsumkalum	J	11.05-04.04	LSK	NSKEst	LSK+NSKEst
Odd-year	540	Bulkley	J	11.05-04.05	MSK	NSKEst	MSK+NSKEst
Odd-year	566	Kispiox	J	11.05-04.06	MSK	NSKEst	MSK+NSKEst
Odd-year	488	Kitwanga	J	11.05-04.07	MSK	NSKEst	MSK+NSKEst
Odd-year	556	Morice	J	11.05-04.08	MSK	NSKEst	MSK+NSKEst
Odd-year	592	Babine	J	11.05-04.08	MSK	NSKEst	MSK+NSKEst

Even-year	Asia	Takushibet		01.01			
Even-year	Asia	Ichani		01.02			
Even-year	Asia	Kushiro		01.03			
Even-year	Asia	Tokoro		01.03			

Race	GFE_ID	Sites	genetic cluster	genetic class	FAZ	MAZ	JAZ
Even-year	1813	Kwakusdis	A	02-01	HecLow	HStr	HecLow+HStr
Even-year	938	Dallery	A	02-02	RSI	HStr	RSI+HStr
Even-year	948	Chuckwalla	A	02-02	RSI	HStr	RSI+HStr
Even-year	978	Skowquiltz	A	02-03	NC	HStr	NC+HStr
Even-year	1010	Kainet	A	02-03	NC	HStr	NC+HStr
Even-year	1090	Hartley Bay	A	02-03	HecLow	HStr	HecLow+HStr
Even-year	1836	Duthie	B	03	NC	HStr	NC+HStr
Even-year	1082	Gilttoyees	C	04-01	NC	HStr	NC+HStr
Even-year	1080	Bish	C	04-02	NC	HStr	NC+HStr
Even-year	7990614	Kitlope	C	04-03	NC	HStr	NC+HStr
Even-year	1086	Quaal	C	04-04	NC	HStr	NC+HStr
Even-year	1756	Kwinamass	C	04-04	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	1497	Tlell	D	05-01	QCI	HStr	QCI+HStr
Even-year	2307	Crow Lagoon	D	05-02	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	1560	Lignite	D	05-03	QCI	NQCI	QCI+NQCI
Even-year	1568	Datlamen	D	05-03	QCI	NQCI	QCI+NQCI
Even-year	1570	Mamin	D	05-03	QCI	NQCI	QCI+NQCI
Even-year	1571	Yakoun	D	05-03	QCI	NQCI	QCI+NQCI
Even-year	1541	Gregory	D	05-04	QCI	WQCI	QCI+WQCI
Even-year	1656	Tasu	D	05-05.1	QCI	WQCI	QCI+WQCI
Even-year	1531	Kana Inlet	D	05-05.2	QCI	WQCI	QCI+WQCI
Even-year	1551	Celestial	D	05-05.2	QCI	WQCI	QCI+WQCI
Even-year	1671	Security	D	05-05.3	QCI	WQCI	QCI+WQCI
Even-year	1678	Browns Cabin	D	05-05.3	QCI	WQCI	QCI+WQCI
Even-year	1597	Big Goose	D	05-06	QCI	HStr	QCI+HStr
Even-year	1007	Salmon Bay	D	05-07	HecLow	HStr	HecLow+HStr
Even-year	1709	Windy Bay	D	05-07	QCI	HStr	QCI+HStr
Even-year	1606	Echo Harbour	D	05-08	QCI	HStr	QCI+HStr
Even-year	1584	Pallant	D	05-09.1	QCI	HStr	QCI+HStr
Even-year	1579	Copper	D	05-09.2	QCI	HStr	QCI+HStr
Even-year	1683	Deena	D	05-09.3	QCI	HStr	QCI+HStr
Even-year	1512	Tarundl	D	05-09.4	QCI	HStr	QCI+HStr
Even-year	1511	Honna	D	05-09.5	QCI	HStr	QCI+HStr
Even-year	1692	Skedans	D	05-10	QCI	HStr	QCI+HStr
Even-year	1755	Mouse	E	06	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	1955	Oona	E	07-01	HecLow	NSKEst	HecLow+NSKEst
Even-year	1751	Ensheshese	E	07-02	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	1768	Dogfish	E	08-01	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	1752	Big Tsamspanaknok	E	08-02	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	1752	Little Tsamspanaknok	E	08-02	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	1932	Alpha	F	09-01	HecLow	NSKEst	HecLow+NSKEst
Even-year	1097	Kumealon	F	09-02	HecLow	NSKEst	HecLow+NSKEst
Even-year	1914	Pa-aat	F	09-03	HecLow	NSKEst	HecLow+NSKEst
Even-year	1769	Lizard	F	09-04	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	989	Clatse	F	10	HecLow	HStr	HecLow+HStr
Even-year	1901	Turn	F	10	HecLow	HStr	HecLow+HStr
Even-year	918	Nekite	F	11-01	RSI	HStr	RSI+HStr
Even-year	1007	Salmon Bay	F	11-01	HecLow	HStr	HecLow+HStr

Race	GFE_ID	Sites	genetic cluster	genetic class	FAZ	MAZ	JAZ
Even-year	1850	Arnoup	F	11-02	NC	HStr	NC+HStr
Even-year	999	Neekas	F	11-02	HecLow	HStr	HecLow+HStr
Even-year	1760	Illiance	H	12.01.01-01	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	1761	Wilauks	H	12.01.01-01	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	949	Clyak	H	12.01.01-02	RSI	HStr	RSI+HStr
Even-year	1890	Borrowman	H	12.01.01-03	HecLow	HStr	HecLow+HStr
Even-year	878	Embley	H	12.01.01-04	SC	SFj	SC+SFj
Even-year	984	Elcho	H	12.01.02-02.01	NC	HStr	NC+HStr
Even-year	986	Martin	H	12.01.02-02.01	NC	HStr	NC+HStr
Even-year	861	Ahta	H	12.01.02-02.03	SC	SFj	SC+SFj
Even-year	510	Clearwater	H	12.01.02-02.03	LSK	NSKEst	LSK+NSKEst
Even-year	847	Glendale	H	12.01.02-02.03	SC	SFj	SC+SFj
Even-year	852	Ahnuhati	H	12.01.02-03.01	SC	SFj	SC+SFj
Even-year	1091	Belowe	H	12.01.02-03.02	HecLow	HStr	HecLow+HStr
Even-year	995	Bullock Channel	H	12.01.02-03.02	HecLow	HStr	HecLow+HStr
Even-year	530	Clear	H	12.01.02-03.02	LSK	NSKEst	LSK+NSKEst
Even-year	1869	Barnard	H	12.01.03-01	HecLow	HStr	HecLow+HStr
Even-year	1085	Kitkiata	H	12.01.03-02	NC	HStr	NC+HStr
Even-year	1897	Gill Creek	H	12.01.03-03	HecLow	HStr	HecLow+HStr
Even-year	1137	Crane Bay	H	12.01.04-01	SC	SFj	SC+SFj
Even-year	1750	Toon	H	12.01.04-02	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	874	Wakeman	H	12.01.04-02.02	SC	SFj	SC+SFj
Even-year	860	Kakweiken	H	12.01.04-02.03	SC	SFj	SC+SFj
Even-year	853	Kwalate	H	12.01.04-02.03	SC	SFj	SC+SFj
Even-year	1030	Kiltuish	H	12.01.04-03	NC	HStr	NC+HStr
Even-year	1820	Kitasoo	H	12.01.04-03.01	HecLow	HStr	HecLow+HStr
Even-year	1789	Stewart	H	12.01.04-04	HecLow	HStr	HecLow+HStr
Even-year	993	Quarcha	H	12.01.04-05	NC	HStr	NC+HStr
Even-year	952	Milton	H	12.01.04-06	RSI	HStr	RSI+HStr
Even-year	446	Green	G	12.02.01	LSK	NSKEst	LSK+NSKEst
Even-year	1021	Khutze	G	12.02.01	NC	HStr	NC+HStr
Even-year	1748	Lachmach	G	12.02.02	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	1951	Hankin	G	12.02.03-01.01	HecLow	NSKEst	HecLow+NSKEst
Even-year	1754	Khuzeymateen	G	12.02.03-01.01	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	1870	West Arm	G	12.02.03-01.01	NC	HStr	NC+HStr
Even-year	1959	Head	G	12.02.03-01.02	HecLow	NSKEst	HecLow+NSKEst
Even-year	1739	La Hou	G	12.02.03-01.02	HecLow	NSKEst	HecLow+NSKEst
Even-year	1742	Sandy Bay	G	12.02.03-01.02	HecLow	NSKEst	HecLow+NSKEst
Even-year	1948	Shaw	G	12.02.03-01.02	HecLow	NSKEst	HecLow+NSKEst
Even-year	1737	Silver	G	12.02.03-01.02	HecLow	NSKEst	HecLow+NSKEst
Even-year	1050	Kitimat	G	12.02.03-02.01	NC	HStr	NC+HStr
Even-year	592	Babine	G	12.02.03-02.02	MSK	NSKEst	MSK+NSKEst
Even-year	540	Bulkley	G	12.02.03-02.02	MSK	NSKEst	MSK+NSKEst
Even-year	521	Kalum	G	12.02.03-02.02	LSK	NSKEst	LSK+NSKEst
Even-year	566	Kispiox	G	12.02.03-02.02	MSK	NSKEst	MSK+NSKEst
Even-year	488	Kitwanga	G	12.02.03-02.02	MSK	NSKEst	MSK+NSKEst
Even-year	477	Kleanza	G	12.02.03-02.02	LSK	NSKEst	LSK+NSKEst
Even-year	505	Lakelse	G	12.02.03-02.02	LSK	NSKEst	LSK+NSKEst

Race	GFE_ID	Sites	genetic cluster	genetic class	FAZ	MAZ	JAZ
Even-year	1754	Khutzeymateen	G	12.02.03-03.01	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	1753	Larch	G	12.02.03-03.01	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	531	Cedar	G	12.02.03-03.02	LSK	NSKEst	LSK+NSKEst
Even-year	631	Chambers	G	12.02.03-03.02	LNR-P	NSKEst	LNR-P+NSKEst
Even-year	1906	Evelyn	G	12.02.03-03.02	NC	HStr	NC+HStr
Even-year	664	Kiteen	G	12.02.03-04.01	UNR	NSKEst	UNR+NSKEst
Even-year	1015	Mussel	G	12.02.03-04.01	NC	HStr	NC+HStr
Even-year	1744	Stumaun	G	12.02.03-04.02	HecLow	NSKEst	HecLow+NSKEst
Even-year	937	Amback	G	12.02.03-04.03	RSI	HStr	RSI+HStr
Even-year	970	Atnarko	G	12.02.03-04.03	BCD	HStr	BCD+HStr
Even-year	1034	Kemano	G	12.02.03-04.03	NC	HStr	NC+HStr
Even-year	850	Klinaklini	G	12.02.03-04.03	HK	SFj	HK+SFj

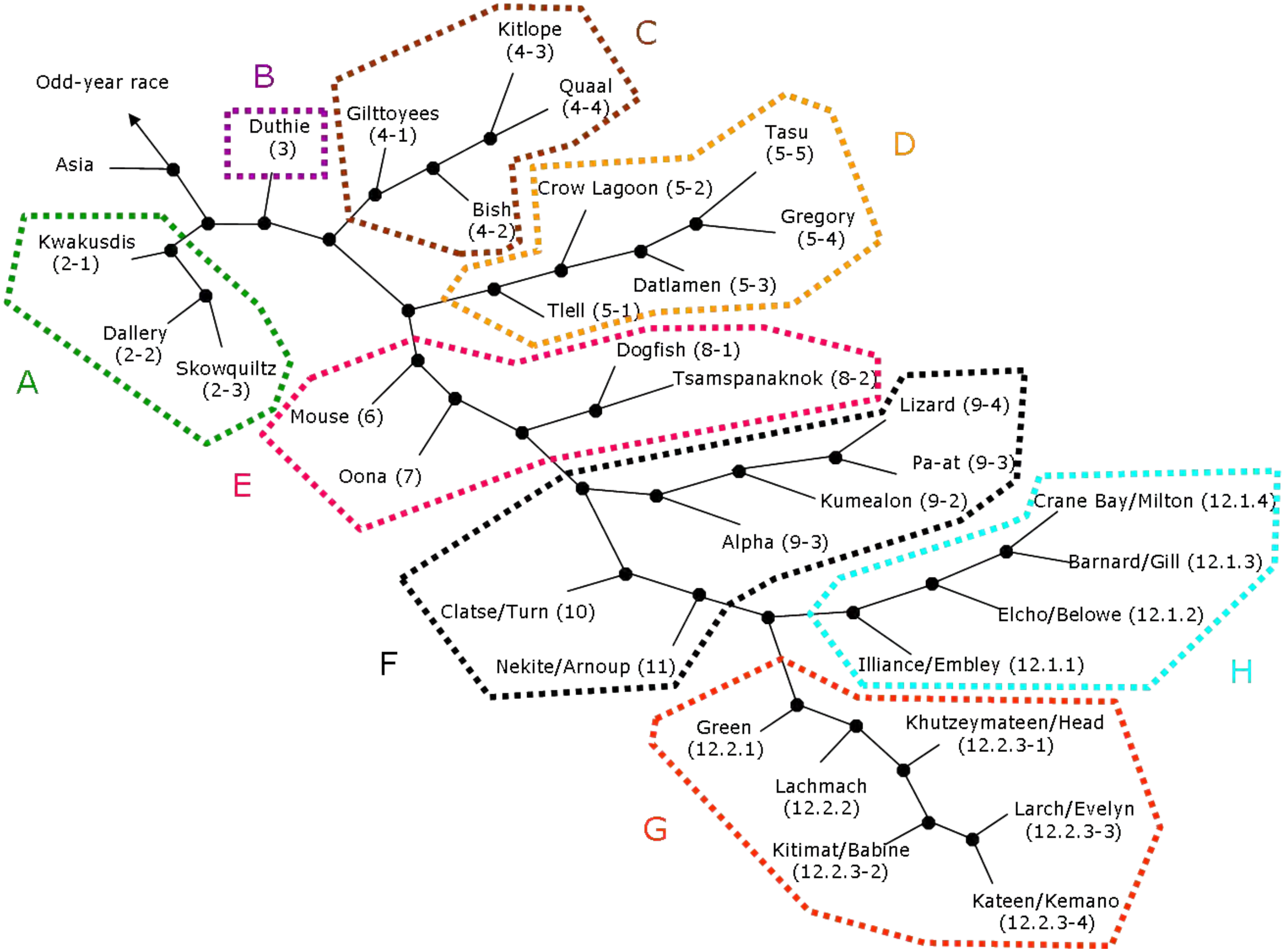


Figure 7. Diagrammatic dendrogram for even-year pink salmon. The dotted lines and letters indicate major genetic groupings. The site names are representative of the sites in each sub-group. The codes in parentheses are for the 5-level hierarchical genetic classification (see Table 3).

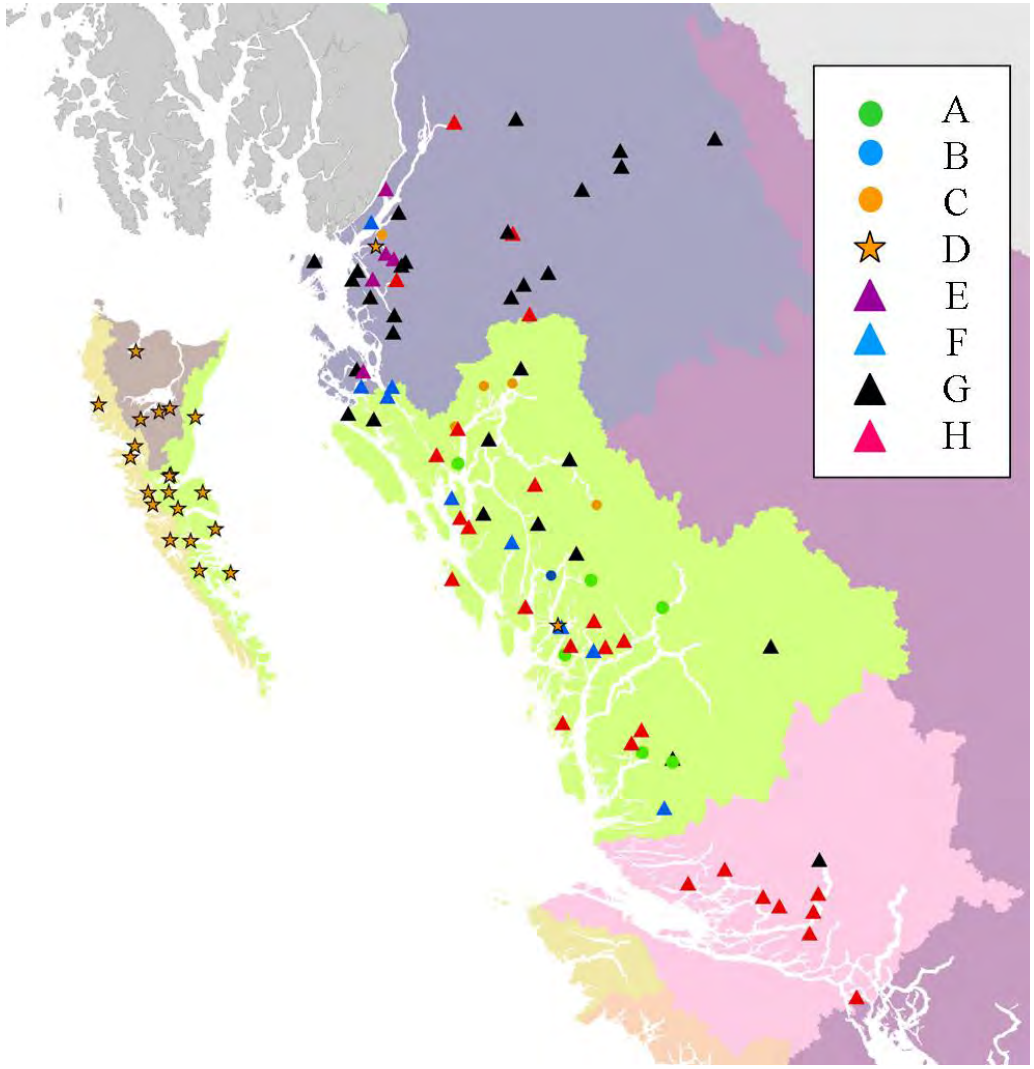


Figure 8. A map showing the distribution of sites within the nine genetic clusters (level-3 in the five-level hierarchical classification) of even-year pink salmon in British Columbia. The colored polygons are the Marine Adaptive Zones.

Table 4. A tabular summary of the genetic-ecotypic crosswalk for even-year pink salmon using the genetic cluster (level-3 of the 5-level hierarchical classification).

JAZ		genetic cluster									
acronym	index	A	B	C	D	E	F	G	H	total sites in JAZ	number of clusters in JAZ
SC+SFj	12								8	8	1
HK+SFj	17							1		1	1
RSI+HStr	18	2					1	1	2	6	4
BCD+HStr	19							1		1	1
QCI+HStr	20				10					10	1
QCI+WQCI	21				6					6	1
QCI+NQCI	22				4					4	1
HecLow+HStr	23	2			1		4		7	14	4
NC+HStr	24	2	1	4			1	6	5	19	6
HecLow+NSKEst	25					1	3	7		11	3
LSK+NSKEst	26							5	2	7	2
MSK+NSKEst	27							4		4	1
LNR-P+NSKEst	29			1	1	5	1	5	3	16	6
UNR+NSKEst	30							1		1	1
Grand Total		6	1	5	22	6	10	31	27	108	8
JAZ in cluster		3	1	2	5	2	5	9	6	14	

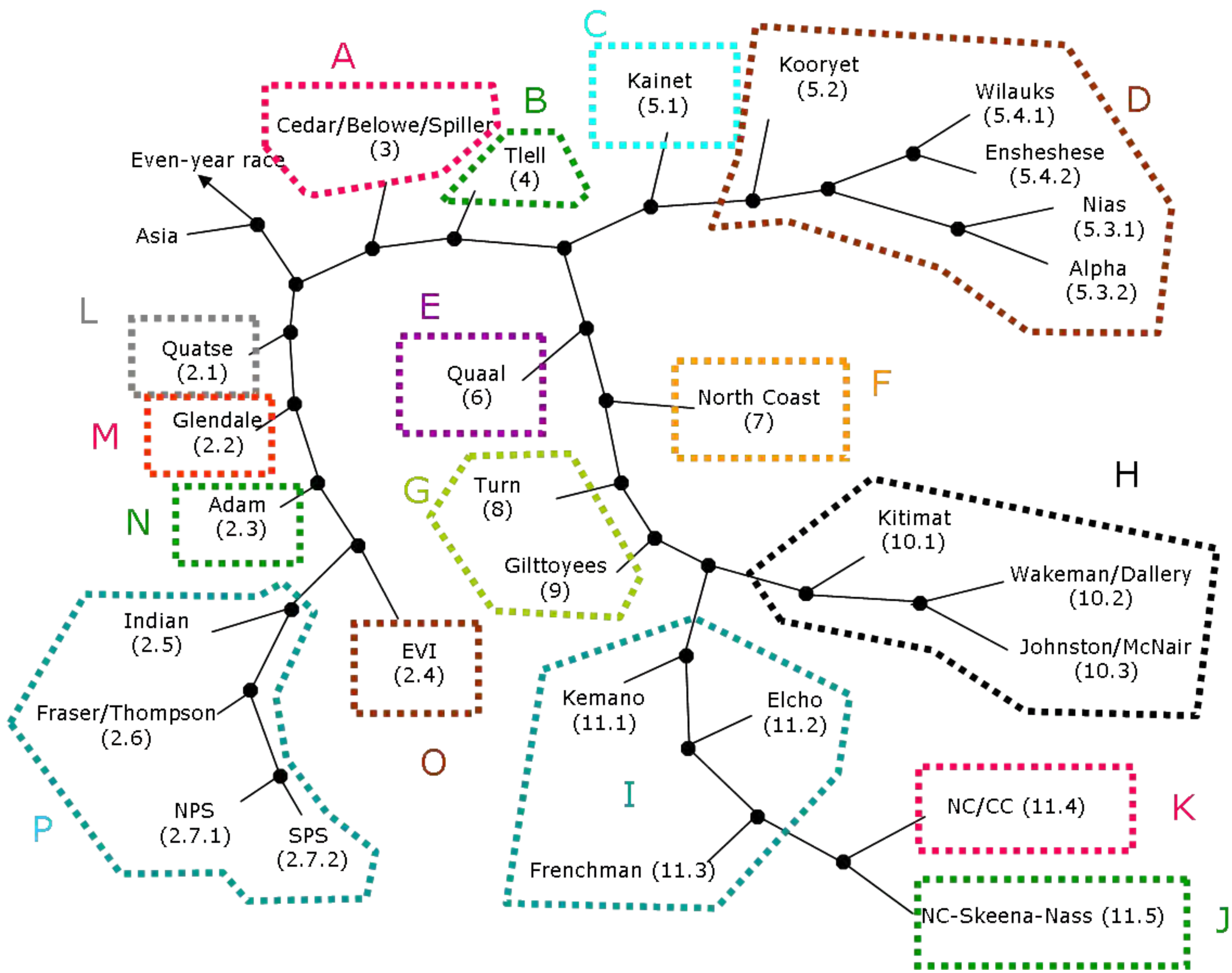


Figure 9. Diagrammatic dendrogram for odd-year pink salmon. The dotted lines and letters indicate genetic clusters. The site names are representative of the sites in each sub-group. The codes in parentheses are the cluster specific portion of the genetic class (see Table 3).

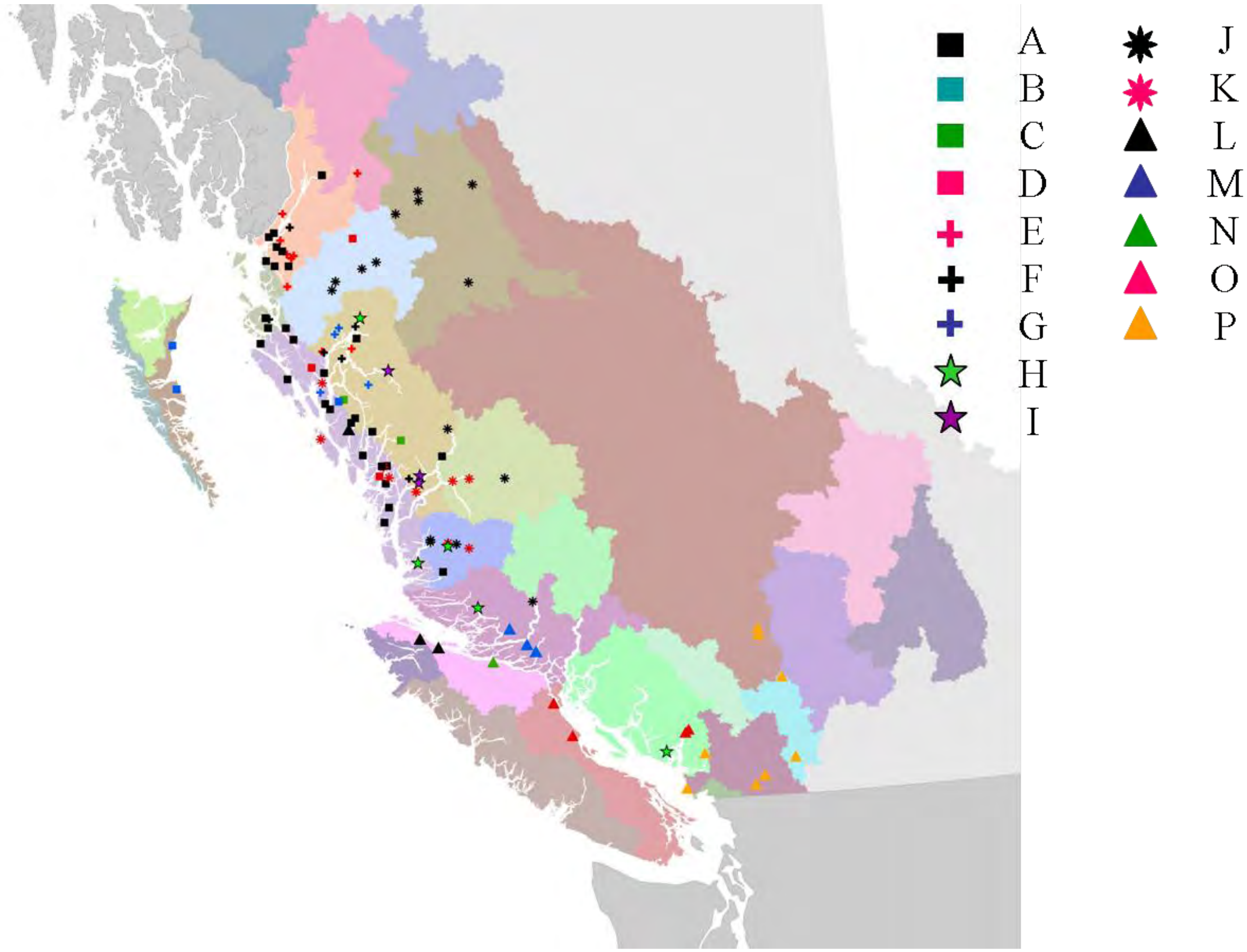


Figure 10. A map showing the distribution of sites within the 16 genetic clusters (level-3 in the five-level hierarchical classification) of odd-year pink salmon in British Columbia.

Table 5. A tabular summary of the genetic-ecotypic crosswalk for odd-year pink salmon using the genetic cluster (level-3 of the five-level genetic classification). The genetic classifications of the odd-year and even-year races are independent and cannot be compared using the cluster IDs.

JAZ		cluster																	
Cluster	index	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	sites in JAZ	clusters in JAZ
LFR+GStr	3																3	3	1
FRCany+GStr	5																1	1	1
MFR+GStr	6																2	2	1
LTh+GStr	8																1	1	1
SC+GStr	11								1							2	3	6	3
SC+SFj	12								1					3				4	2
EVI+GStr	13															2		2	1
EVI+SFj	14												2		1			3	2
HK+SFj	17										2							2	1
RSI+HStr	18				1				1		3	2						7	4
BCD+HStr	19										1	2						3	2
QCI+HStr	20		2															2	1
QCI+WQCI	21																	0	0
QCI+NQCI	22																	0	0
HecLow+HStr	23	2			10			1	1			4	1					19	6
NC+HStr	24		1	2	5	2	4	3	1	3	1	1						23	10
HecLow+NSKEst	25				6		1											7	2
LSK+NSKEst	26	1									4							5	2
MSK+NSKEst	27										5							5	1
LNR-P+NSKEst	29				8	7	1											16	3
UNR+NSKEst	30					1												1	1
WA	99																16	16	1
sites in cluster		3	3	2	30	10	6	4	5	3	16	9	3	3	1	4	26	128	16
JAZ in clusters		3	3	2	6	4	4	3	6	2	7	5	3	2	2	3	7	23	

Table 6. Regional variation in spawn timing (DOY) in pink salmon. Both races are combined and grouped by their JAZ ordered roughly south to north. Predictions of the mean date of spawning were made using the GLM model shown in Table 7. Note that no data on spawning time was available for the sole site in the Taku River.

		DOY of peak spawning						
JAZ	index	N	minimum	mean	maximum	SD	model prediction	residual (O-E)
LFR+GStr	3	35	258.0	297.1	341.0	13.36	295.4	1.89
LILL+GStr	4	3	258.0	269.6	283.0	12.61	284.7	-15.16
FRCany+GStr	5	11	278.0	284.6	291.4	4.35	289.9	-5.24
MFR+GStr	6	13	258.0	284.6	319.0	15.40	278.5	6.92
LTh+GStr	8	4	271.5	276.9	281.1	4.26	287.4	-10.46
STh+GStr	9	4	282.8	284.9	288.0	2.21	281.2	3.74
NTh+GStr	10	1	274.3	274.3	274.3		277.4	-3.05
SC+GStr	11	77	237.0	262.5	290.0	10.03	262.6	0.10
SC+SFj	12	134	231.2	262.4	294.5	11.58	263.3	-0.86
EVI+GStr	13	45	257.8	270.7	303.0	8.19	268.8	1.96
EVI+SFj	14	41	248.0	261.9	278.7	6.90	263.5	-1.63
WVI+WVI	15	134	240.5	268.3	319.0	11.92	267.5	0.80
WVI+WQCI	16	37	227.0	257.5	289.0	14.66	263.1	-5.66
HK+SFj	17	6	241.5	255.5	279.5	18.34	253.0	2.57
RSI+HStr	18	46	227.0	252.8	273.0	10.17	255.1	-2.37
BCD+HStr	19	35	232.0	246.5	258.5	5.54	246.5	-0.18
QCI+HStr	20	175	237.0	265.4	293.5	8.44	263.2	2.28
QCI+WQCI	21	89	242.5	261.7	288.0	7.58	262.3	-0.56
QCI+NQCI	22	29	244.2	253.6	260.5	3.97	254.7	-1.09
HecLow+HStr	23	290	227.0	259.8	289.0	9.40	260.0	-0.19
NC+HStr	24	197	225.1	250.1	288.0	11.32	249.5	0.53
HecLow+NSKEst	25	107	241.9	256.1	265.6	4.20	255.7	0.37
LSK+NSKEst	26	107	228.0	248.8	262.3	7.25	249.6	-0.87
MSK+NSKEst	27	91	227.0	248.1	273.5	8.87	246.8	1.36
USK+NSKEst	28	3	245.6	251.7	256.6	5.62	235.2	16.56
LNR-P+NSKEst	29	117	227.0	242.1	269.0	8.56	244.2	-2.12
UNR+NSKEst	30	8	247.0	251.3	259.0	4.38	241.7	9.30
Taku+TBFj	34	1					203.0	
Overall		1840	225.1	258.6	341.0	13.64		

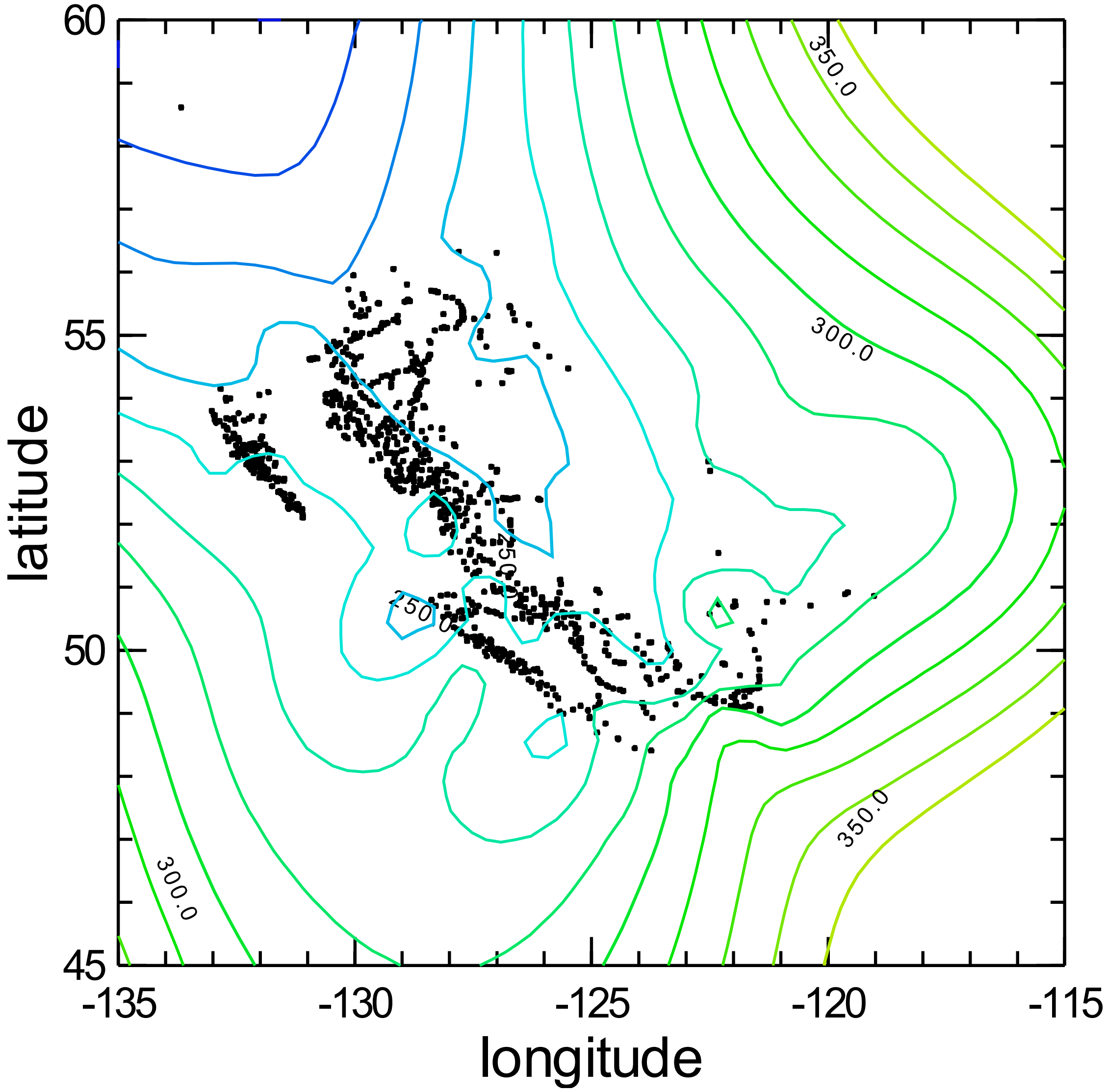


Figure 11. A contour plot showing the geographical distribution of the day of peak spawning (DOY) for pink salmon of both races. Each dot is a race×site pair and values plotted are the mean DOYs for each pair.

Table 7 The GLM for mean day of spawning in British Columbian pink salmon populations. The variables used are described in 13.

Dependent Variable	DOY_PK_SPAWN (site mean of the ay of year of peak spawning)
N	1803
Multiple R	0.756
Squared Multiple R	0.571

Estimates of Effects $B = (X'X)^{-1}X'Y$

Factor		Level	DOY_PK_SPAWN
CONSTANT			292.106
SPECIES$	either PKE (even-year) or PKO (odd-year)	PKE	0.542
LAT	latitude (decimal degrees N)		-2.793
LONG	longitude (-decimal degrees W)		-0.832
TUNDRA_PC	% upstream watershed area of high elevation tundra		-0.100
AT_AUG	mean air temperature in August		1.434
AT_NOV	mean air temperature in November		2.778
MAX_P_MAG	primary drainage network total link magnitude		0.000480
ELEV_MEAN	mean elevation		0.012
VFW_MEAN	mean width (m) of the valley floor		-0.514
KFAC_LOG	$\log_{10}$of the mean annual peak flow		-6.178

Analysis of Variance

Source	Type III SS	df	Mean Squares	F-ratio	p-value
SPECIES$	507.698	1	507.7	6.3	0.012
LAT	4480.735	1	4480.7	55.9	0.000
LONG	1098.851	1	1098.9	13.7	0.000
TUNDRA_PC	1096.880	1	1096.9	13.7	0.000
AT_AUG	1004.139	1	1004.1	12.5	0.000
AT_NOV	8110.668	1	8110.7	101.1	0.000
MAX_P_MAG	39513.678	1	39513.7	492.6	0.000
ELEV_MEAN	1811.502	1	1811.5	22.6	0.000
VFW_MEAN	3256.950	1	3256.9	40.6	0.000
KFAC_LOG	2439.805	1	2439.8	30.4	0.000
Error	143758.500	1792	80.2		

Least Squares Means

Factor	Level	LS Mean	Standard Error	N
SPECIES$	PKE	259.1	0.299219	915
SPECIES$	PKO	258.0	0.303829	888

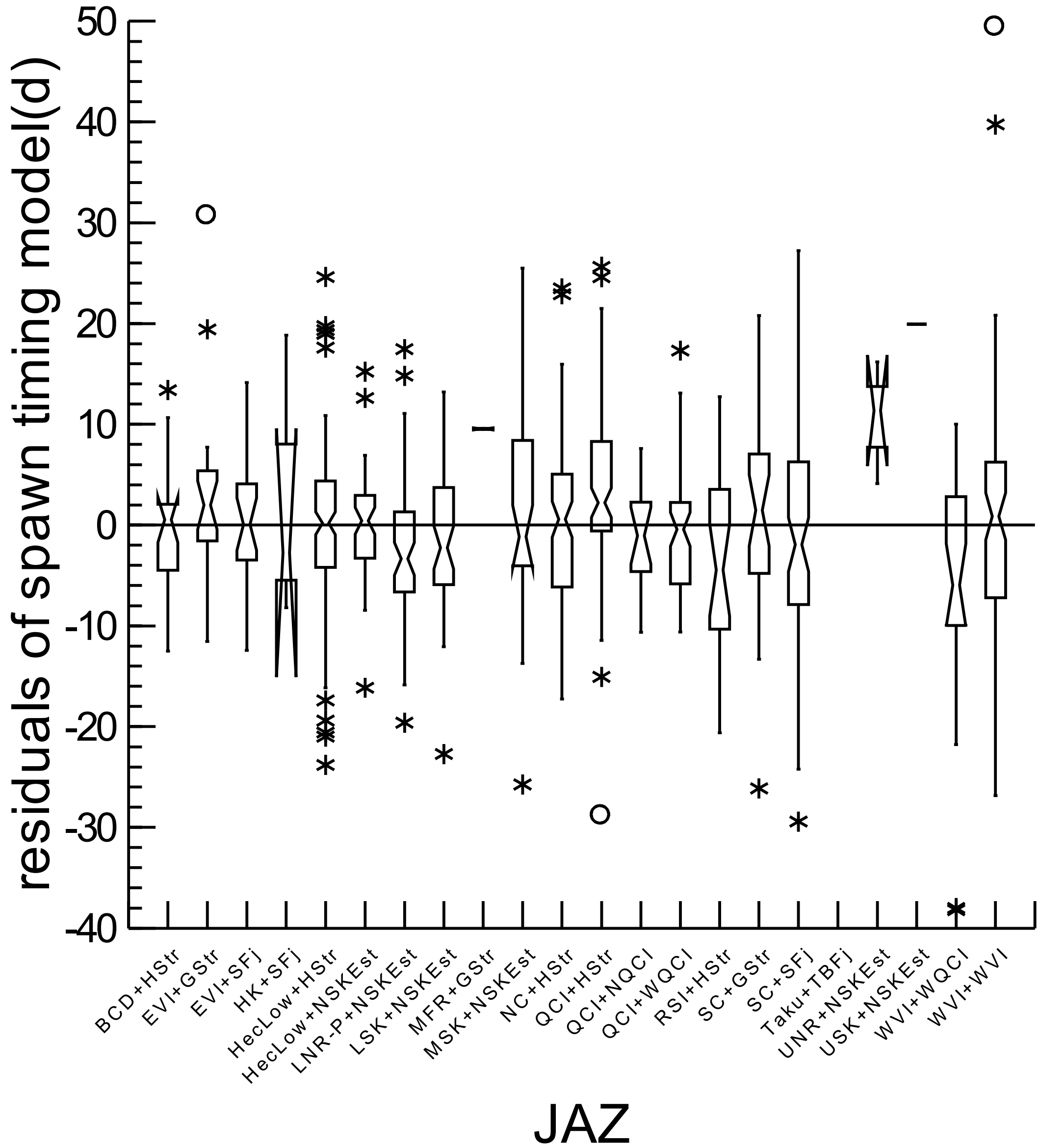


Figure 12. Notched box plots of the residuals for the model (Table 7) for the DOY of peak spawning in even-year pink salmon categorized by their JAZ. The order of the JAZ is alphabetical. A negative residual indicates that spawning was earlier then the model predicted.

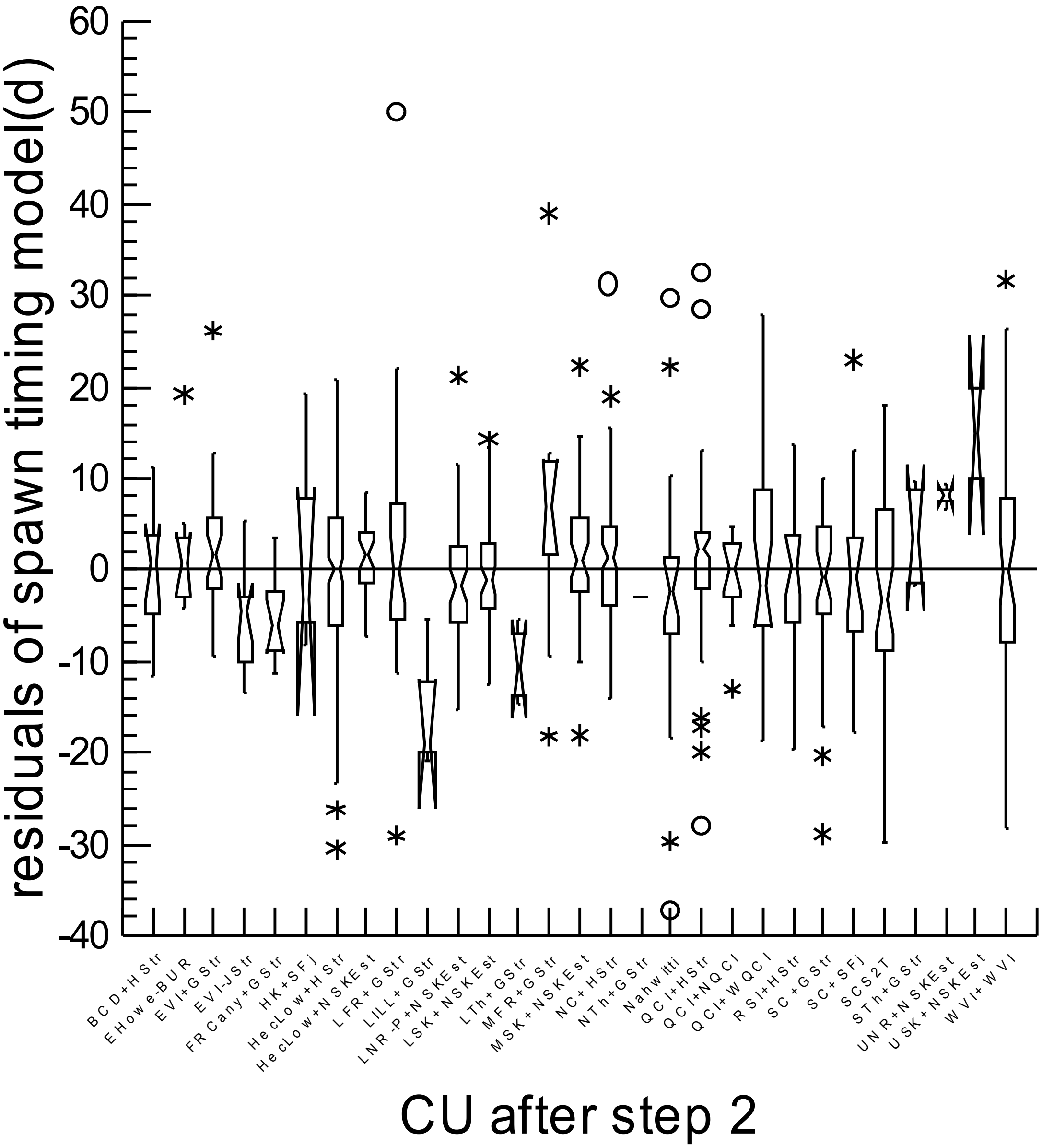


Figure 13. Notched box plots of the residuals for the model (Table 7) for the DOY of peak spawning in odd-year pink salmon categorized by the provisional CU after step 2. The order of the CUs is alphabetical. A negative residual indicates that spawning was earlier then the model predicted.

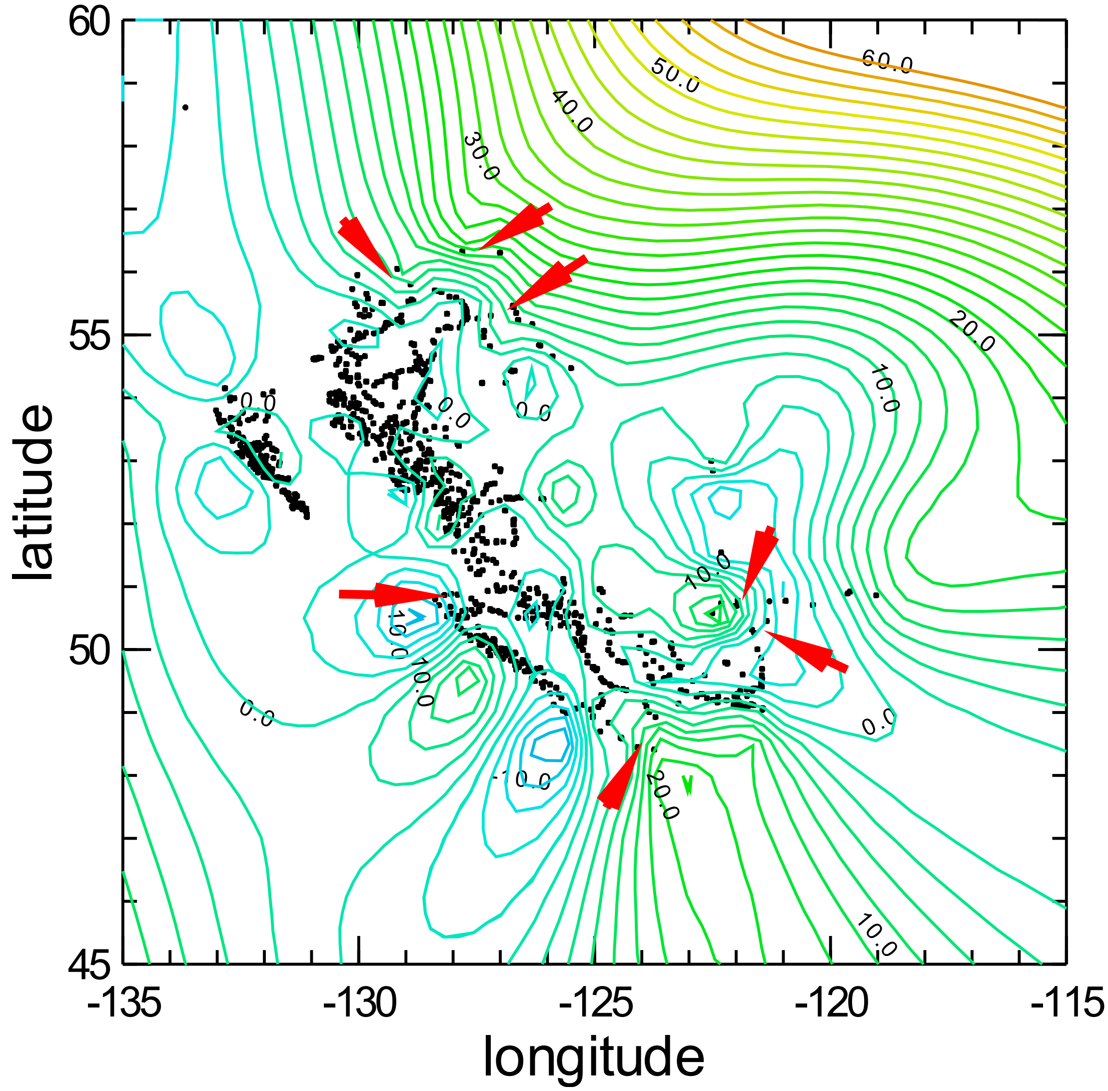


Figure 14. A counter plot of the model residuals for DOY of peak spawning in pink salmon, both races combined. The red arrows indicate locations of consistent and large residuals.

Table 8. Conservation Units for even-year pink salmon (PKE). The table shows the application of the described method. Even-year pink salmon are probably present in the Fraser River drainage but their persistence has not been confirmed and so no CU is recognized. Very little information was available for even-year pink salmon in the northern transboundary rivers. Consequently, the CU recognized in that area is speculative and based on its MAZ ecotype. The number of sites indicated is the total in our database and is not to be interpreted as the number of sites where even-year pink salmon are persistently found.

Even-Year Pink Salmon Conservation Units						
Conservation Unit	Acronym	Index	Number of Sites	Number of Genetic Clusters	Classification Step	Comments
Georgia Strait	GStr	1	55	No Information	Ecotypic/Timing	
W Vancouver Island	WVI	2	83	No Information	Ecotypic	Confirmed by Timing
NorthW Vancouver Island	NWVI	3	24	No Information	Ecotypic	Confirmed by Timing
Southern Fjords	SFj	4	92	2	ecotypic/timing	
Hecate Lowlands	HStr-HecLow	5	163	7	ecotypic/timing	Confirmed by timing
Hecate Strait-Fjords	HStr-Fj	6	145	7	ecotypic/timing	
Nass-Skeena Estuary	NSKEst	7	150	6	ecotypic/timing	
Middle-Upper Skeena	M&U-SKNA	8	45	1	ecotypic/timing	
North Queen Charlotte Islands	NQCI	9	15	1	genetic	
East Queen Charlotte Islands	EQCI	10	95	1	genetic	Distinctive timing
West Queen Charlotte Islands	WQCI	11	59	1	genetic	
Upper Nass	UNASS	12	5	1	ecotypic/timing	Distinctive timing
Transboundary Fjords	TBFj	13	1	no information	ecotypic	No information is available for even-year pink in this JAZ

Table 9. Conservation Units for odd-year pink salmon (PKO). The table shows the application of the described method. Very little information was available for odd-year pink salmon in the northern transboundary rivers. Consequently, the CU recognized in that area is speculative and based on its MAZ ecotype. The number of sites indicated is the total in our database and is not to be interpreted as the number of sites where odd-year pink salmon are persistently found.

Odd-Year Pink Salmon Conservation Units

Conservation Unit	Acronym	Index	Number of Sites	Number of Genetic Clusters	Classification Step	Comments
Fraser River	FR	1	69	1	genetic/timing	Genetically Homogeneous, No Timing Differences
East Howe Sound-Burrard Inlet	EHOWE-BUR	2	10	1	genetic	Genetic Cluster with Specific Geography. Area Is CU in Other Species
Georgia Strait	GStr	3	64	2	genetic/timing	Genetically Homogeneous, No Timing Differences
EVI-Johnstone Strait	EVI-JStr	4	12	1	ecotypic/genetic	
Nahwitti	Nahwitti	5	21	1	ecotypic/genetic	Genetics Conforms to Provincial Eco-Section
W Vancouver Island	WVI	6	49	No Information	ecotypic	Based on MAZ
Southern Fjords	SC+SFj	7	47	1	ecotypic/genetic	Northern Boundary of SC+SFj JAZ Shifted South to Tribune Channel to Accommodate Genetic Clusters
Homathko-Klinaklini-Rivers-Smith-Bella Coola Dean	HK-RSI-BCD	8	56	4	ecotypic/genetic	Predominant Genetic Clusters in Closely Related FAZ
East Queen Charlotte Islands	EQCI	9	80	1	ecotypic/genetic	Distinctive Genetic Cluster in Specific JAZ
North Queen Charlotte Islands	NQCI	10	14	No Information	ecotypic	Speculative in Absence of Genetic Information Although No Differences in Timing Across the QC Islands
West Queen Charlotte Islands	WQCI	11	30	No Information	ecotypic	Speculative in Absence of Genetic Information Although No Differences in Timing Across the QC Islands
Hecate Strait-Lowlands	HStr-HecLow	12	165	6	ecotypic/timing	timing differences with HStr-Fj led to separate management
Hecate Strait-Fjords	HStr-Fj	13	97	10	ecotypic/timing	
Nass-Skeena Estuary	NSKEst	14	33	2	ecotypic/timing	distinctive timing within the MAZ
Lower Skeena| River	LSK	15	54	2	genetics/timing	Skeena is genetically distinct and LSK timing is distinctive
Middle & Upper Skeena River	M&USK	16	49	1	genetics/timing	see comment for LSK
Nass-Portland-Observatory	NR-PORT-OBS	17	57	3	ecotypic/genetic	no habitat model and no timing differences across the JAZ
Upper Nass	UNASS	18	4	1	ecotypic/timing	upper Nass has distinctive timing
Transboundary Fjords	TBFj	19	?	No information	ecotypic	speculative since no information available for sites in this CU. JAZ were grouped on MAZ

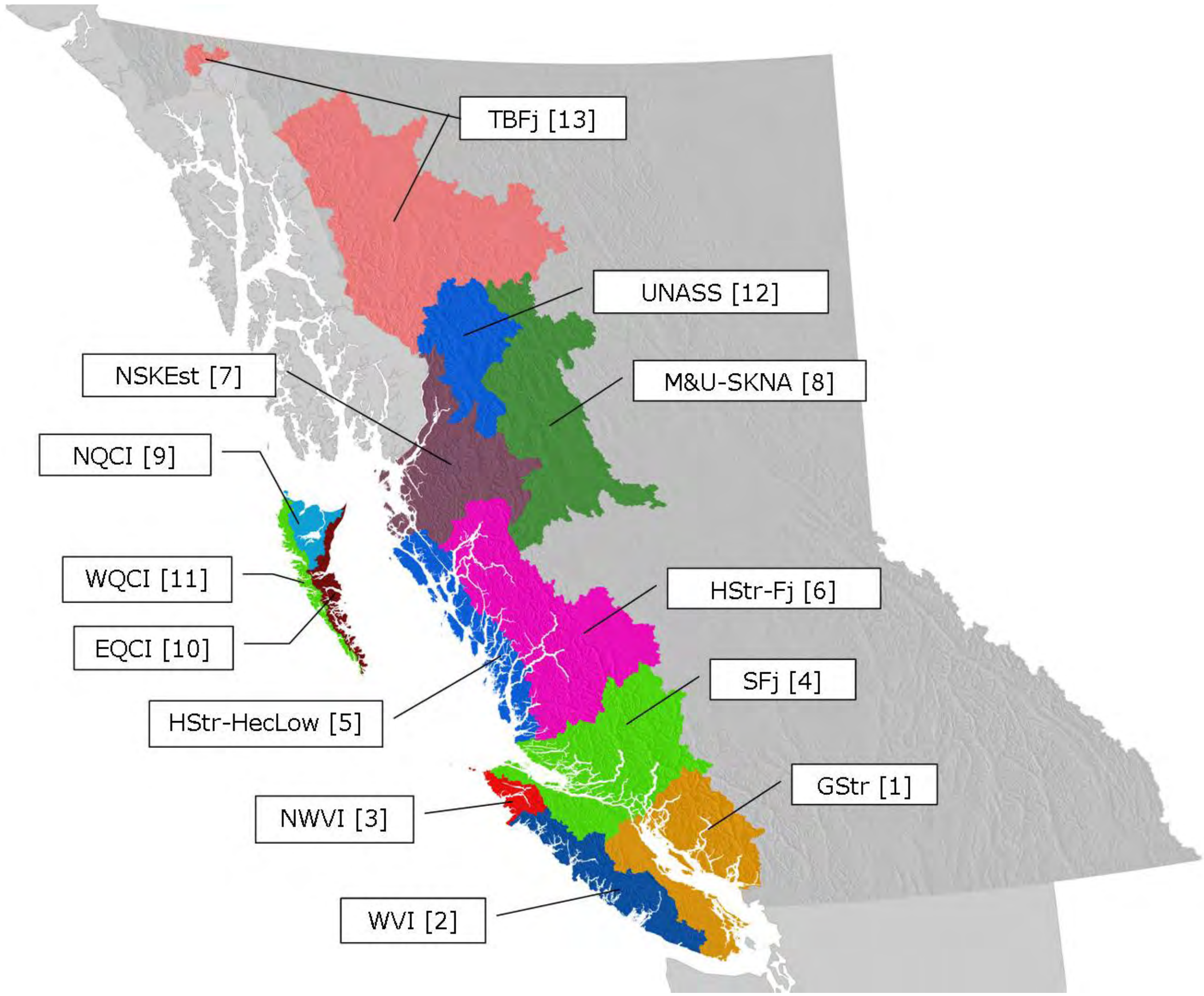


Figure 15. The 12 Conservation Units of even-year pink salmon in British Columbia.

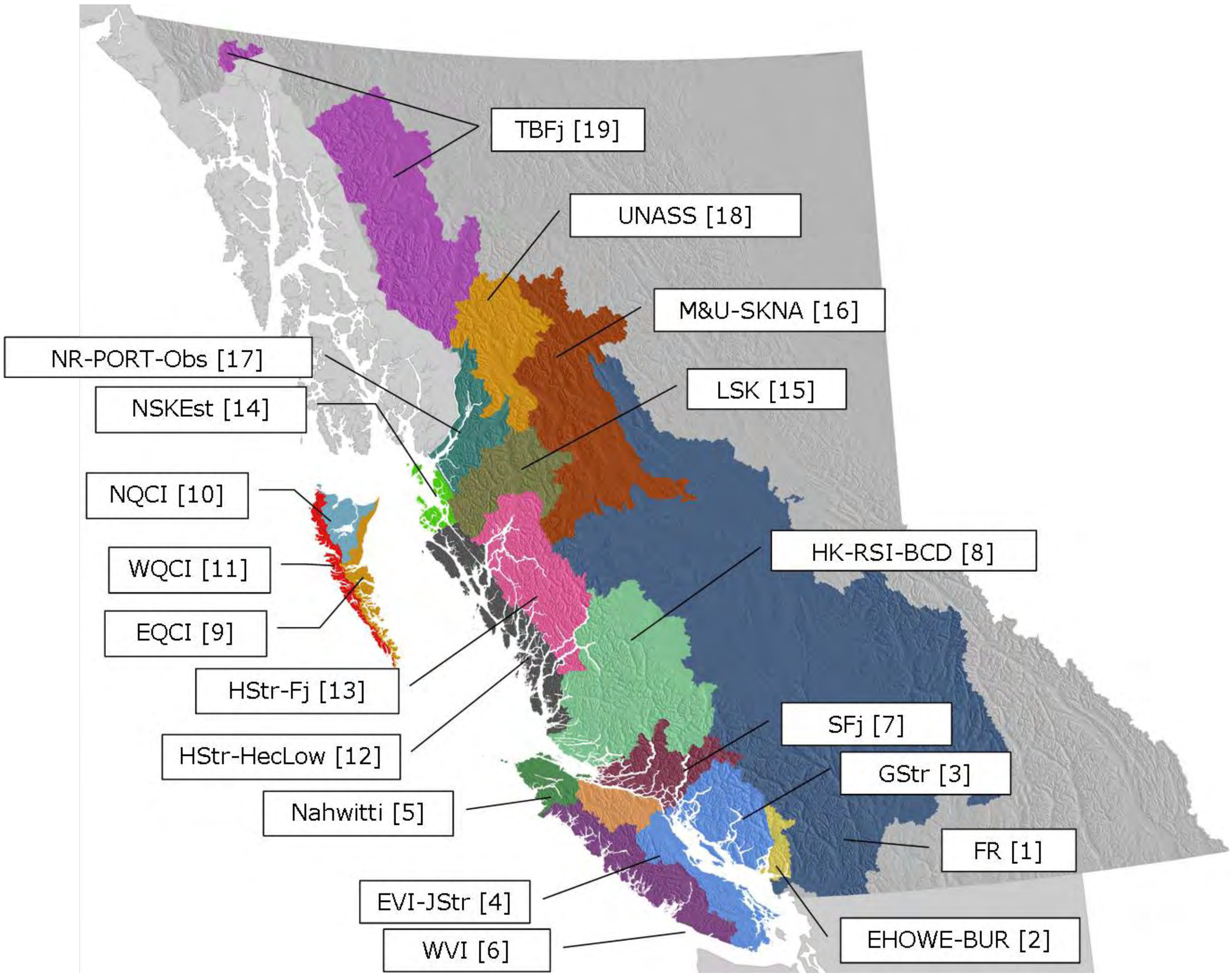


Figure 16. The 19 Conservation Units of odd-year pink salmon in British Columbia.

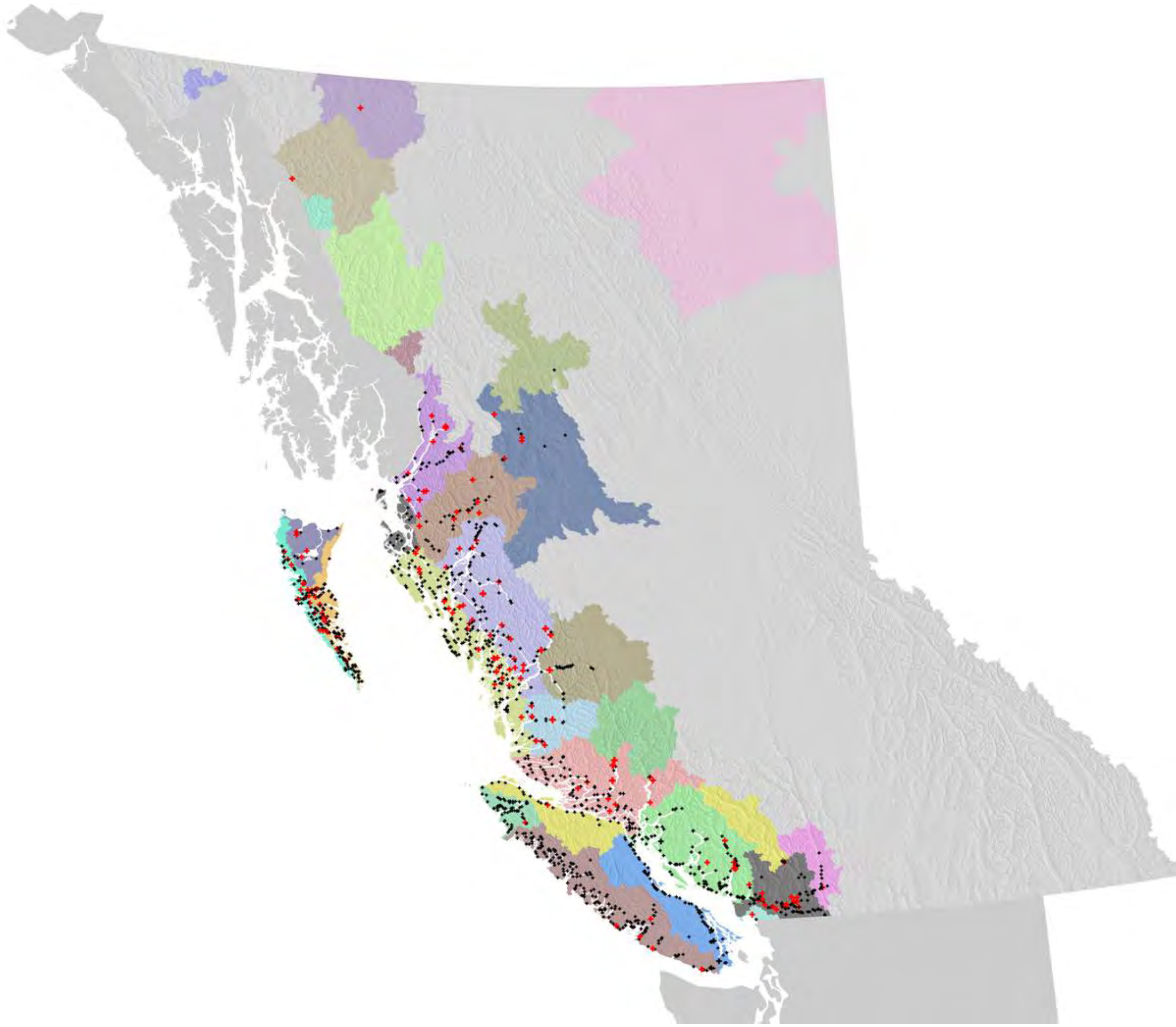


Figure 17. The map shows the locations of all sites in our database with chum salmon populations for British Columbia only (black dots). The red crosses indicate that a genetic sample was available from the site. The colored polygons are JAZ ecotypes where chum salmon either has been documented or is probably present.

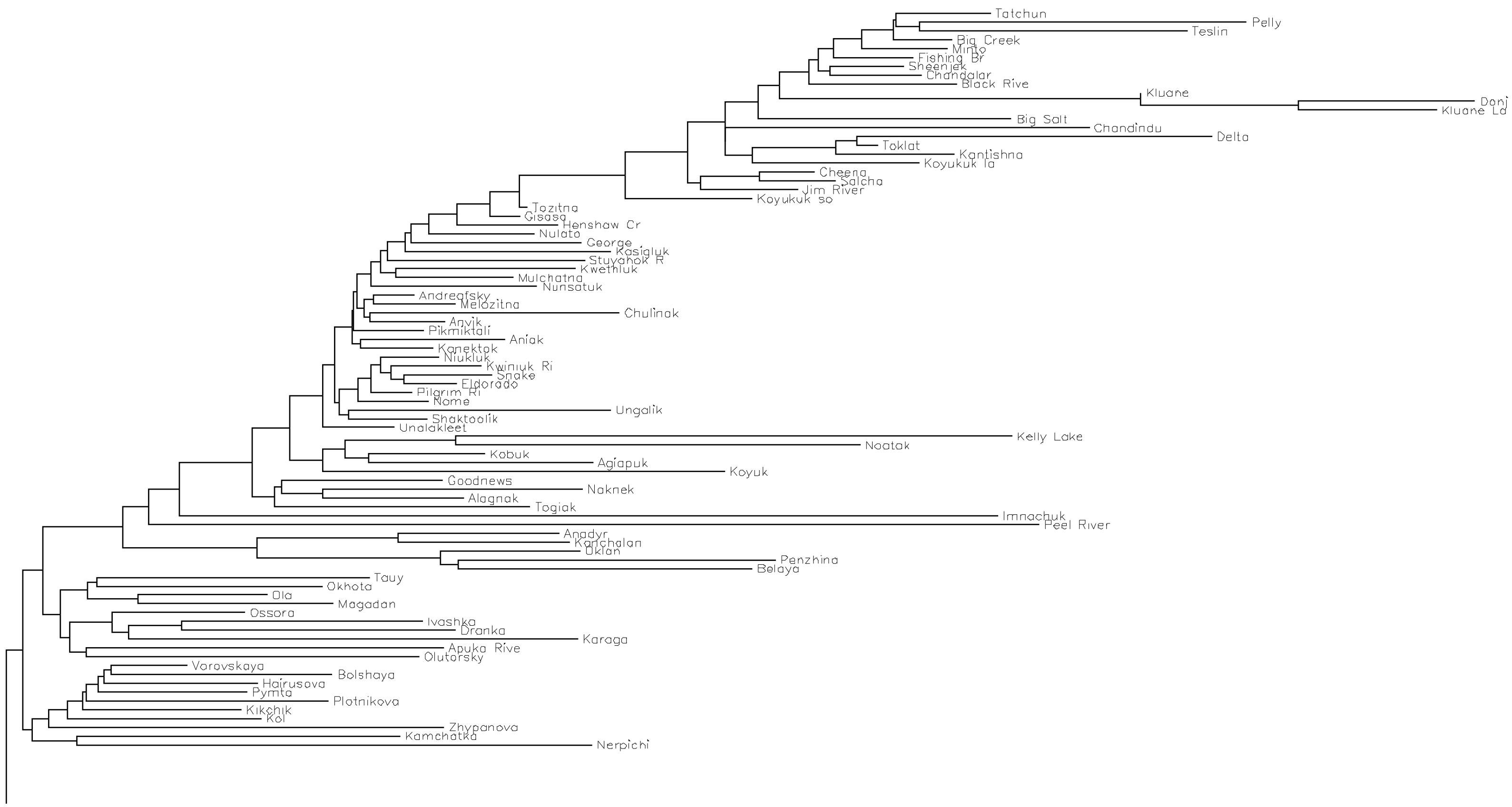
Table 10. Chum presence, relative abundance, and genetic population structure within the JAZ ecotypes of British Columbia. The number sites and number of sites present are taken from our database and do indicate the total number of sites within a JAZ that may have a persistent presence.

JAZ	JAZ Acronym	JAZ code	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic cluster
Okanagan |OR-WA Coastal	OK+ORWA	1	-	1	-	unlikely	-	-
Boundary Bay |Georgia Strait	BB+GStr	2	2	8	25%	documented	2.15-3.2	P
Lower Fraser |Georgia Strait	LFR+GStr	3	78	133	59%	documented	2.15-2 2.15-3.1 2.15-4 2.15-5	P
Lillooet |Georgia Strait	LILL+GStr	4	3	16	19%	documented	2.15-5	P
Fraser Canyon |Georgia Strait	FRCany+GStr	5	13	20	65%	documented	2.15-3.3	P
Middle Fraser |Georgia Strait	MFR+GStr	6	-	176	-	possible	-	-
Upper Fraser |Georgia Strait	UFR+GStr	7	-	45	-	possible	-	-
Lower Thompson |Georgia Strait	LTh+GStr	8	-	20	-	possible	-	-
South Thompson |Georgia Strait	STh+GStr	9	-	66	-	possible	-	-
North Thompson |Georgia Strait	NTh+GStr	10	-	47	-	possible	-	-
S Coastal Streams |Georgia Strait	SC+GStr	11	117	131	89%	documented	2.14-2.1 2.14-2.2 2.14-5 2.14-6	N
S Coastal Streams |QCStr-JStr-SFjords	SC+SFj	12	96	109	88%	documented	2.09.2-2.1 2.11-1 2.11-2 2.14-1 2.14-3 2.14-4	K,N,R
E Vancouver Island |Georgia Strait	EVI+GStr	13	65	90	72%	documented	2.14-2.2	N
E Vancouver Island |QCStr-JStr-SFjords	EVI+SFj	14	20	33	61%	documented	2.13-1	M
W Vancouver Island |	WVI+WVI	15	182	249	73%	documented	2.12-1	L,N

JAZ	JAZ Acronym	JAZ code	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic cluster
Vancouver Island Coastal Current							2.12-2 2.14-2.1	
W Vancouver Island |Outer Graham Island	WVI+WQCI	16	61	64	95%	documented	2.12-2	L
Homathko - Klinaklini Rivers | QCStr-JStr-SFjords	HK+SFj	17	3	4	75%	documented	2.09.2-2.1 2.14-4	N,R
Rivers-Smith Inlets |Hecate Strait - Q.C. Sound	RSI+HStr	18	20	30	67%	documented	2.09.1-2 2.09.1-3 2.09.2-2.1 2.09.3-2	Q,R,S
Bella Coola - Dean Rivers | Hecate Strait - Q.C. Sound	BCD+HStr	19	24	40	60%	documented	2.09.2-2.1	R
Queen Charlottes |Hecate Strait - Q.C. Sound	QCI+HStr	20	125	142	88%	documented	2.10-2 2.10-3.2	J
Queen Charlottes |Outer Graham Island	QCI+WQCI	21	75	83	90%	documented	2.10-3.1 2.10-3.2	J
Queen Charlottes |North Graham Island	QCI+NQCI	22	12	18	67%	documented	2.10-1 2.10-2	J
Hecate Lowlands |Hecate Strait - Q.C. Sound	HecLow+HStr	23	150	174	86%	documented	2.09.1-2 2.09.3-3.1 2.09.3-3.2 2.14-2.2	N,Q,S
N Coastal Streams |Hecate Strait - Q.C. Sound	NC+HStr	24	105	118	89%	documented	2.07-2 2.09.2-1.1 2.09.2-1.2 2.09.2-1.4 2.09.2-2.1 2.09.2-2.2 2.09.2-2.3 2.09.2-2.4 2.09.3-1 2.09.3-3.1 2.09.3-3.2	H,R,S
Hecate Lowlands |Nass - Skeena Estuary	HecLow+NSKEst	25	35	67	52%	documented	2.09.2-1.3 2.09.3-3.2	R,S
Lower Skeena |Nass - Skeena Estuary	LSK+NSKEst	26	33	107	31%	documented	2.05-1 2.08-2 2.08-3	E,I

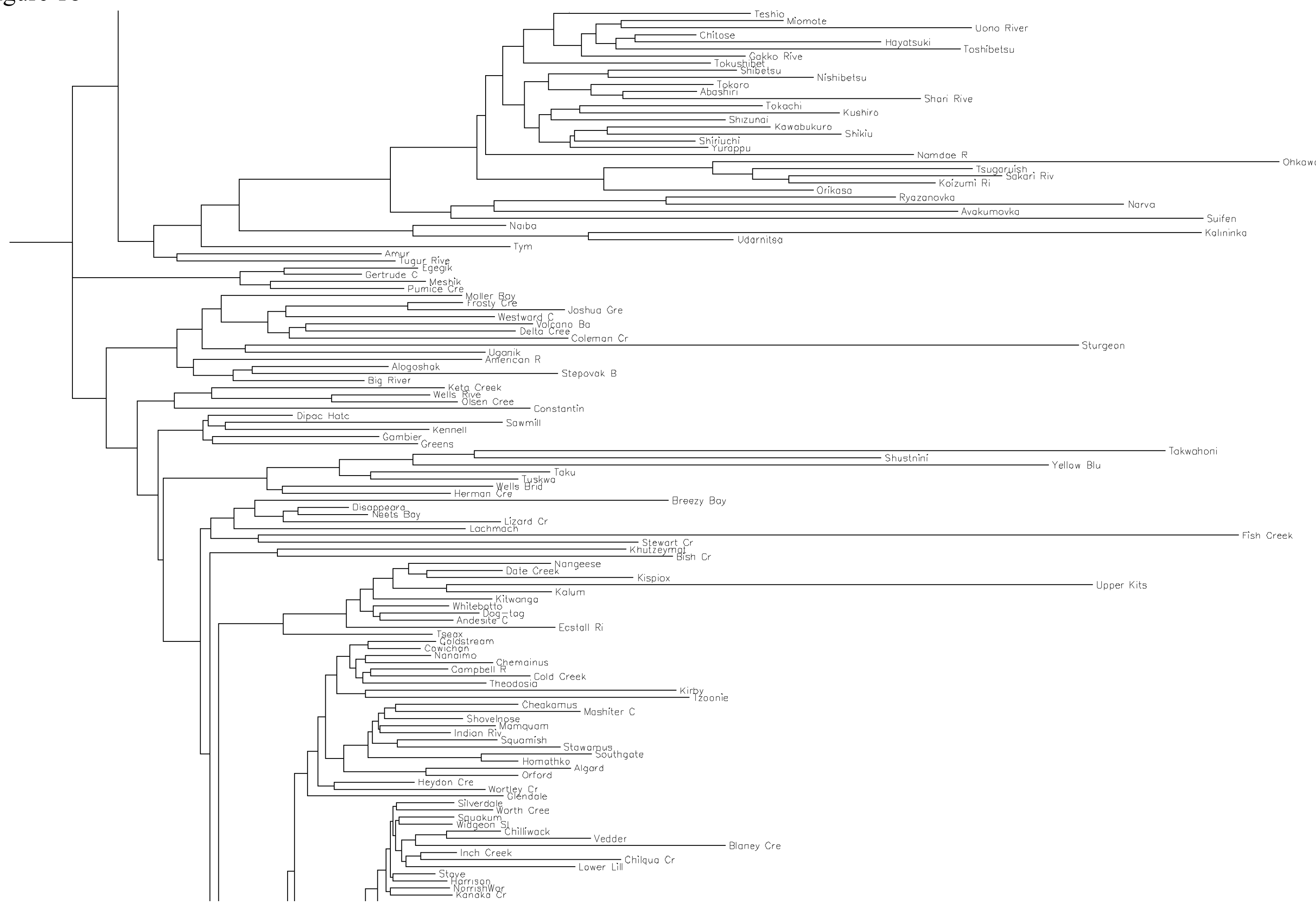
JAZ	JAZ Acronym	JAZ code	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic cluster
Middle Skeena |Nass - Skeena Estuary	MSK+NSKEst	27	9	113	8%	documented	2.08-3	I
Upper Skeena |Nass - Skeena Estuary	USK+NSKEst	28	1	19	5%	documented		
Lower Nass - Portland |Nass - Skeena Estuary	LNR-P+NSKEst	29	46	75	61%	documented	2.06.1-1 2.06.1-2 2.07-1 2.08-1 2.09.2-1.3 2.09.2-1.4	F,H,I,R
Upper Nass |Nass - Skeena Estuary	UNR+NSKEst	30	-	23	-	possible	-	-
Unuk River |Transboundary Fjords	Unuk+TBFj	31	-	2	-	probable		
Lower Stikine |Transboundary Fjords	LStk+TBFj	32	-	18	-	probable		
Whiting River |Transboundary Fjords	Whtng+TBFj	33	-	1	-	probable		
Taku |Transboundary Fjords	Taku+TBFj	34	5	19	26%	documented	2.05-2 2.05-3 2.05-4 2.05-5	E
Lynn Canal |Transboundary Fjords	LYNN+TBFj	35	-	4	-	probable		
Alsek |Alaska Coastal Downwelling	Alsek+AKCst	36	-	6	-	possible		
Teslin Headwaters |Bering Sea	TesHW+Ber	37	1	4	25%	documented	1.14-2	D
Lower Liard |Arctic Ocean	Liard+AO	38	-	1	?	probable		
Yukon River |Bering Sea	Yuk+Ber	37	-	?	?	documented	1.11-1 1.13-1 1.13-2 1.14-1 1.14-2	B,C,D
Mackenzie River |Arctic Ocean	MacR+AO	39	-	1	?	documented	1.05-1	A

Figure 18



Tatchun
Pelly
Teslin
Big Creek
Minto
Fishing Br
Sheenjek
Chandalar
Black Rive
Kluane
Donj
Kluane La
Big Salt
Chandindu
Delta
Toklat
Kantishna
Koyukuk la
Cheena
Salcha
Jim River
Koyukuk so
Tozitna
Gisasa
Henshaw Cr
Nulato
George
Kasigluk
Stuyahok R
Kwethluk
Mulchatna
Nunsatuk
Andreafsky
Melozitna
Chulinak
Anvik
Pikmiktalik
Aniak
Kanektok
Niukluk
Kwiniuk Ri
Snake
Eldorado
Pilgrim Ri
Nome
Ungalik
Shaktoolik
Unalakleet
Kelly Lake
Noatak
Kobuk
Agiapuk
Koyuk
Goodnews
Naknek
Alagnak
Togiak
Imnachuk
Peel River
Anadyr
Kanchalan
Uklan
Penzhina
Belaya
Tauy
Okhota
Ola
Magadan
Ossora
Ivashka
Dranka
Karaga
Apuka Rive
Olutorsky
Vorovskaya
Bolshaya
Hairusova
Pymta
Plotnikova
Kikchik
Kol
Zhypanova
Kamchatka
Nerpichi

Figure 18



Teshio
Miomote
Uono River
Chitose
Hayatsuki
Toshibetsu
Gakko Rive
Tokushibet
Shibetsu
Nishibetsu
Tokoro
Abashiri
Shari Rive
Tokachi
Kushiro
Shizunai
Kawabukuro
Shikiu
Shiriuchi
Yurappu
Namdae R
Ohkawa
Tsugaruish
Sakari Riv
Koizumi Ri
Orikasa
Ryazanovka
Narva
Avakumovka
Suifen
Naiba
Kalininka
Udarnitsa
Tym
Amur
Tugur Rive
Egegik
Gertrude C
Meshik
Pumice Cre
Moller Bay
Frosty Cre
Joshua Gre
Westward C
Volcano Ba
Delta Cree
Coleman Cr
Sturgeon
Uganik
American R
Alogoshak
Stepovak B
Big River
Keta Creek
Wells Rive
Olsen Cree
Constantin
Dipac Hatc
Sawmill
Kennell
Gambier
Greens
Takwahoni
Shustnini
Yellow Blu
Taku
Tuskwa
Wells Brid
Herman Cre
Breezy Bay
Disappeara
Neets Bay
Lizard Cr
Lachmach
Fish Creek
Stewart Cr
Khutzeymat
Bish Cr
Nangeese
Date Creek
Kispiox
Upper Kits
Kalum
Kitwanga
Whitebotto
Dog-tag
Andesite C
Ecstall Ri
Tseax
Goldstream
Cowichan
Nanaimo
Chemainus
Campbell R
Cold Creek
Theodosia
Kirby
Tzoonie
Cheakamus
Mashiter C
Shovelnose
Mamquam
Indian Riv
Squamish
Stawamus
Southgate
Homathko
Algard
Orford
Heydon Cre
Wortley Cr
Glendale
Silverdale
Worth Cree
Squakum
Widgeon Sl
Chilliwack
Vedder
Blaney Cre
Inch Creek
Chilqua Cr
Lower Lill
Stave
Harrison
NorrishWor
Kanaka Cr

Figure 18. Neighbor-joining dendrogram of Cavalli-Sforza and Edwards chord distance for chum salmon surveyed at 14 microsatellite loci (Beacham et. al. unpublished data).

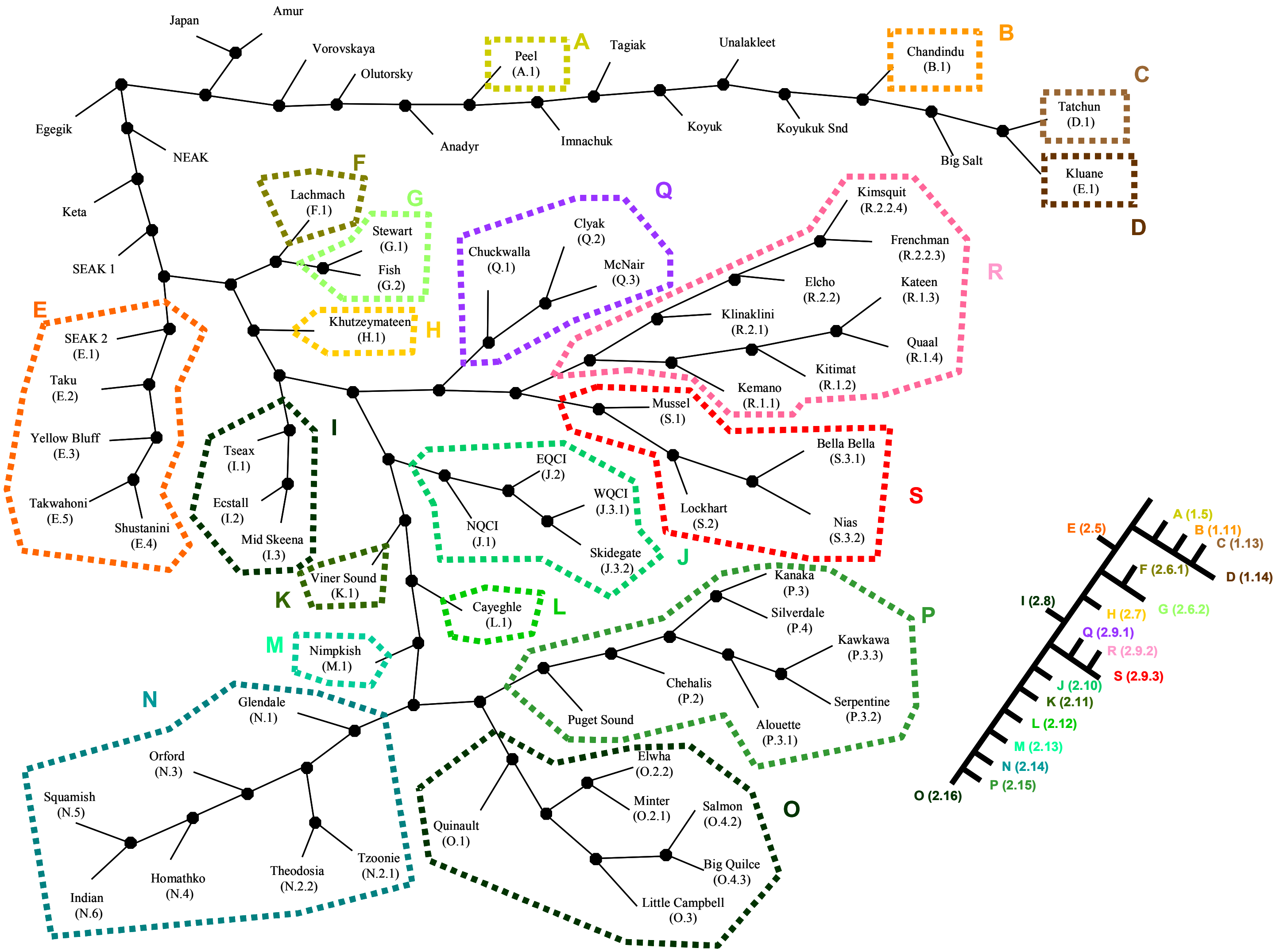


Figure 19. Two diagrammatic representations of the genetic population structure of chum salmon. The stick diagram (lower right) shows the relationships between the genetic cluster (letters and dotted lines), while the larger diagram shows structure within the clusters as indicated by the genetic classification (bracketed numbers).

Table 11. A simple genetic classification of the chum populations from Beacham et al. (unpublished data) shown in Figure 18. A five level hierarchical genetic classification was used. The genetic class and, for populations south and east of mainland Alaska, the genetic cluster of each site are shown. Ecotypic classifications for sites outside of B. C. are not definitive. The GFE_ID is the SEDS population identifier for populations in British Columbia.

site	GFE_ID	genetic cluster	genetic class	FAZ	MAZ	JAZ
Amur	Asia		1.01.1-			
Tugur River	Asia		1.01.1-			
Abashiri	Asia		1.01.2-			
Avakumovka	Asia		1.01.2-			
Chitose	Asia		1.01.2-			
Gakko River	Asia		1.01.2-			
Hayatsuki	Asia		1.01.2-			
Kalininka	Asia		1.01.2-			
Kawabukuro	Asia		1.01.2-			
Koizumi River	Asia		1.01.2-			
Kushiro	Asia		1.01.2-			
Miomote	Asia		1.01.2-			
Naiba	Asia		1.01.2-			
Namdae River	Asia		1.01.2-			
Narva	Asia		1.01.2-			
Nishibetsu	Asia		1.01.2-			
Ohkawa	Asia		1.01.2-			
Orikasa	Asia		1.01.2-			
Ryazanovka	Asia		1.01.2-			
Sakari River	Asia		1.01.2-			
Shari River	Asia		1.01.2-			
Shibetsu	Asia		1.01.2-			
Shiku	Asia		1.01.2-			
Shiriuchi	Asia		1.01.2-			
Shizunai	Asia		1.01.2-			
Suifen	Asia		1.01.2-			
Teshio	Asia		1.01.2-			
Tokachi	Asia		1.01.2-			
Tokoro	Asia		1.01.2-			
Tokushibet	Asia		1.01.2-			
Toshibetsu	Asia		1.01.2-			
Tsugaruish	Asia		1.01.2-			
Tym	Asia		1.01.2-			
Udarnitsa	Asia		1.01.2-			
Uono River	Asia		1.01.2-			
Yurappu	Asia		1.01.2-			
Bolshaya	Asia		1.02-			
Hairusova	Asia		1.02-			
Kamchatka	Asia		1.02-			
Kol	Asia		1.02-			
Nerpichi	Asia		1.02-			

site	GFE_ID	genetic cluster	genetic class	FAZ	MAZ	JAZ
Plotnikova	Asia		1.02-			
Pymta	Asia		1.02-			
Vorovskaya	Asia		1.02-			
Zhypanova	Asia		1.02-			
Kikchik	Asia		1.02-			
Apuka River	Asia		1.03-			
Karago	Asia		1.03-			
Magadan	Asia		1.03-			
Okhota	Asia		1.03-			
Ola	Asia		1.03-			
Olutorsky	Asia		1.03-			
Ossora	Asia		1.03-			
Tauy	Asia		1.03-			
Dranka	Asia		1.03-			
Ivashka	Asia		1.03-			
Anadyr	Asia		1.04-			
Belaya	Asia		1.04-			
Kanchalan	Asia		1.04-			
Oklan	Asia		1.04-			
Penzhina	Asia		1.04-			
Peel River	Yuk-Mackenzie	A	1.05-1	MacR	AO	MacR+AO
Imnachuk	AK		1.06-			
Alagnak	AK		1.07-			
Goodnews	AK		1.07-			
Naknek	AK		1.07-			
Togiak	AK		1.07-			
Agiapuk	AK		1.08-			
Kelly Lake	AK		1.08-			
Kobuk	AK		1.08-			
Koyuk	AK		1.08-			
Noatak	AK		1.08-			
Andreafsky	AK		1.09-			
Aniak	AK		1.09-			
Anvik	AK		1.09-			
Chulinak	AK		1.09-			
Eldorado	AK		1.09-			
George	AK		1.09-			
Glsasa	AK		1.09-			
Henshaw Creek	AK		1.09-			
Kanetok	AK		1.09-			
Kasigluk	AK		1.09-			
Kwethluk	AK		1.09-			
Kwiniuk	AK		1.09-			
Melozitna	AK		1.09-			
Mulchatna	AK		1.09-			
Niukluk	AK		1.09-			
Nome	AK		1.09-			
Nulato	AK		1.09-			

site	GFE_ID	genetic cluster	genetic class	FAZ	MAZ	JAZ
Nunsatuk	AK		1.09-			
Pikmiktali	AK		1.09-			
Pilgrim River	AK		1.09-			
Shaktoolik	AK		1.09-			
Snake	AK		1.09-			
Styuahok	AK		1.09-			
Tozitna	AK		1.09-			
Unalakleet	AK		1.09-			
Ungalik	AK		1.09-			
Kantishna	AK		1.10-			
Koyukuk Lake	AK		1.10-			
Koyukuk Sound	AK		1.10-			
Salcha	AK		1.10-			
Cheena	AK		1.10-			
Delta	AK		1.10-			
Jim River	AK		1.10-			
Toklat	AK		1.10-			
Chandindu	2492	B	1.11-1	Yuk	Ber	Yuk+Ber
Big Salt	AK		1.12-			
Kluane	2509	C	1.13-1	Yuk	Ber	Yuk+Ber
Kluane Lake	2504	C	1.13-2	Yuk	Ber	Yuk+Ber
Donjek	2505	C	1.13-2	Yuk	Ber	Yuk+Ber
Sheenlek	AK		1.14-			
Black River	AK		1.14-			
Chandalar	AK		1.14-			
Fishing Branch	2522	D	1.14-1	Yuk	Ber	Yuk+Ber
Minto	2554	D	1.14-1	Yuk	Ber	Yuk+Ber
Big Creek	AK		1.14-1			
Tatchun	2493	D	1.14-2	Yuk	Ber	Yuk+Ber
Teslin	2499	D	1.14-2	TesHW	Ber	TesHW+Ber
Pelly	2510	D	1.14-2	Yuk	Ber	Yuk+Ber
Egegik	AK		2.01-			
Gertrude Creek	AK		2.01-			
Meshik	AK		2.01-			
Pumice Creek	AK		2.01-			
Alogoshak	AK		2.02-			
American River	AK		2.02-			
Big River	AK		2.02-			
Delta Creek	AK		2.02-			
Frosty Creek	AK		2.02-			
Joshua Creek	AK		2.02-			
Sturgeon	AK		2.02-			
Uganik	AK		2.02-			
Volcano Bay	AK		2.02-			
Westward Creek	AK		2.02-			
Moller Bay	AK		2.02-			
Coleman Creek	AK		2.02-			
Stepovak Bay	AK		2.02-			

site	GFE_ID	genetic cluster	genetic class	FAZ	MAZ	JAZ
Constantine	AK		2.03-			
Keta Creek	AK		2.03-			
Olsen Creek	AK		2.03-			
Wells River	AK		2.03-			
Greens	AK		2.04-			
Kennell	AK		2.04-			
Dipac Hatchery	AK		2.04-			
Gambier	AK		2.04-			
Sawmill	AK		2.04-			
Wells Bridge	AK	E	2.05-1			
Breezy Bay	AK	E	2.05-1			
Disappearance	AK	E	2.05-1			
Neets Bay	AK	E	2.05-1			
Herman Creek	508	E	2.05-1	LSK	NSKEst	LSK+NSKEst
Tuskwa	2180	E	2.05-2	Taku	TBFj	Taku+TBFj
Taku	2203	E	2.05-2	Taku	TBFj	Taku+TBFj
Yellow Bluff	220303	E	2.05-3	Taku	TBFj	Taku+TBFj
Shustnini	220302	E	2.05-4	Taku	TBFj	Taku+TBFj
Takwahoni	220301	E	2.05-5	Taku	TBFj	Taku+TBFj
Lachmach	1748	F	2.06.1-1	LNR-P	NSKEst	LNR-P+NSKEst
Lizard Creek	1769	F	2.06.1-2	LNR-P	NSKEst	LNR-P+NSKEst
Stewart Creek	AK	G	2.06.2-1			
Fish Creek	AK	G	2.06.2-2			
Khutzeymateen	1754	H	2.07-1	LNR-P	NSKEst	LNR-P+NSKEst
Bish Creek	1080	H	2.07-2	NC	HStr	NC+HStr
Tseax	651	I	2.08-1	LNR-P	NSKEst	LNR-P+NSKEst
Ecstall River	447	I	2.08-2	LSK	NSKEst	LSK+NSKEst
Dog Tag	463	I	2.08-3	LSK	NSKEst	LSK+NSKEst
Andesite	468	I	2.08-3	LSK	NSKEst	LSK+NSKEst
Kitwanga	488	I	2.08-3	MSK	NSKEst	MSK+NSKEst
Upper Kitsumkalum River	520	I	2.08-3	LSK	NSKEst	LSK+NSKEst
Kitsumkalum River	521	I	2.08-3	LSK	NSKEst	LSK+NSKEst
Kispiox	566	I	2.08-3	MSK	NSKEst	MSK+NSKEst
Date Creek	567	I	2.08-3	MSK	NSKEst	MSK+NSKEst
Nangeese	581	I	2.08-3	MSK	NSKEst	MSK+NSKEst
Whitebotom	2737	I	2.08-3	LSK	NSKEst	LSK+NSKEst
Chuckwalla	948	Q	2.09.1-2	RSI	HStr	RSI+HStr
MacNair Creek	953	Q	2.09.1-2	HecLow	HStr	HecLow+HStr
Clyak	949	Q	2.09.1-3	RSI	HStr	RSI+HStr
Carroll	SEAK	R	2.09.2-			
Kemano	1034	R	2.09.2-1.1	NC	HStr	NC+HStr
Kitimat River	1050	R	2.09.2-1.2	NC	HStr	NC+HStr
Gilttoyees	1082	R	2.09.2-1.2	NC	HStr	NC+HStr
Kumealon	1097	R	2.09.2-1.3	HecLow	NSKEst	HecLow+NSKEst
Toon	1750	R	2.09.2-1.3	LNR-P	NSKEst	LNR-P+NSKEst
Ensheshese	1751	R	2.09.2-1.3	LNR-P	NSKEst	LNR-P+NSKEst
Kateen	1754	R	2.09.2-1.3	LNR-P	NSKEst	LNR-P+NSKEst
Neets Bay	AK	R	2.09.2-1.3			

site	GFE_ID	genetic cluster	genetic class	FAZ	MAZ	JAZ
Quaal River	1086	R	2.09.2-1.4	NC	HStr	NC+HStr
Stagoo	1758	R	2.09.2-1.4	LNR-P	NSKEst	LNR-P+NSKEst
Illiance	1760	R	2.09.2-1.4	LNR-P	NSKEst	LNR-P+NSKEst
Wilauks Creek	1761	R	2.09.2-1.4	LNR-P	NSKEst	LNR-P+NSKEst
Kitsault River	1762	R	2.09.2-1.4	LNR-P	NSKEst	LNR-P+NSKEst
Kshwan	1764	R	2.09.2-1.4	LNR-P	NSKEst	LNR-P+NSKEst
Dak	2236	R	2.09.2-1.4	LNR-P	NSKEst	LNR-P+NSKEst
Klinaklini	850	R	2.09.2-2.1	HK	SFj	HK+SFj
Ahnuhati	852	R	2.09.2-2.1	SC	SFj	SC+SFj
Ashlum	939	R	2.09.2-2.1	RSI	HStr	RSI+HStr
Nooseseck	973	R	2.09.2-2.1	BCD	HStr	BCD+HStr
Dean River	975	R	2.09.2-2.1	BCD	HStr	BCD+HStr
Kimsquit	977	R	2.09.2-2.1	NC	HStr	NC+HStr
Skowquiltz	978	R	2.09.2-2.1	NC	HStr	NC+HStr
Kiltuish	1030	R	2.09.2-2.1	NC	HStr	NC+HStr
Elcho Creek	984	R	2.09.2-2.2	NC	HStr	NC+HStr
Jenny Bay	1798	R	2.09.2-2.2	NC	HStr	NC+HStr
Frenchman	985	R	2.09.2-2.3	NC	HStr	NC+HStr
Kimsquit B	977	R	2.09.2-2.4	NC	HStr	NC+HStr
Lard	1009	S	2.09.3-1	NC	HStr	NC+HStr
Kainet Creek	1010	S	2.09.3-1	NC	HStr	NC+HStr
Mussel River	1015	S	2.09.3-1	NC	HStr	NC+HStr
Walkum	917	S	2.09.3-2	RSI	HStr	RSI+HStr
Nekite	918	S	2.09.3-2	RSI	HStr	RSI+HStr
Draney	928	S	2.09.3-2	RSI	HStr	RSI+HStr
Lockhart-Gordon	929	S	2.09.3-2	RSI	HStr	RSI+HStr
Martin	986	S	2.09.3-3.1	NC	HStr	NC+HStr
Clatse Creek	989	S	2.09.3-3.1	HecLow	HStr	HecLow+HStr
Roscoe Creek	991	S	2.09.3-3.1	NC	HStr	NC+HStr
Bullock Channel	995	S	2.09.3-3.1	HecLow	HStr	HecLow+HStr
Cheenis Lagoon	998	S	2.09.3-3.1	HecLow	HStr	HecLow+HStr
Neekas Creek	999	S	2.09.3-3.1	HecLow	HStr	HecLow+HStr
Bella Bella	1796	S	2.09.3-3.1	HecLow	HStr	HecLow+HStr
Hooknose	1796	S	2.09.3-3.1	HecLow	HStr	HecLow+HStr
Deer Pass	1806	S	2.09.3-3.1	HecLow	HStr	HecLow+HStr
McLoughlin	1809	S	2.09.3-3.1	HecLow	HStr	HecLow+HStr
Kwakusdis	1813	S	2.09.3-3.1	HecLow	HStr	HecLow+HStr
Cooper Inlet	300100	S	2.09.3-3.1	HecLow	HStr	HecLow+HStr
Salmon Bay	1007	S	2.09.3-3.2	HecLow	HStr	HecLow+HStr
Kitasu	1820	S	2.09.3-3.2	HecLow	HStr	HecLow+HStr
Duthie Creek	1836	S	2.09.3-3.2	NC	HStr	NC+HStr
Arnoup Creek	1850	S	2.09.3-3.2	NC	HStr	NC+HStr
Nias Creek	1852	S	2.09.3-3.2	NC	HStr	NC+HStr
Tyler	1854	S	2.09.3-3.2	HecLow	HStr	HecLow+HStr
Barnard	1869	S	2.09.3-3.2	HecLow	HStr	HecLow+HStr
West Arm Creek	1870	S	2.09.3-3.2	NC	HStr	NC+HStr
East Arm Creek	1871	S	2.09.3-3.2	NC	HStr	NC+HStr
Gil Creek	1897	S	2.09.3-3.2	HecLow	HStr	HecLow+HStr

site	GFE_ID	genetic cluster	genetic class	FAZ	MAZ	JAZ
Blackrock	1900	S	2.09.3-3.2	HecLow	HStr	HecLow+HStr
Turn Creek	1901	S	2.09.3-3.2	HecLow	HStr	HecLow+HStr
Pa-aat River	1914	S	2.09.3-3.2	HecLow	NSKEst	HecLow+NSKEst
Wilson Creek	1927	S	2.09.3-3.2	HecLow	NSKEst	HecLow+NSKEst
Markle Inlet	1928	S	2.09.3-3.2	HecLow	NSKEst	HecLow+NSKEst
Naden	1559	J	2.10-1	QCI	NQCI	QCI+NQCI
Ain	1563	J	2.10-1	QCI	NQCI	QCI+NQCI
Awun	1567	J	2.10-1	QCI	NQCI	QCI+NQCI
Stanley	1557	J	2.10-2	QCI	NQCI	QCI+NQCI
Pallant	1584	J	2.10-2	QCI	HStr	QCI+HStr
Lagoon Inlet	1588	J	2.10-2	QCI	HStr	QCI+HStr
Thorsen	1595	J	2.10-2	QCI	HStr	QCI+HStr
Little Goose	1596	J	2.10-2	QCI	HStr	QCI+HStr
Pacofi	1598	J	2.10-2	QCI	HStr	QCI+HStr
Salmon River	1605	J	2.10-2	QCI	HStr	QCI+HStr
Hutton Head	1609	J	2.10-2	QCI	HStr	QCI+HStr
Bag Hargour	1624	J	2.10-2	QCI	HStr	QCI+HStr
Sedgewick	1713	J	2.10-2	QCI	HStr	QCI+HStr
Dawson Inlet	1527	J	2.10-3.1	QCI	WQCI	QCI+WQCI
Clapp Basin	1534	J	2.10-3.1	QCI	WQCI	QCI+WQCI
Mountain Creek	1536	J	2.10-3.1	QCI	WQCI	QCI+WQCI
Seal Inlet	1545	J	2.10-3.1	QCI	WQCI	QCI+WQCI
Mace Creek	1550	J	2.10-3.1	QCI	WQCI	QCI+WQCI
Steel Creek	1553	J	2.10-3.1	QCI	WQCI	QCI+WQCI
Fairfax Inlet	1650	J	2.10-3.1	QCI	WQCI	QCI+WQCI
Botany Creek	1652	J	2.10-3.1	QCI	WQCI	QCI+WQCI
Gold Harbour	1663	J	2.10-3.1	QCI	WQCI	QCI+WQCI
Security	1670	J	2.10-3.1	QCI	WQCI	QCI+WQCI
Honna	1511	J	2.10-3.2	QCI	HStr	QCI+HStr
Tarundl Creek	1512	J	2.10-3.2	QCI	HStr	QCI+HStr
Slatechuck	1514	J	2.10-3.2	QCI	HStr	QCI+HStr
Lagins	1517	J	2.10-3.2	QCI	HStr	QCI+HStr
North Arm	1523	J	2.10-3.2	QCI	WQCI	QCI+WQCI
Buck Channel	1676	J	2.10-3.2	QCI	WQCI	QCI+WQCI
Government	1678	J	2.10-3.2	QCI	WQCI	QCI+WQCI
Deena	1683	J	2.10-3.2	QCI	HStr	QCI+HStr
Viner Sound	868	K	2.11-1	SC	SFj	SC+SFj
Ahta	861	K	2.11-2	SC	SFj	SC+SFj
Smith Creek	1298	L	2.12-1	WVI	WVI	WVI+WVI
Nitinat	1242	L	2.12-2	WVI	WVI	WVI+WVI
Sugsaw	1250	L	2.12-2	WVI	WVI	WVI+WVI
Nahmint	1270	L	2.12-2	WVI	WVI	WVI+WVI
Cayeghle	1450	L	2.12-2	WVI	WQCI	WVI+WQCI
Nimpkish	1112	M	2.13-1	EVI	SFj	EVI+SFj
Heydon Creek	831	N	2.14-1	SC	SFj	SC+SFj
Wortley Creek	832	N	2.14-1	SC	SFj	SC+SFj
Glendale	847	N	2.14-1	SC	SFj	SC+SFj
Tzoonie	776	N	2.14-2.1	SC	GStr	SC+GStr

site	GFE_ID	genetic cluster	genetic class	FAZ	MAZ	JAZ
Kirby	1227	N	2.14-2.1	WVI	WVI	WVI+WVI
Theodosia	800	N	2.14-2.2	SC	GStr	SC+GStr
Cold Creek	958	N	2.14-2.2	HecLow	HStr	HecLow+HStr
Campbell River	1141	N	2.14-2.2	EVI	GStr	EVI+GStr
Nanaimo	1194	N	2.14-2.2	EVI	GStr	EVI+GStr
Chemainus	1204	N	2.14-2.2	EVI	GStr	EVI+GStr
Cowichan	1208	N	2.14-2.2	EVI	GStr	EVI+GStr
Goldstream	1211	N	2.14-2.2	EVI	GStr	EVI+GStr
Algard	816	N	2.14-3	SC	SFj	SC+SFj
Orford	816	N	2.14-3	SC	SFj	SC+SFj
Southgate	817	N	2.14-4	SC	SFj	SC+SFj
Homathko	819	N	2.14-4	HK	SFj	HK+SFj
Stawamus	705	N	2.14-5	SC	GStr	SC+GStr
Squamish	708	N	2.14-5	SC	GStr	SC+GStr
Indian River	688	N	2.14-6	SC	GStr	SC+GStr
Mamquam	709	N	2.14-6	SC	GStr	SC+GStr
Mashiter	714	N	2.14-6	SC	GStr	SC+GStr
Cheakamus	719	N	2.14-6	SC	GStr	SC+GStr
Shovelnose	737	N	2.14-6	SC	GStr	SC+GStr
Grant Creek	WA	P	2.15-1			
Siberia Creek	WA	P	2.15-1			
County Line	WA	P	2.15-1			
Nooksack	WA	P	2.15-1			
Skagit	WA	P	2.15-1			
Chehalis	181	P	2.15-2	LFR	GStr	LFR+GStr
Alouette N	14	P	2.15-3.1	LFR	GStr	LFR+GStr
Serpentine	681	P	2.15-3.2	BB	GStr	BB+GStr
Kawkawa	114	P	2.15-3.3	FRCany	GStr	FRCany+GStr
Kanaka	27	P	2.15-4	LFR	GStr	LFR+GStr
Stave	34	P	2.15-4	LFR	GStr	LFR+GStr
Norrish	51	P	2.15-4	LFR	GStr	LFR+GStr
Harrison	179	P	2.15-4	LFR	GStr	LFR+GStr
Blaney Creek	16	P	2.15-5	LFR	GStr	LFR+GStr
Widgeon	21	P	2.15-5	LFR	GStr	LFR+GStr
Silverdale	36	P	2.15-5	LFR	GStr	LFR+GStr
Chilqua	43	P	2.15-5	LFR	GStr	LFR+GStr
Inch Creek	52	P	2.15-5	LFR	GStr	LFR+GStr
Worth Creek	53	P	2.15-5	LFR	GStr	LFR+GStr
Chilliwack	62	P	2.15-5	LFR	GStr	LFR+GStr
Vedder	62	P	2.15-5	LFR	GStr	LFR+GStr
Lower Lillooet	177	P	2.15-5	LILL	GStr	LILL+GStr
Squawkum	180	P	2.15-5	LFR	GStr	LFR+GStr
Bitter Creek	WA	O	2.16-1			
Ellsworth	WA	O	2.16-1			
Quinault	WA	O	2.16-1			
Satsop	WA	O	2.16-1			
Kennedy Creek	WA	O	2.16-2.1			
Minter Creek	WA	O	2.16-2.1			

site	GFE_ID	genetic cluster	genetic class	FAZ	MAZ	JAZ
Elwha	WA	O	2.16-2.2			
Hoodsport	WA	O	2.16-2.2			
Tulalip	WA	O	2.16-2.2			
Little Campbell	WA	O	2.16-3			
Big Quilce	WA	O	2.16-4.1			
Salmon Creek	WA	O	2.16-4.2			

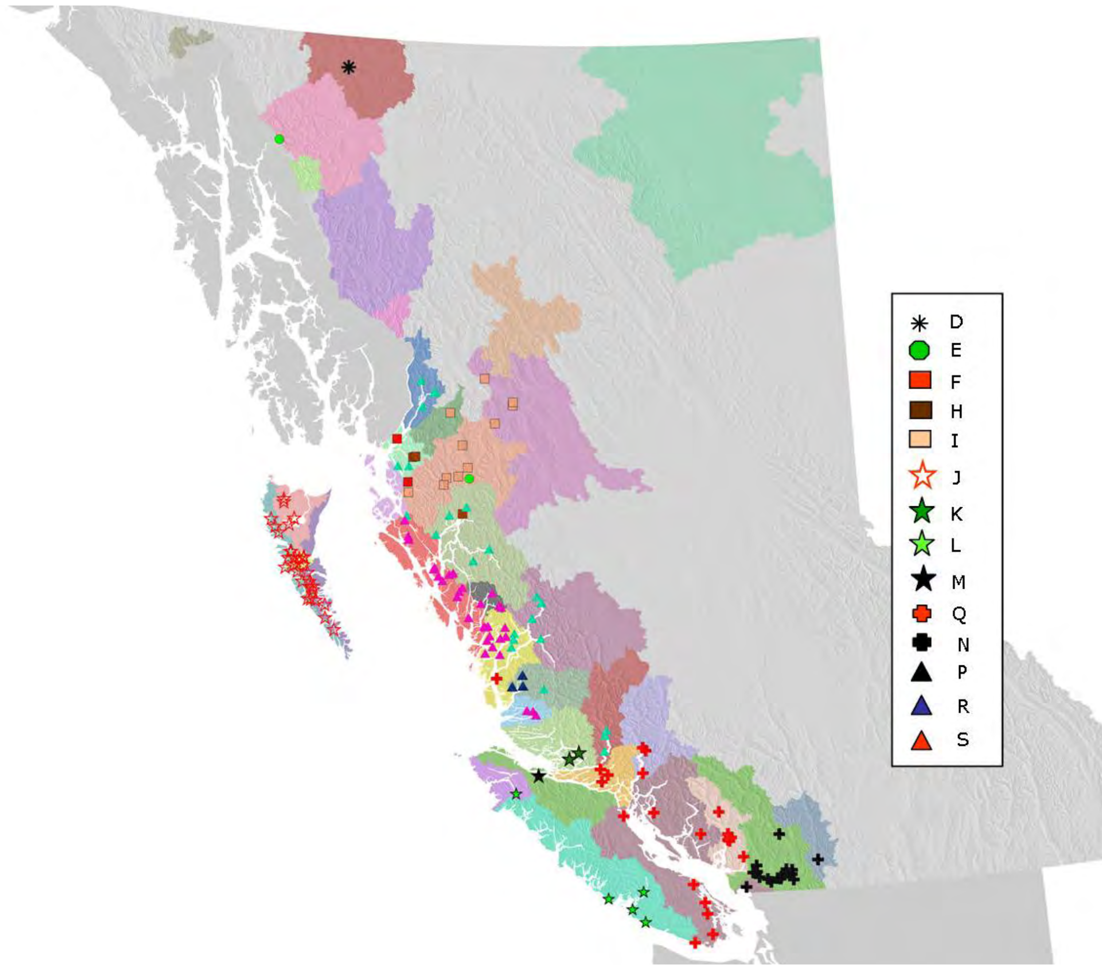


Figure 20. The genetic cluster of each sampled population of chum salmon is shown here superimposed on a map of the JAZ ecotypes in British Columbia. The associations of the clusters are shown by the symbol shapes.

Table 12. The initial ecotypic X genetic crosswalk for chum salmon. The crosswalk indicates that some ecotypic zones, notably on the mainland side of Hecate Strait and in the lower Nass-Portland Sound areas, are genetically diverse, while other genetic groups (e.g. 2.09.2-2.1) are wide distributed geographically. Sites with a genetic class but no genetic cluster are not in Canada.

<u>Northern British Columbia</u>

genetic classification		Joint Adaptive Zone (JAZ)										
cluster	class	NC+ HStr	HecLow+ NSKEst	LSK+ NSKEst	MSK+ NSKEst	LNR-P+ NSKEst	Taku+ TBFj	TesHW+ Ber	Yuk+ Ber	MacR+ AO	foreign	row total
	1.01.1-										2	2
	1.01.2-										34	34
	1.02-										10	10
	1.03-										10	10
	1.04-										5	5
A	1.05-1									1		1
	1.06-										1	1
	1.07-										4	4
	1.08-										5	5
	1.09-										26	26
	1.10-										8	8
B	1.11-1								1			1
	1.12-										1	1
C	1.13-1								1			1
	1.13-2								2			2
D	1.14-										3	3
	1.14-1								2		1	3
	1.14-2							1	2			3
	2.01-										4	4
	2.02-										13	13
	2.03-										4	4
	2.04-										5	5
E	2.05-1			1							4	5
	2.05-2						2					2
	2.05-3						1					1
	2.05-4						1					1
	2.05-5						1					1

genetic classification		Joint Adaptive Zone (JAZ)										
cluster	class	NC+ HStr	HecLow+ NSKEst	LSK+ NSKEst	MSK+ NSKEst	LNR-P+ NSKEst	Taku+ TBFj	TesHW+ Ber	Yuk+ Ber	MacR+ AO	foreign	row total
F	2.06.1-1					1						1
	2.06.1-2					1						1
G	2.06.2-1										1	1
	2.06.2-2										1	1
H	2.07-1					1						1
	2.07-2	1										1

Central Coast, Vancouver Island, Strait of Georgia

genetic classification		JAZ																	
cluster	class	SC+ GStr	SC+ SFj	EVI+ GStr	EVI+ SFj	WVI+ WVI	WVI+ WQCI	HK+ SFj	RSI+ HStr	BCD+ HStr	QCI+ HStr	QCI+ WQCI	QCI+ NQCI	HecLow + HStr	NC+ HStr	HecLow + NSKEst	LSK+ NSKEst	MSK+ NSKEst	LNR-P+ NSKEst	row total
I	2.08-1																		1	1
	2.08-2																1			1
	2.08-3																5	4		9
Q	2.09.1-2								1					1						2
	2.09.1-3								1											1
R	2.09.2-																			1
	2.09.2-1.1														1					1
	2.09.2-1.2														2					2
	2.09.2-1.3															1			3	5
	2.09.2-1.4														1				6	7
	2.09.2-2.1		1					1	1	2					3					8
	2.09.2-2.2														2					2
	2.09.2-2.3														1					1
	2.09.2-2.4														1					1
S	2.09.3-1														3					3
	2.09.3-2								4											4
	2.09.3-3.1													10	2					12
	2.09.3-3.2													7	5	3				15
J	2.10-1												3							3
	2.10-2										9		1							10
	2.10-3.1											10								10
	2.10-3.2										5	3								8

genetic classification		JAZ																		
cluster	class	SC+ GStr	SC+ SFj	EVI+ GStr	EVI+ SFj	WVI+ WVI	WVI+ WQCI	HK+ SFj	RSI+ HStr	BCD+ HStr	QCI+ HStr	QCI+ WQCI	QCI+ NQCI	HecLow + HStr	NC+ HStr	HecLow + NSKEst	LSK+ NSKEst	MSK+ NSKEst	LNR-P+ NSKEst	row total
K	2.11-1		1																	1
	2.11-2		1																	1
L	2.12-1					1														1
	2.12-2					3	1													4
M	2.13-1				1															1
N	2.14-1		3																	3
	2.14-2.1	1				1														2
	2.14-2.2	1		5										1						7
	2.14-3		2																	2
	2.14-4		1					1												2
	2.14-5	2																		2
	2.14-6	5																		5

Fraser River

genetic classification		JAZ					
cluster	class	BB+ GStr	LFR+ GStr	LILL+ GStr	FRCany+ GStr	foreign	row total
P	2.15-1					5	5
	2.15-2		1				1
	2.15-3.1		1				1
	2.15-3.2	1					1
	2.15-3.3				1		1
	2.15-4		4				4
	2.15-5		9	1			10
O	2.16-1					4	4
	2.16-2.1					2	2
	2.16-2.2					3	3
	2.16-3					1	1
	2.16-4.1					1	1
	2.16-4.2					1	1
	column total	1	15	1	1	161	335

Table 13. The crosswalk of the genetic classification with the provisional CUs created in step 2 for chum salmon. The same color coding has been used to facilitate comparison with Table 12. Considerable genetic diversity remains in the north and central coasts and in the Portland Sound and lower Nass River. Genetic classes (rows) having only non-Canadian sites were not included in this table but the excluded sites are included in the row and column totals.

cluster	genetic class	NC+ HStr	LSK+ NSKEst	MSK+ NSKEst	LNR-P+ NSKEst	PCOb+ NSKEst	Taku+ TBFj	TesHW+ Ber	Yuk+ Ber	Mac+ AO	row total
A	1.05-1									1	1
B	1.11-1								1		1
C	1.13-1								1		1
	1.13-2								2		2
D	1.14-										3
	1.14-1								2		3
	1.14-2							1	2		3
E	2.05-1		1								5
	2.05-2						2				2
	2.05-3						1				1
	2.05-4						1				1
	2.05-5						1				1
F	2.06.1-1				1						1
	2.06.1-2				1						1
H	2.07-1				1						1
	2.07-2	1									1
I	2.08-1				1						1
	2.08-2		1								1
	2.08-3		5	4							9

cluster	genetic class	UKNIGHT+ SFj	SI+ HStr	RI+ HStr	BCD+ HStr	HecLow+ HStr	NC+ HStr	QCI+ HStr	SKID	QCI+ WQCI	QCI+ NQCI	LNR-P+ NSKEst	PCOb+ NSKEst	row total
Q	2.09.1-2			2										2
	2.09.1-3			1										1
R	2.09.2-1.1						1							1
	2.09.2-1.2						2							2
	2.09.2-1.3					1						3		5
	2.09.2-1.4						1						6	7
	2.09.2-2.1	2		1	4		1							8
	2.09.2-2.2						2							2
	2.09.2-2.3						1							1
	2.09.2-2.4				1									1
S	2.09.3-1						3							3
	2.09.3-2		4											4
	2.09.3-3.1						12							12
	2.09.3-3.2					15								15
J	2.10-1										3			3
	2.10-2							9			1			10
	2.10-3.1									10				10
	2.10-3.2								8					8

cluster	genetic class	BB+ GStr	FRCany+ GStr	LFR+ GStr	LILL+ GStr	HOWE+ GStr	GStr+ GStr	EVI+ SFj	LOUGH+ SFj	BUTE+ SFj	SC+ SFj	WVI+ WVI	WVI+ WQCI	NC+ HStr	row total
K	2.11-1										1				1
	2.11-2										1				1
L	2.12-1											1			1
	2.12-2											3	1		4

cluster	genetic class	BB+ GStr	FRCany+ GStr	LFR+ GStr	LILL+ GStr	HOWE+ GStr	GStr+ GStr	EVI+ SFj	LOUGH+ SFj	BUTE+ SFj	SC+ SFj				
M	2.13-1							1							1
N	2.14-1								3						3
	2.14-2.1						2								2
	2.14-2.2						6							1	7
	2.14-3									2					2
	2.14-4									2					2
	2.14-5					2									2
	2.14-6					5									5
P	2.15-2			1											1
	2.15-3.1			1											1
	2.15-3.2	1													1
	2.15-3.3		1												1
	2.15-4			4											4
	2.15-5			9	1										10
	column total	1	1	15	1	7	8	1	3	4	2	4	1	25	335

Table 14. Statistical summaries of the mean DOY of peak spawning for British Columbian chum populations. The populations were grouped by the JAZ after adjustments made for genetic population structure (step 2). 'N' is the number of populations within each JAZ. The range is the number of days between the latest and earliest spawning populations. The standardized seasonal classification of dates can be found in Appendix 6.

		Population mean DOY and season of peak spawning						
		minimum		mean		maximum		Range
JAZ	N	DOY	season	DOY	season	DOY	season	(days)
BB+GStr	1			323.6	LFALL			
GStr+GStr	136	279.7	EFALL	315.2	MFALL	359.0	EWIN	79
HOWE+GStr	55	135.0	MSPR	318.1	MFALL	354.0	LFALL	219
LFR+GStr	78	282.6	EFALL	319.1	MFALL	394.0	MWIN	111
LILL+GStr	3	296.5	MFALL	307.4	MFALL	319.1	MFALL	23
FRCany+GStr	12	281.9	EFALL	299.3	MFALL	334.4	LFALL	52
BUTE+SFj	5	278.7	EFALL	299.3	MFALL	313.2	MFALL	34
LOUGH+SFj	37	273.7	EFALL	302.8	MFALL	319.0	MFALL	45
SC+SFj	50	258.0	LSUM	278.0	EFALL	319.2	MFALL	61
UKNIGHT+SFj	6	245.3	LSUM	275.6	EFALL	303.1	MFALL	58
EVI+SFj	20	272.5	EFALL	294.4	MFALL	333.9	LFALL	61
WVI+WVI	169	288.0	EFALL	300.3	MFALL	320.0	MFALL	32
WVI+WQCI	60	281.3	EFALL	293.0	EFALL	319.0	MFALL	38
RI+HStr	15	238.4	LSUM	264.6	EFALL	306.6	MFALL	68
SI+HStr	10	258.0	LSUM	270.2	EFALL	285.5	EFALL	27
BCD+HStr	29	220.0	MSUM	241.1	LSUM	284.8	EFALL	65
QCI+HStr	97	273.5	EFALL	285.3	EFALL	298.5	MFALL	25
SKID	43	265.5	EFALL	278.7	EFALL	289.0	EFALL	23
QCI+WQCI	58	265.7	EFALL	276.7	EFALL	285.5	EFALL	20
QCI+NQCI	12	253.4	LSUM	285.3	EFALL	297.5	MFALL	44
HecLow+HStr	134	245.8	LSUM	262.9	LSUM	283.5	EFALL	38
NC+HStr	128	220.2	MSUM	255.8	LSUM	286.0	EFALL	66
HecLow+NSKEst	16	249.0	LSUM	261.7	LSUM	293.0	EFALL	44
LSK+NSKEst	31	227.0	MSUM	248.8	LSUM	258.8	LSUM	32
MSK+NSKEst	9	213.0	MSUM	241.2	LSUM	250.4	LSUM	37
USK+NSKEst	1			259.0	LSUM			
LNR-P+NSKEst	32	227.0	MSUM	252.2	LSUM	309.0	MFALL	82
PCOb+NSKEst	13	226.7	MSUM	235.1	LSUM	253.9	LSUM	27
overall	1261	135.0	MSPR	284.7	EFALL	394.0	MWIN	259

Table 15 Liner regression model for mean day of spawning in British Columbian chum salmon populations.

Dependent Variable	day of peak spawning (DOY) [var: DOY_PK_SPAWN]
N	1259
Multiple R	0.889
Squared Multiple R	0.791
Adjusted Squared Multiple R	0.790
Standard Error of Estimate	12.00

Regression Coefficients $B = (X'X)^{-1}X'Y$

Effect	Coefficient	Standard Error	t	p-value	
CONSTANT	292.0	33.35	8.75	<<0.001	
LAT	-8.895	0.536	-16.6	<<0.001	latitude (°N)
LONG	-2.545	0.283927	-8.96	<<0.001	longitude (–°W)
TRIB_GRAD	-0.199	0.0599	-3.31	0.001	mean elevation of all tributaries (m)
PPT_ANN	-0.00399	0.000376	-10.6	<<0.001	mean annual precipitation (mm)
AT_SEP	10.65	0.709	15.0	<<0.001	mean air temperature in September (°C)
MAX_P_MAG	0.000082	0.000026	3.18	0.0015	a measure of stream stability
ELEV_MEAN	0.0373	0.00287	13.0	<<0.001	mean elevation of watershed (m)

Analysis of Variance

Source	SS	df	Mean Squares	F-ratio	p-value
Regression	6.816552E+005	7	97379.3	676.2	<<0.001
Residual	1.801574E+005	1251	144.01		

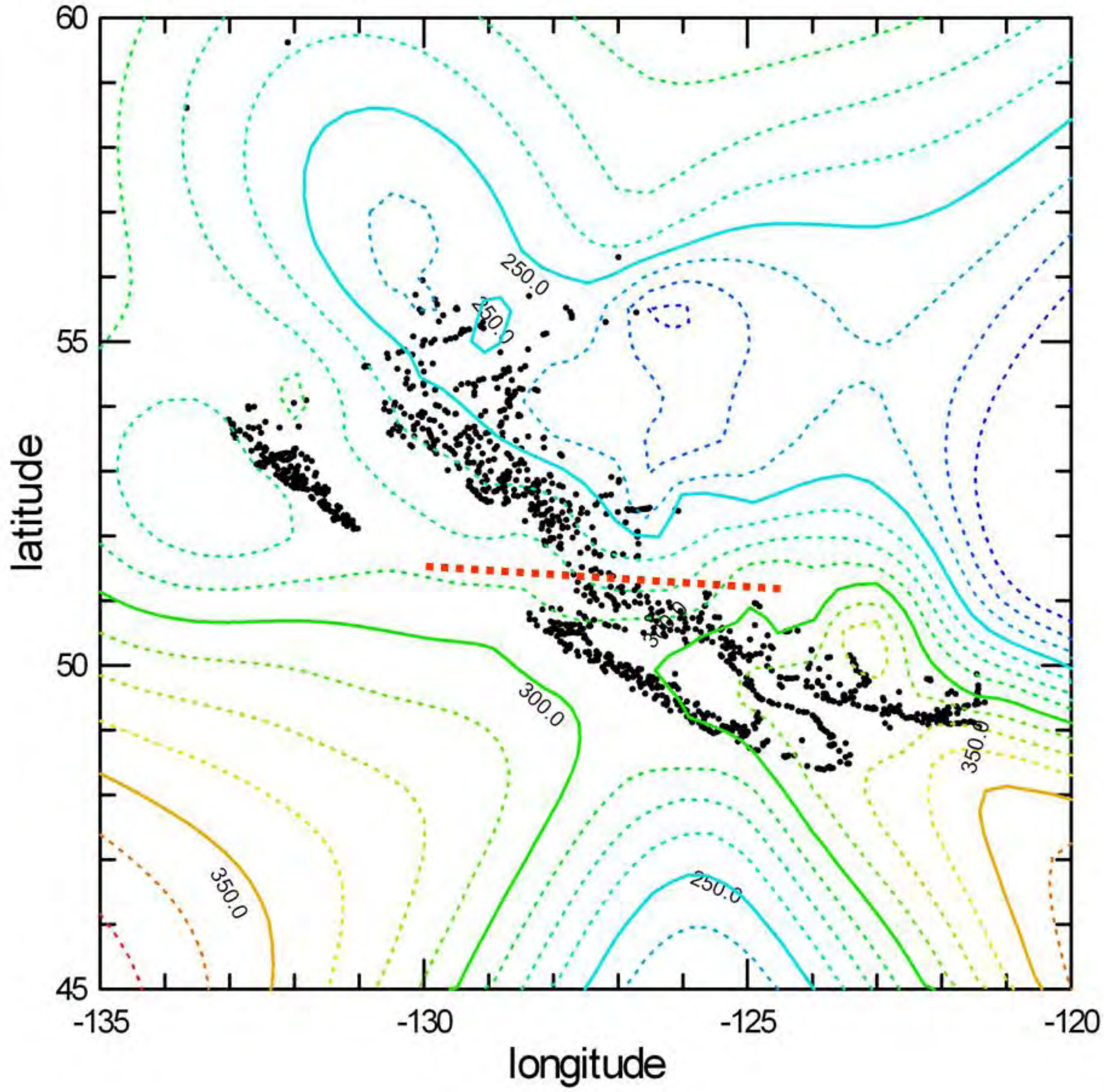


Figure 21. Contour plot of the day of peak spawning for the chum salmon populations in British Columbia. Variation in spawning time is oriented to the coast and so tends to be earlier to the northwest (i.e., along the coast) and northeast (i.e., inland). The red dotted line lies at the latitude of Rivers Inlet. Note how the isopleths lie approximately E-W in this area of the coast. This latitude marks a N-S divide in mean time of spawning.

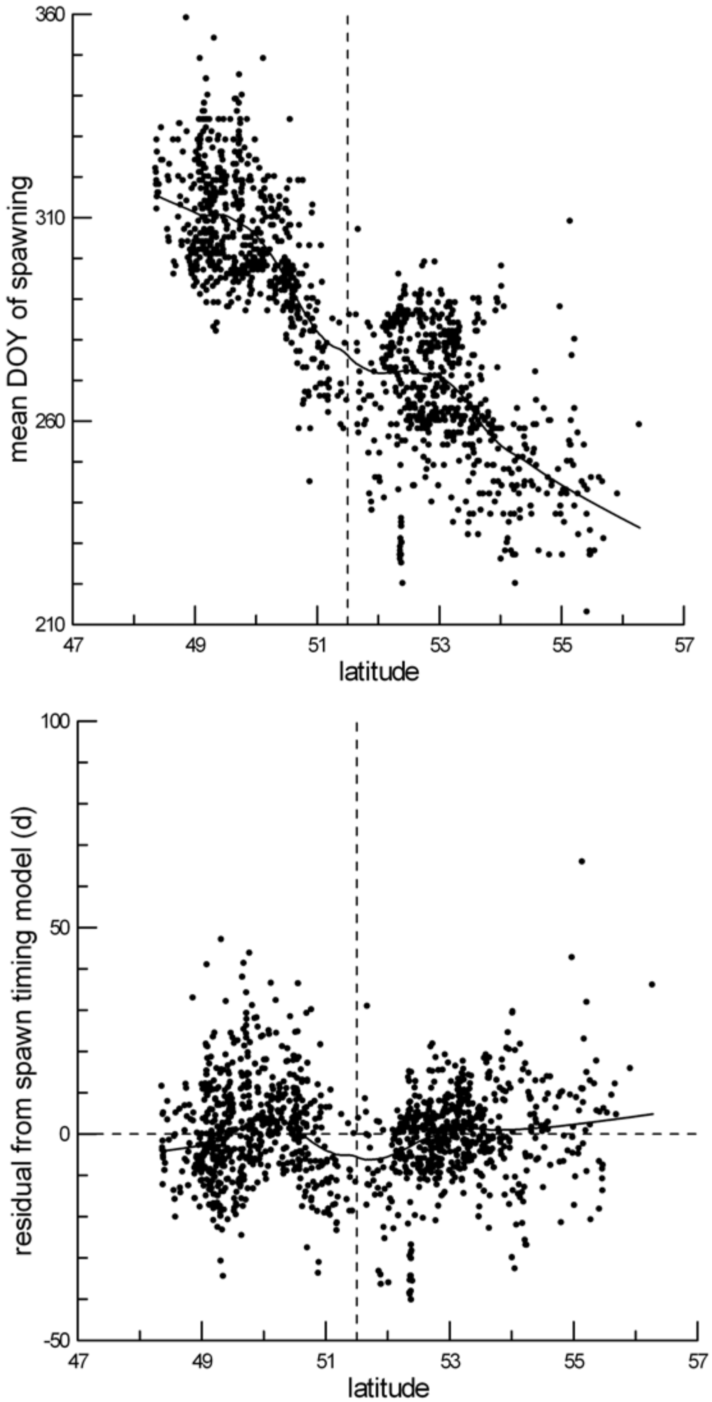


Figure 22. For chum salmon, plots of the mean DOY of spawning (top) and the residuals of the spawn timing model versus latitude. The vertical dotted line marks the N-S transition shown in the preceding figure. The solid lines are LOWESS smoothing function. Note how the clear N-S dichotomy of the top figure is absent in the residual plot. Apparently, physiographic and climatic differences along the coast, which are included in the model account for the sharp transition in spawning time.

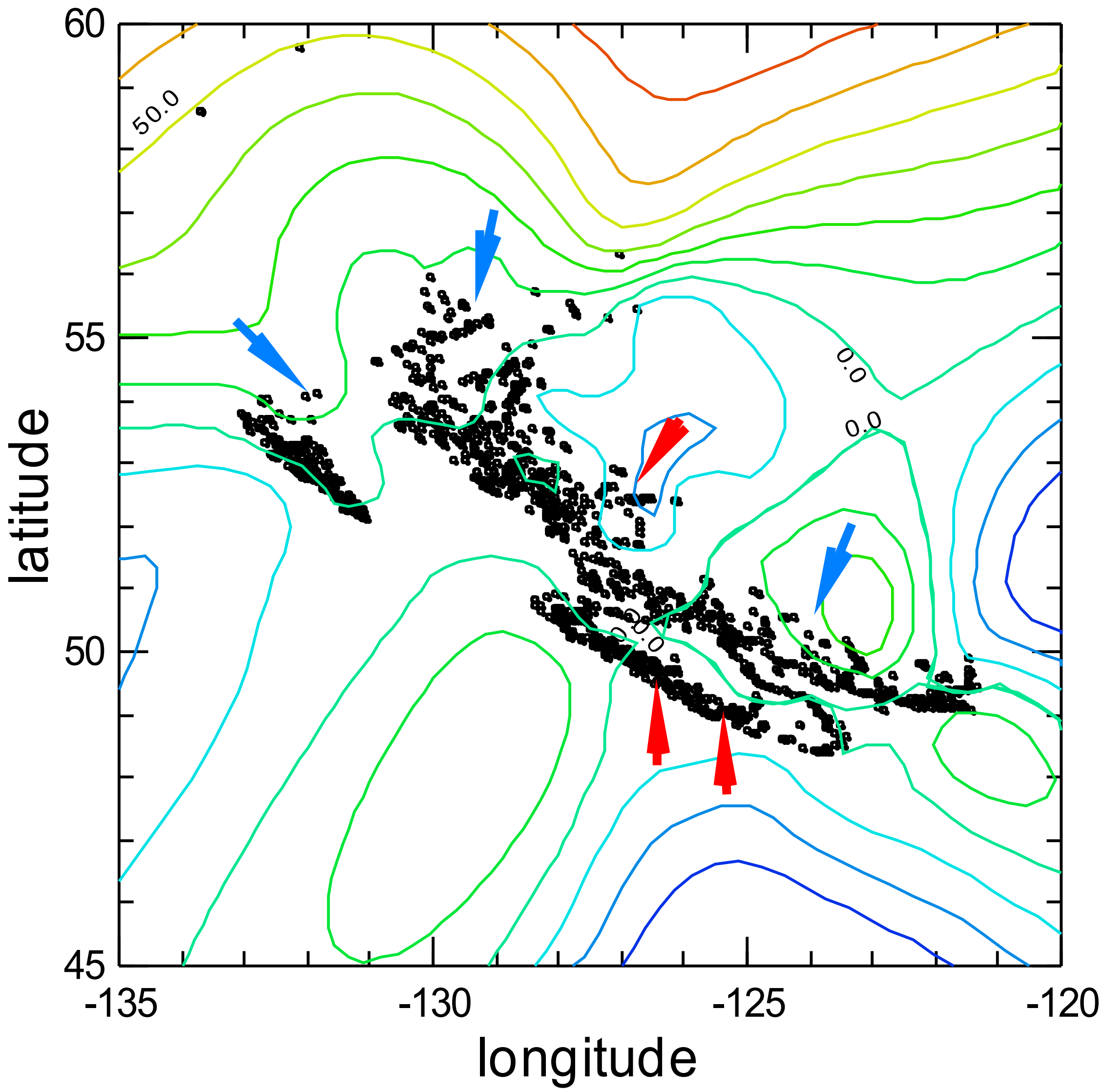


Figure 23. A contour map of the residuals from the spawning time model for chum salmon in British Columbia. The blue arrows indicate areas where the model predicted earlier spawning than was observed (i.e., positive residuals). The red arrows indicate areas where spawning was consistently earlier than predicted.

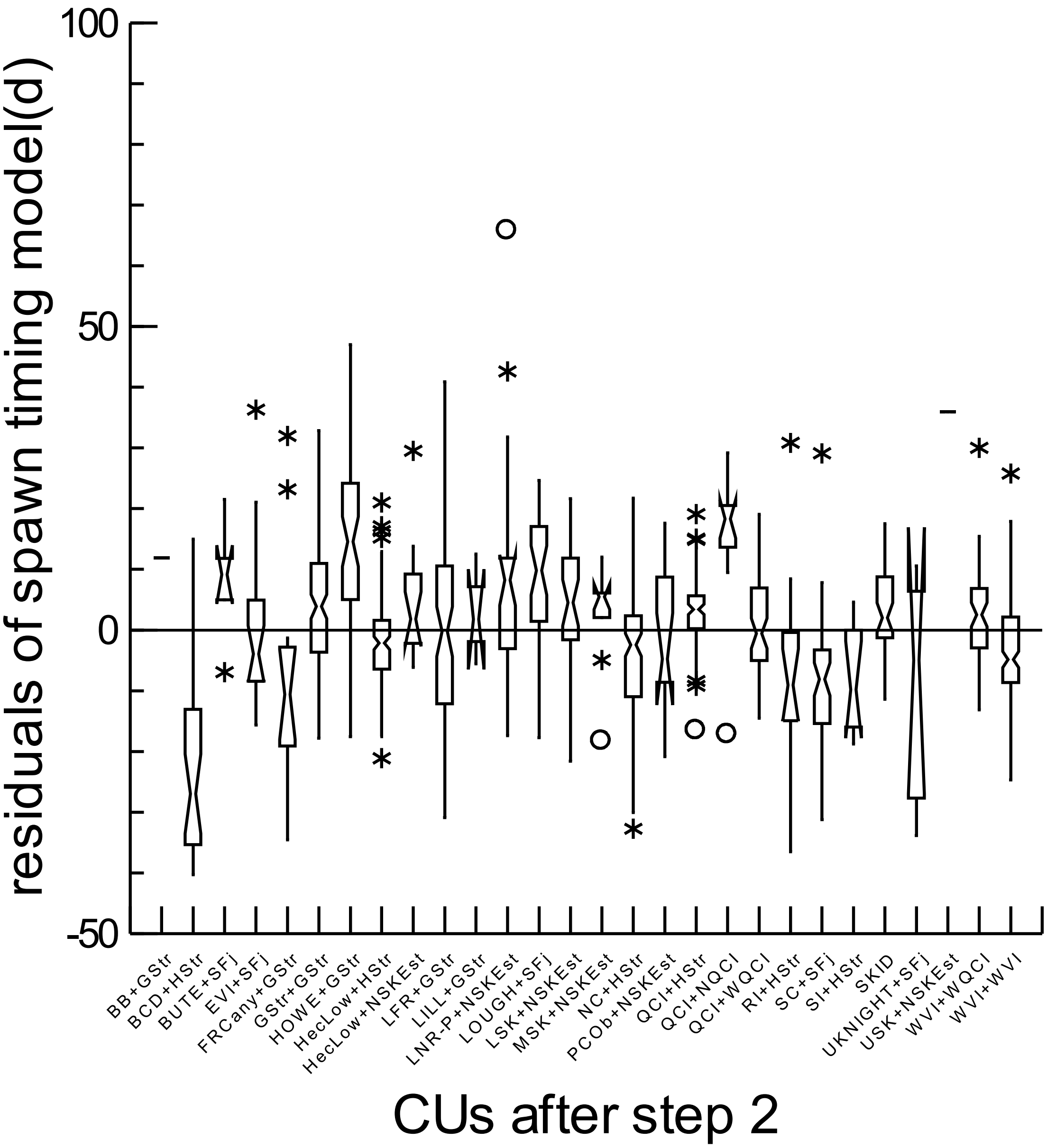


Figure 24. Box plots of the residuals of the spawning time model for chum salmon categorized by the Conservation Units established at step 2 - the consideration of genetic population structure. The groups are arranged alphabetically. A positive residual indicates that spawning occurred later than the model prediction.

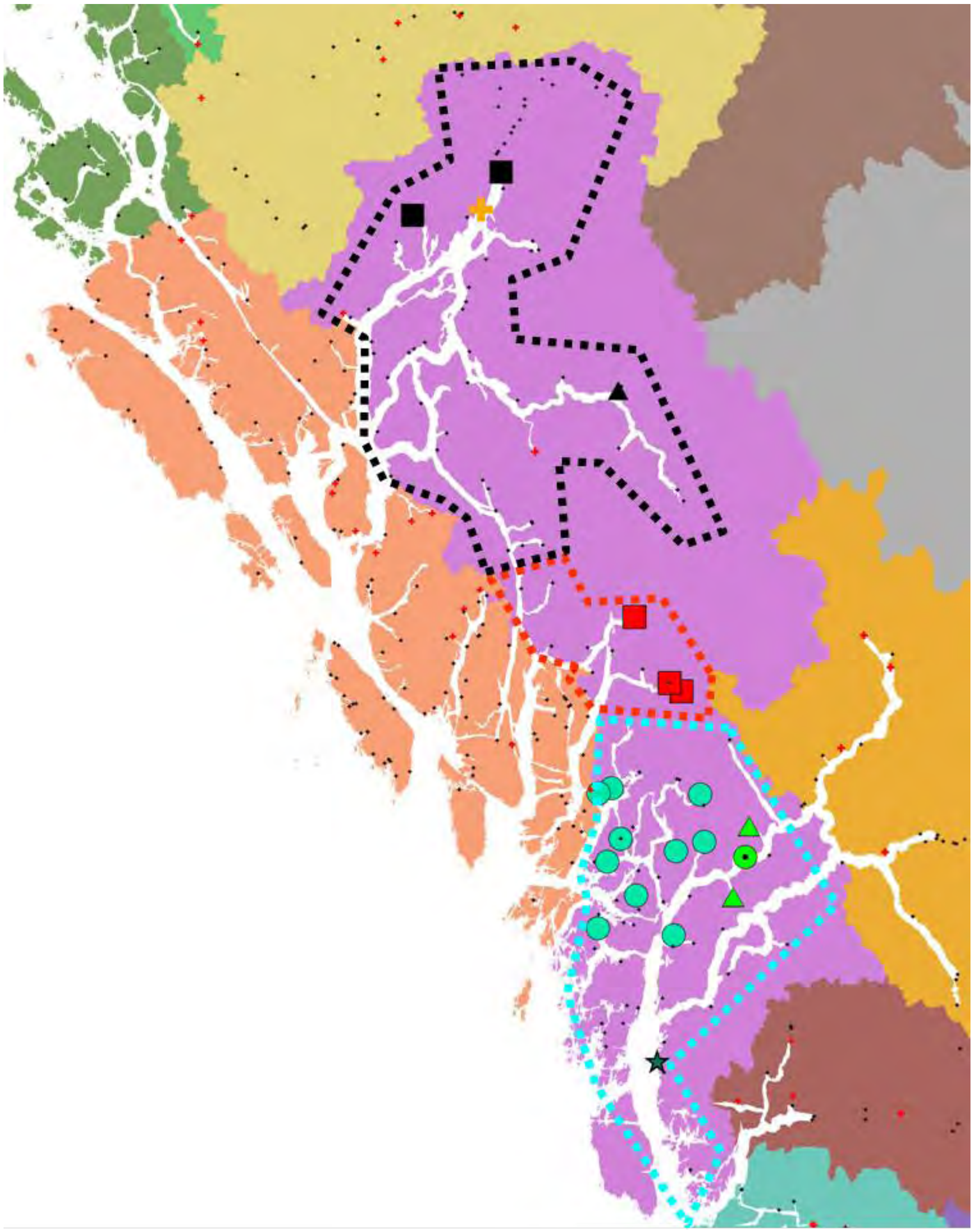


Figure 25. A map showing the locations of eight genetic classes of chum salmon within the NC+HStr provisional CU after step 2. The classes are: 2.07-2 (✚); 2.09.2-1.1 (▲); 2.09.2-1.2 (■); 2.09.2-2.2 (▲); 2.09.2-2.3 (◉); 2.09.3-1 (■); 2.09.3-3.1 (●); and 2.14-2.2 (★). The three outlined areas are CUs suggested by spawn timing similarities: Douglas-Gardner (- - - -), Mussel-Kynoch (- - - -) and Spiller-Fitz Hugh-Burke (- - - -).

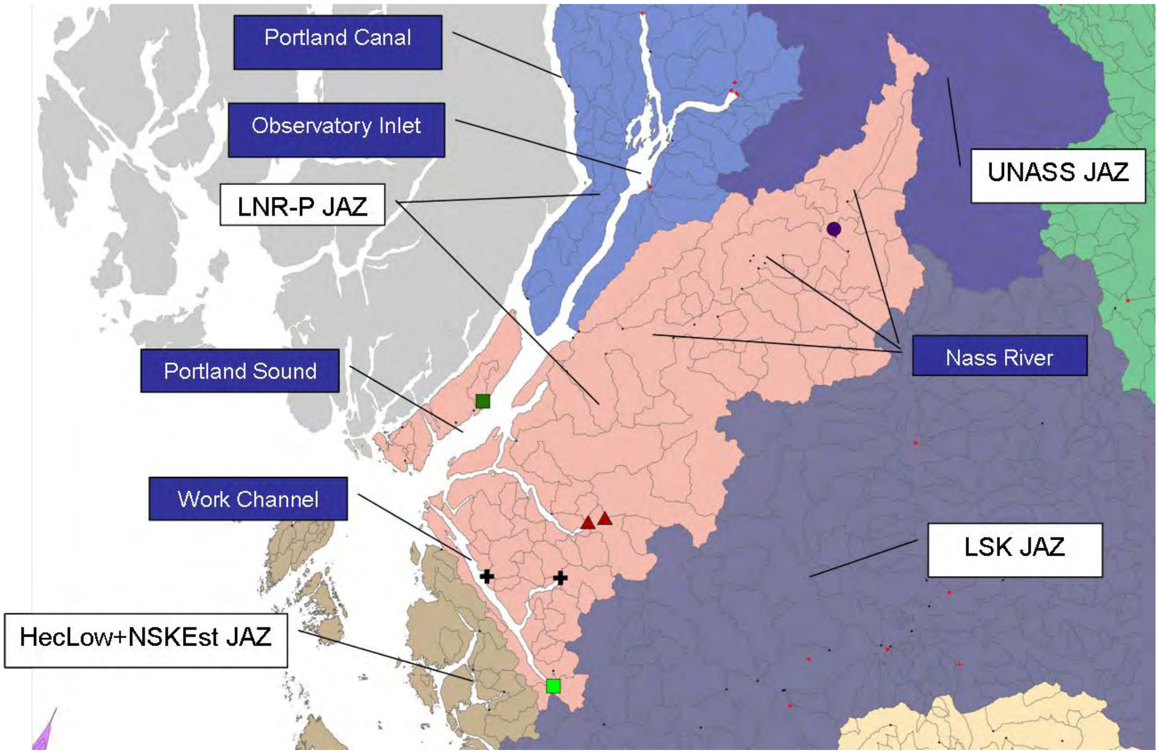


Figure 26. A map showing the locations of five genetic classifications within the LNR-P+NSKEst provisional CU following step 2. The genetic classifications are 2.06.1-1 (■), 2.06.1-2 (■) 2.07-1 (▲), 2.08-1 (●); and 2.09.2-1.3 (✚).

Table 16. Summary of the discriminant function analysis for the Lower Nass-Portland Inlet ecotypic CU of chum salmon.

Group Frequencies

Portland Inlet	lower Nass River
12	21

Group Means

variable	Portland Inlet	lower Nass River
MS_GRAD	3.374	4.253
TRIB_GRAD	16.432	22.811
GLAC_PC	0.602	1.633
TUNDRA_PC	8.498	18.833
HIGHLEV_PC	9.100	20.466
DD0_ANN	1859.222	1360.552
PPT_ANN	3794.716	2337.272
AT_ANN	5.123	3.762
MAX_P_MAG	25.500	12427.000
WS_ORDER	2.833	4.429
MELTONS	0.143	0.188
ELEV_MEAN	446.333	692.667
VFW_MEAN	1.034	2.482
KFAC_LOG	4.114	4.266

Stepping Summary

	F(+ent,-rem)	Wilks's Lambda	Approx. F-ratio	p-value
MAX_P_MAG	3223943.349	0.000	3223943.349	0.000
AT_ANN	20.616	0.000	2632020.297	0.000
VFW_MEAN	7.892	0.000	2157809.369	0.000
TRIB_GRAD	3.520	0.000	1758984.381	0.000
WS_ORDER	4.207	0.000	1568352.461	0.000

Classification Matrix (Cases in row categories classified into columns)

	Portland Inlet	lower Nass River	%correct
Portland Inlet	12	0	100
lower Nass River	0	21	100
Total	12	21	100

Canonical Discriminant Functions : Standardized by Within Variances

TRIB_GRAD	0.764
AT_ANN	1.575
MAX_P_MAG	1.673
WS_ORDER	0.890
VFW_MEAN	-1.430

Canonical Scores of Group Means

Portland Inlet	-690.984
lower Nass River	394.848

Table 17. A summary of the habitat discriminant function for the lower Fraser River, Lillooet, and Fraser Canyon ecotypic CUs of chum salmon.

Group Frequencies

Fraser canyon	lower Fraser River
12	78

Group Means

	Fraser canyon	lower Fraser River
MS_GRAD	2.667	2.690
TRIB_GRAD	21.378	17.029
GLAC_PC	0.002	0.885
TUNDRA_PC	1.583	5.129
HIGHLEV_PC	1.585	6.015
DD0_ANN	1864.923	2733.663
PPT_ANN	2207.371	2243.465
AT_ANN	5.144	7.522
MAX_P_MAG	61800.000	61800.000
WS_ORDER	5.083	4.718
MELTONS	0.160	0.164
ELEV_MEAN	978.000	574.051
VFW_MEAN	0.654	3.829
KFAC_LOG	3.977	4.155

Stepping Summary

	F(+ent,-rem)	Wilks's Lambda	Approx. F-ratio	p-value
KFAC_LOG	86.679	0.504	86.679	0.000
TUNDRA_PC	6.344	0.470	49.143	0.000
PPT_ANN	3.623	0.451	34.958	0.000

Classification Matrix (Cases in row categories classified into columns)

	Fraser canyon	lower Fraser River	%correct
Fraser canyon	11	1	92
lower Fraser River	2	76	97
Total	13	77	97

Canonical Discriminant Functions : Standardized by Within Variances

TUNDRA_PC	0.408
PPT_ANN	-0.285
KFAC_LOG	1.049

Canonical Scores of Group Means

	1
Fraser canyon	-2.784
lower Fraser River	0.428

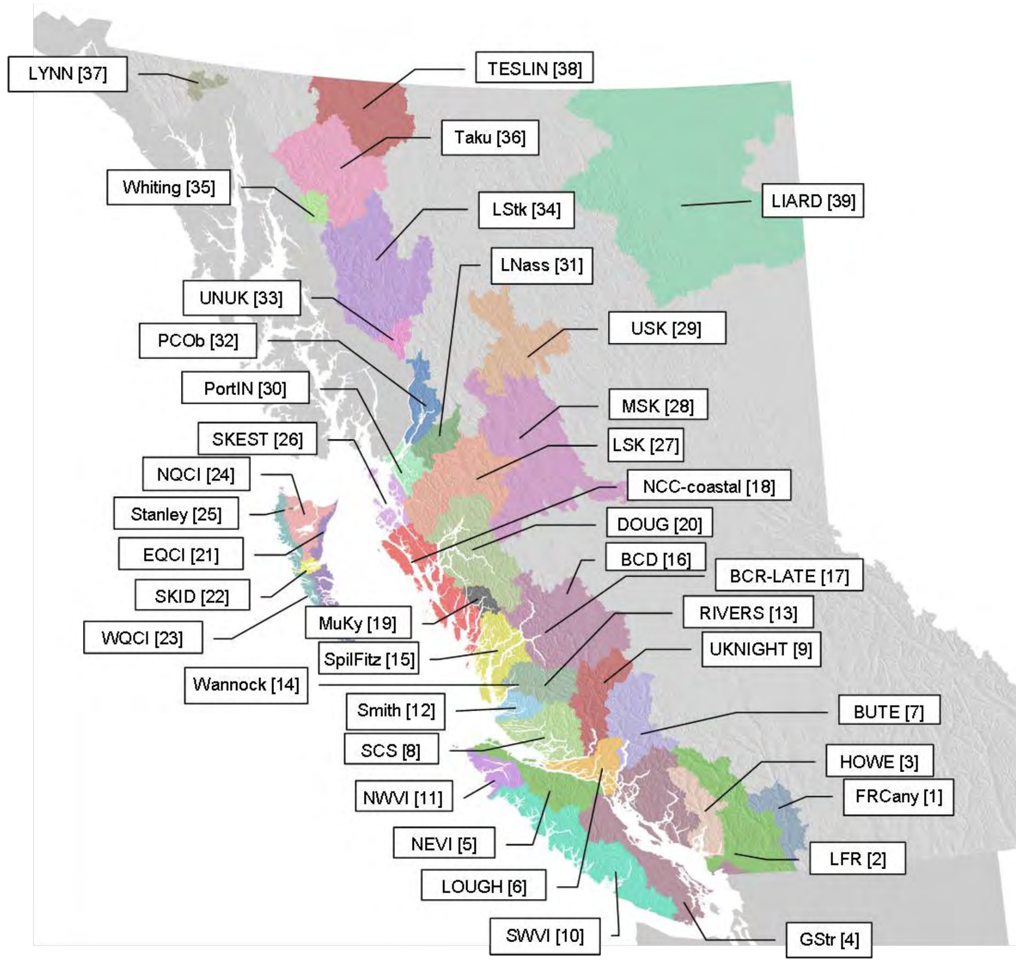


Figure 27. The 39 Conservation Units of chum salmon in British Columbia. Conservation Units in the Mackenzie River and Yukon River drainages are not shown, except for the Teslin CU[38], which may change when the Yukon River CUs are fully described.

Table 18. A summary of the 39 Conservation Units for chum salmon in index order, which is roughly geographical from south to north. The number of sites indicated is the total in our database and is not to be interpreted as the number of sites where chum salmon are persistently found.

Chum salmon Conservation Units

Conservation Unit	acronym	index	number of sites	classification step	comments
Fraser Canyon	FRCany	1	13	habitat	suggested by genetics
Lower Fraser	LFR	2	81	habitat	2 ecotypic CUs merged
Howe Sound-Burrard Inlet	HOWE	3	55	genetic	
Georgia Strait	GStr-SFj	4	140	genetic	2 ecotypic CUs merged
East Vancouver Island	NEVI	5	20	ecotypic	confirmed by genetics
Loughborough	LOUGH	6	37	genetic	
Bute Inlet	BUTE	7	5	genetic	
Southern Coastal Streams	SCS	8	51	genetic	
Upper Knight	UKNIGHT	9	6	timing	ecotype split
Southwest Vancouver Island	SWVI	10	171	timing	
Northwest Vancouver Island	NWVI	11	61	timing	
Smith Inlet	SMITH	12	10	genetic	ecotype split
Rivers Inlet	RIVERS	13	14	timing	ecotype split
Wannock	WANNOCK	14	1	timing	
Spiller-Fitz Hugh-Burke	SpilFitz	15	54	genetic/timing	suggested by genetics/confirmed by timing
Bella Coola - Dean Rivers	BCD	16	30	timing	ecotype split
Bella Coola River - Late	BCR-LATE	17	1	timing	
Hecate Lowlands	NCC-coastal	18	136	ecotypic	confirmed by genetics
Mussel-Kynoch	MuKy	19	12	genetic/timing	suggested by genetics/confirmed by timing
Douglas-Gardner	DOUG	20	61	genetic/timing	suggested by genetics/confirmed by timing
East QCI	EQCI	21	98	ecotypic	confirmed by genetics
Skidegate	SKID	22	43	genetic	ecotype split
West QCI	WQCI	23	59	ecotypic	confirmed by genetics
North QCI	NQCI	24	11	ecotypic	confirmed by genetics
North QCI-Stanley Creek	Stanley	25	1	genetic/timing	unique timing

Chum salmon Conservation Units					
Conservation Unit	acronym	index	number of sites	classification step	comments
Skeena Estuary	SKEST	26	16	ecotypic	confirmed by genetics
Lower Skeena	LSK	27	33	ecotypic	
Middle Skeena	MSK	28	9	ecotypic	
Upper Skeena	USK	29	1	ecotypic	confirmed by genetics
Portland Inlet	PortIN	30	13	habitat	supported by genetics
Lower Nass	LNASS	31	19	genetic/habitat	
Portland Canal-Observatory	PCOb	32	14	genetic	
Unuk	UNUK	33	?	ecotypic	
Lower Stikine	LStk	34	?	ecotypic	
Whiting	WHTNG	35	?	ecotypic	
Taku	TAKU	36	5	ecotypic	confirmed by genetics
Lynn Canal	LYNN	37	?	ecotypic	
Teslin†	TESLIN	38	1	ecotypic	
Lower Liard	LIARD	39	?	ecotypic	
Yukon‡	YUK	?	0	ecotypic	
Mackenzie River‡	MACR	?	0	ecotypic	Peel River is genetically distinctive; other CUs within the Mackenzie are possible.

† The Teslin River headwaters is likely part of an Upper Yukon CU whose structure has yet to be determined
‡ There are likely several CUs of chum salmon in the Yukon River and at least one in the Mackenzie River in addition to the lower Liard. Their structure has yet to be determined.

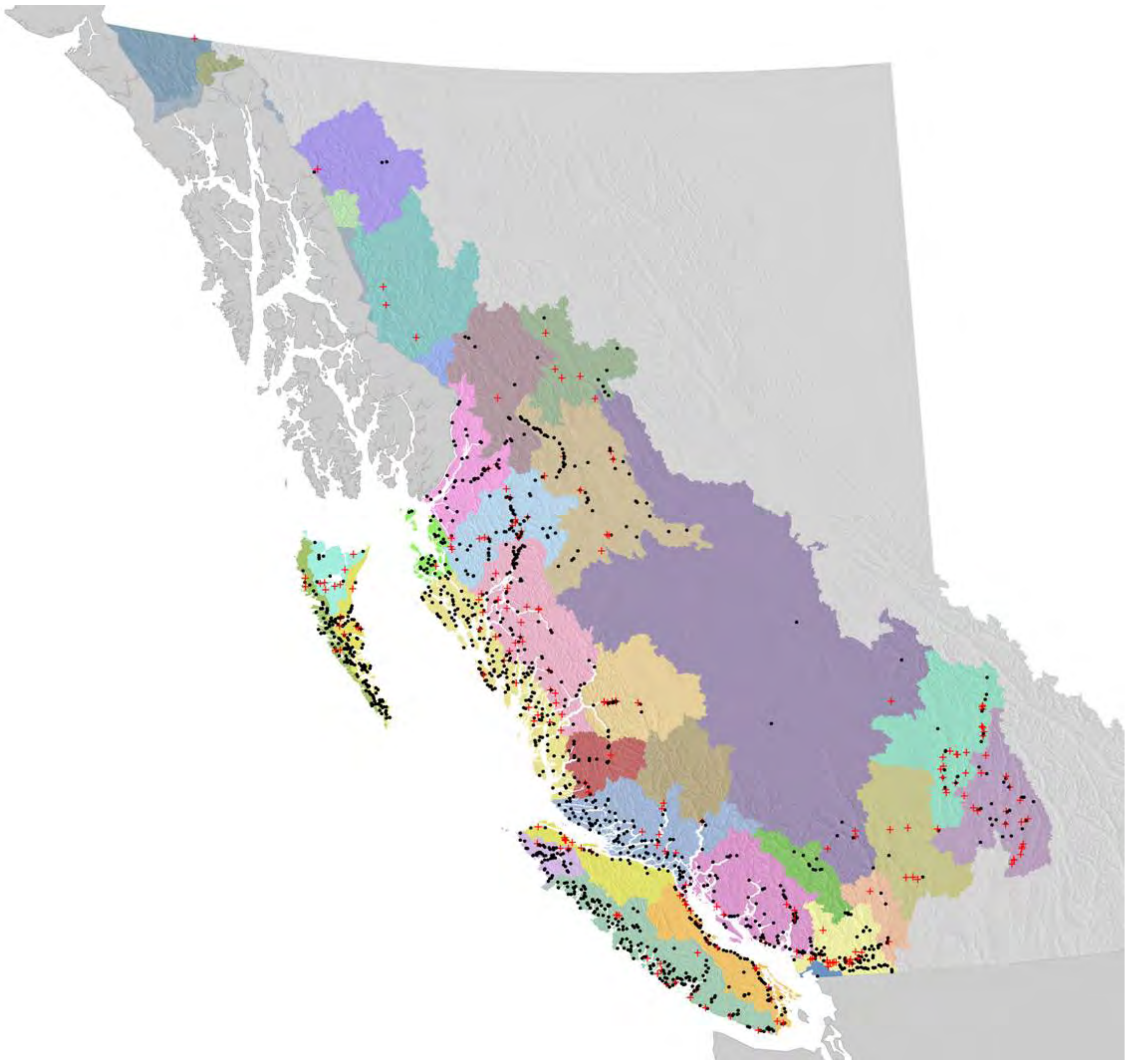


Figure 28. A map showing the location of the 1542 sites within British Columbia with coho salmon. The red crosses are sites where genetic samples were available. The colored polygons are the JAZ ecotypic CUs either where coho salmon has been documented or where the species is probably present.

Table 19. Coho salmon presence, relative abundance, and genetic population structure within the JAZ ecotypes of British Columbia. The number sites and number of sites present are taken from our database and do not indicate the total number of sites within a JAZ that may have a persistent presence.

JAZ	JAZ Acronym	JAZ index	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic clusters present in JAZ
Okanagan|OR-WA Coastal	OK+ORWA	1	-	1	-	unlikely	-	-
Boundary Bay| Georgia Strait	BB+GStr	2	1	8	13%	documented	0	0
Lower Fraser|Georgia Strait	LFR+GStr	3	92	133	69%	documented	3.04.04- 3.04.05-1 3.04.05-2 3.04.05-3 3.04.05-4	L,M
Lillooet| Georgia Strait	LILL+GStr	4	13	16	81%	documented	0	0
Fraser Canyon| Georgia Strait	FRCany+GStr	5	9	20	45%	documented	3.04.06- 3.04.07-	N
Middle Fraser|Georgia Strait	MFR+GStr	6	12	176	7%	documented	3.04.09-1	P
Upper Fraser|Georgia Strait	UFR+GStr	7	-	45	-	possible	-	-
Lower Thompson| Georgia Strait	LTh+GStr	8	7	20	35%	documented	3.04.09-3	P
South Thompson| Georgia Strait	STh+GStr	9	40	66	61%	documented	3.04.09-2 3.04.09-4 3.04.09-5 3.04.09-6 3.04.09-7	P
North Thompson| Georgia Strait	NTh+GStr	10	38	47	81%	documented	3.04.08-1 3.04.08-2.1 3.04.08-2.2 3.04.08-3 3.04.09-6	O,P
S Coastal Streams| Georgia Strait	SC+GStr	11	101	131	77%	documented	3.04.01- 3.04.03-1	I,K
S Coastal Streams| QCStr-JStr-SFjords	SC+SFj	12	96	109	88%	documented	3.04.01- 3.04.02-2	I,J
E Vancouver Island| Georgia Strait	EVI+GStr	13	83	90	92%	documented	3.04.02-1 3.04.02-2	J,R

JAZ	JAZ Acronym	JAZ index	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic clusters present in JAZ
E Vancouver Island| QCStr-JStr-SFjords	EVI+SFj	14	23	33	70%	documented	3.04.02-3 3.04.02-4 3.07-4 3.04.02-1 3.07-1 3.07-2 3.07-3	J,R
W Vancouver Island| Vancouver Island Coastal Current	WVI+WVI	15	191	249	77%	documented	3.07-5 3.04.02-1 3.05.04-2 3.05.05-3 3.05.06-4 3.06- 3.08-1	G,J,Q,S
W Vancouver Island| Outer Graham Island	WVI+WQCI	16	57	64	89%	documented	3.07-1	R
Homathko - Klinaklini Rivers|QCStr-JStr-SFjords	HK+SFj	17	4	4	100%	documented	3.01.03-3 3.01.03-4	V
Rivers-Smith Inlets| Hecate Strait - Q.C. Sound	RSI+HStr	18	27	30	90%	documented	3.01.02-1 3.05.01-1	F,U
Bella Coola - Dean Rivers| Hecate Strait - Q.C. Sound	BCD+HStr	19	23	40	58%	documented	3.01.03-5 3.01.03-6	V
Queen Charlottes|Hecate Strait - Q.C. Sound	QCI+HStr	20	129	142	91%	documented	1.02-1 3.05.02-1 3.05.02-2 3.05.02-3 3.05.02-4	B,H
Queen Charlottes| Outer Graham Island	QCI+WQCI	21	55	83	66%	documented	3.05.03-1	G
Queen Charlottes| North Graham Island	QCI+NQCI	22	17	18	94%	documented	1.02-1.1 1.02-1.2 1.02-1.3.1 1.02-1.3.2 1.02-1.4 1.02-2	B
Hecate Lowlands| Hecate Strait - Q.C. Sound	HecLow+HStr	23	162	174	93%	documented	3.01.01-1 3.01.01-6.2	E,T

JAZ	JAZ Acronym	JAZ index	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic clusters present in JAZ
							3.03-1	
							3.03-2	
N Coastal Streams| Hecate Strait - Q.C. Sound	NC+HStr	24	103	118	87%	documented	1.01-1	A,D,E,T,V
							1.01-3	
							3.01.01-1	
							3.01.01-2.1	
							3.01.01-2.2	
							3.01.01-3	
							3.01.01-4	
							3.01.01-5	
							3.01.03-1	
							3.01.03-2	
							3.02-1	
							3.03-1	
							3.03-2	
Hecate Lowlands| Nass - Skeena Estuary	HecLow+NSKEst	25	30	67	45%	documented	1.01-2	A
Lower Skeena| Nass - Skeena Estuary	LSK+NSKEst	26	74	107	69%	documented	3.01.04-	W,Y,Z
							3.01.08-	
							3.01.09-	
							3.01.10-	
							3.01.11-	
							3.01.12-1	
Middle Skeena |Nass - Skeena Estuary	MSK+NSKEst	27	76	113	67%	documented	3.01.12-3.2	Z
							3.01.12-3.3	
							3.01.12-5	
							3.01.12-6	
Upper Skeena| Nass - Skeena Estuary	USK+NSKEst	28	12	19	63%	documented	3.01.12-4.1	Z
							3.01.12-4.2	
							3.01.12-4.3	
							3.01.12-4.4	
Lower Nass - Portland| Nass - Skeena Estuary	LNR-P+NSKEst	29	46	75	61%	documented	3.01.02-1	U,Y
							3.01.07-	
Upper Nass| Nass - Skeena Estuary	UNR+NSKEst	30	13	23	57%	documented	3.01.12-2	Z
Unuk River| Transboundary Fjords	UNUK+TBFj	31	-	2	-	probable	-	-

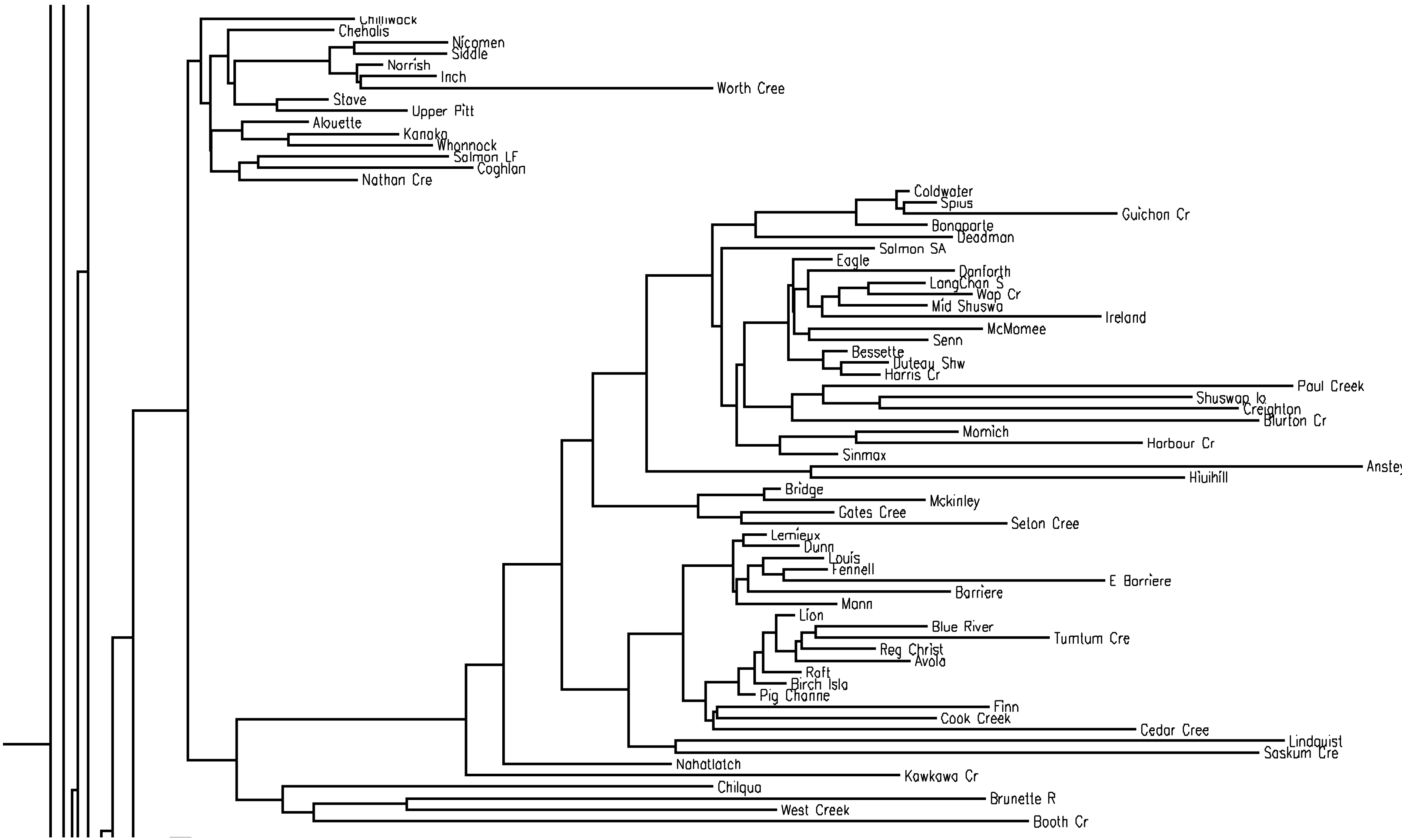
JAZ	JAZ Acronym	JAZ index	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic clusters present in JAZ
Lower Stikine|Transboundary Fjords	LStk+TBFj	32	3	18	17%	documented	3.01.06-1 3.01.06-2 3.01.06-3	X
Whiting River| Transboundary Fjords	Whtng+TBFj	33	-	1	-	probable	-	-
Taku| Transboundary Fjords	Taku+TBFj	34	4	19	21%	documented	3.01.06-4	X
Lynn Canal| Transboundary Fjords	LYNN+TBFj	35	-	4	-	probable	-	-
Alsek| Alaska Coastal Downwelling	Alsek+AKCst	36	1	6	17%	documented	2.03-2	C
Teslin Headwaters| Bering Sea	TesHW+Ber	37	-	4	-	unlikely	-	-
Lower Liard |Arctic Ocean	Liard+AO	38	-	1	-	unlikely	-	-
Yukon River |Bering Sea	Yuk+Ber	37	-	4	-	possible	-	-
Mackenzie River| Arctic Ocean	MacR+AO	39	-	1	-	possible	-	-

Figure 29 – coho dendrogram

Figure 29...

Pallant
Copper
SheldonsBa
GreyBay Cr
Deena
Hanna
Tarundl
Robertson
Thornton C
Maggie Riv
Conuma
Canton
Sucwoa
Tasu
Coates Cre
Mercer Cre
Long Lake
Nekite Riv
Nitinat
Pachena
San Juan
Sarita
Nooksack
Marblemoun
Wallace
Nisqually
Grizzly
Minter
Dungeness
Elwha
Hood Canal
Bingham
Willapa
Lewis
Kalama Fal
Elochoman
Cowlitz
Clackamas
Eagle Cr
Bonneville
Sandy Hatc
Fallert H
Elochoman
Noyo Cal
Eel South
Eel West
Mill Smith
Klamath
Umpqua
Ten Mile L
Siltcoos L
Tahkenitch
Siuslaw
Alsea Rive
Siletz Riv
Beaver Cr
Trask Hatc
Quillayute
Queets
Clearwa US
Shale
Quatse
Glenlion
Storie
Cluxewe
Tsulquase
Keogh
Nahwitti
Stephens
Washlawls
Waukwaas
Quatsese R
Goodspeed
Kennedy
Tranquil
Cypre
Kootowis

Figure 29...



Chilliwack
Chehalis
Nicomen
Siddle
Norrish
Inch
Worth Cree
Stave
Upper Pitt
Alouette
Kanaka
Whonnock
Salmon LF
Coghlan
Nathan Cre
Coldwater
Spius
Guichon Cr
Bonaparte
Deadman
Salmon SA
Eagle
Danforth
LangChan S
Wap Cr
Mid Shuswa
Ireland
McMomee
Senn
Bessette
Duteau Shw
Harris Cr
Paul Creek
Shuswap lo
Creighton
Blurton Cr
Momich
Harbour Cr
Sinmax
Anstey
Hiuihill
Bridge
Mckinley
Gates Cree
Seton Cree
Lemieux
Dunn
Louis
Fennell
E Barriere
Barriere
Mann
Lion
Blue River
Tumtum Cre
Reg Christ
Avola
Raft
Birch Isla
Pig Channe
Finn
Cook Creek
Cedar Cree
Lindquist
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Nahatlatch
Kawkawa Cr
Chilqua
Brunette R
West Creek
Booth Cr

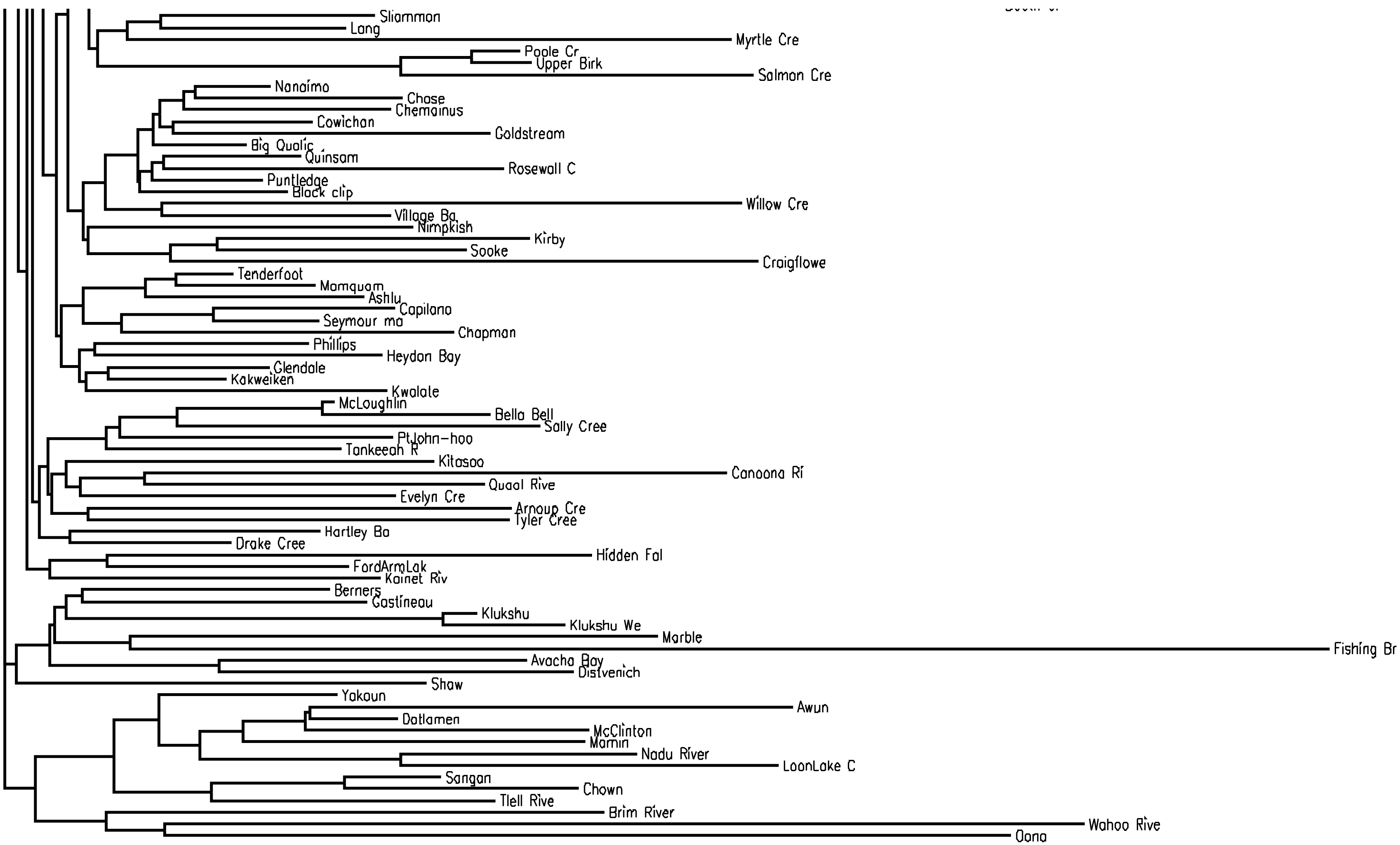


Figure 29. Neighbor-joining dendrogram of Cavalli-Sforza and Edwards (1967) chord distance for populations of coho salmon surveyed with microsatellite DNA (Beacham et al. unpublished data.)

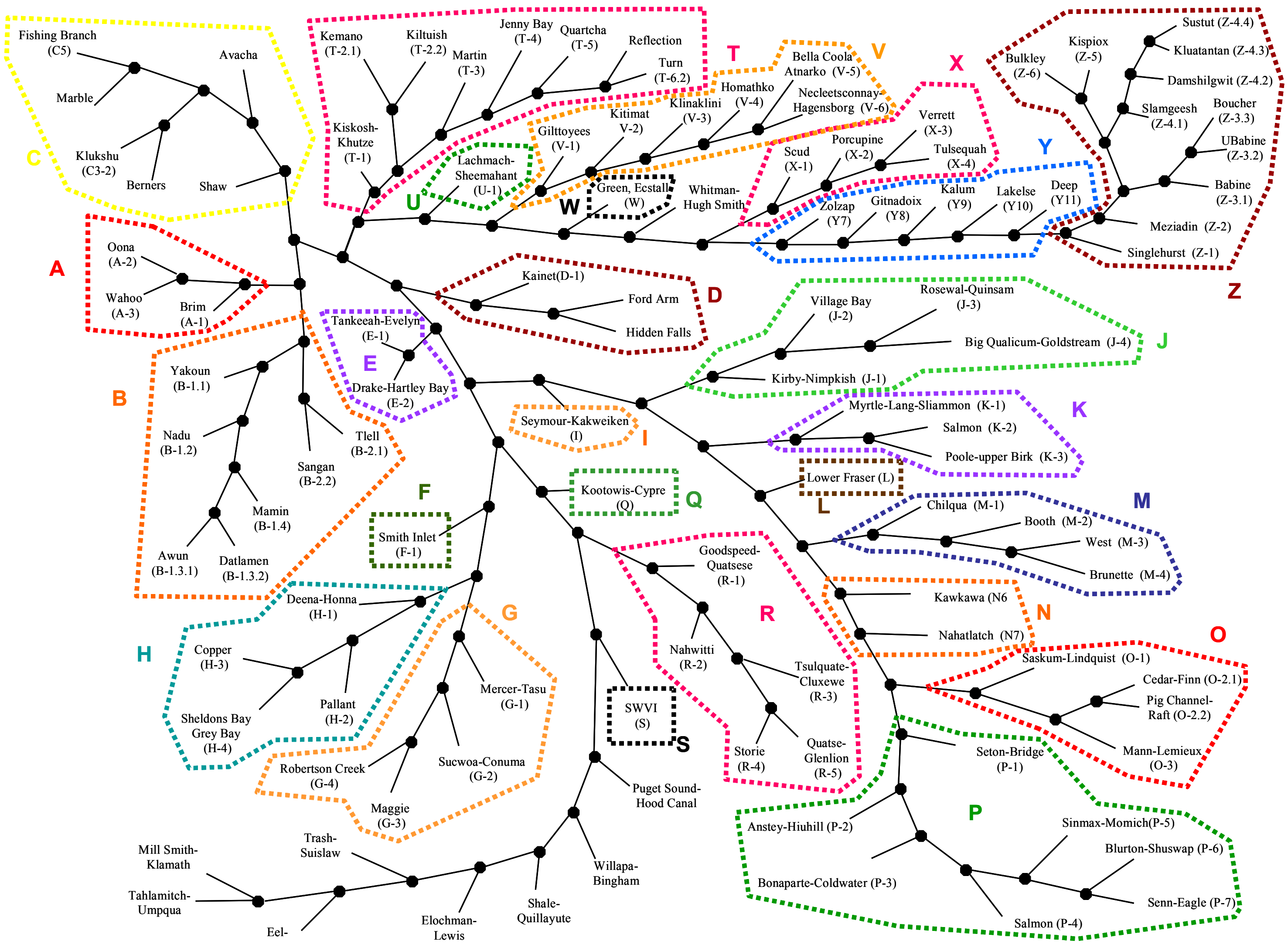


Figure 30. A diagrammatic summary of the coho dendrogram of Figure 29. The genetic clusters are indicated by the dotted lines and their associated letters.

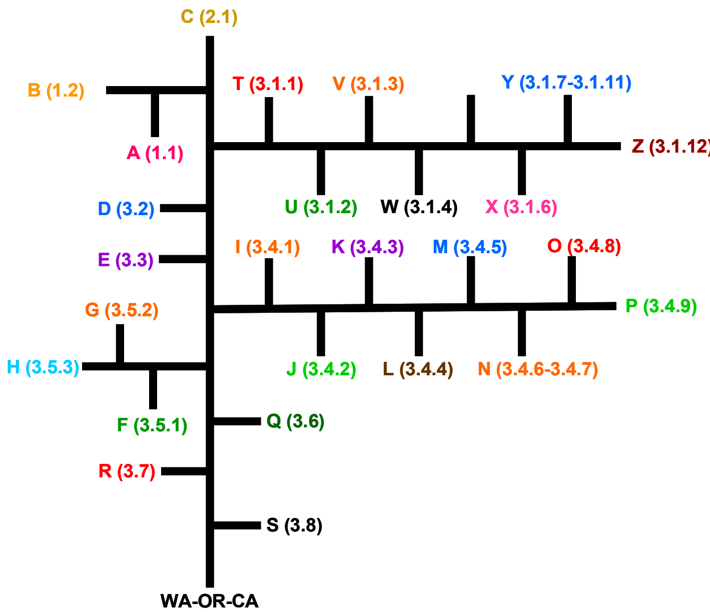


Figure 31. A stick diagram showing the relationship of the 26 genetic clusters for coho salmon in British Columbia.

Table 20. A simple genetic classification of the coho populations from Beacham et al. (unpublished data) shown in Figure 28. A five level hierarchical genetic classification was used. Classifications for sites outside of British Columbia are generally not shown. The GFE_ID is the SEDS population identifier for populations in British Columbia. Horizontal lines divide the genetic clusters, which are defined by the portion of the genetic class to the left of the dash.

GFE_ID	sites	cluster	genetic class	FAZ	MAZ	JAZ
1036	Brim River	A	1.01-1	NC	HStr	NC+HStr
1955	Oona River	A	1.01-2	HecLow	NSKEst	HecLow+NSKEst
1035	Wahoo	A	1.01-3	NC	HStr	NC+HStr
1497	Tlell River	B	1.02-1	QCI	HStr	QCI+HStr
1571	Yakoun	B	1.02-1.1	QCI	NQCI	QCI+NQCI
3545	Nadu	B	1.02-1.2	QCI	NQCI	QCI+NQCI
2001658	Loon Lake Creek	B	1.02-1.2	QCI	WQCI	QCI+WQCI
1567	Awun	B	1.02-1.3.1	QCI	NQCI	QCI+NQCI
1566	McClinton	B	1.02-1.3.2	QCI	NQCI	QCI+NQCI
1568	Datlamen	B	1.02-1.3.2	QCI	NQCI	QCI+NQCI
1570	Mamin	B	1.02-1.4	QCI	NQCI	QCI+NQCI
1575	Sangan	B	1.02-2	QCI	NQCI	QCI+NQCI
2001575	Chown Brook	B	1.02-2	QCI	NQCI	QCI+NQCI
?	Shaw	C	2.01-	?	?	?
2332	Klukshu Weir	C	2.03-2	Alsek	AKCst	Alsek+AKCst
2332	Klukshu	C	2.03-2	Alsek	AKCst	Alsek+AKCst
2522	Fishing Branch	C	2.05-	Yuk	Ber	Yuk+Ber
1010	Kainet Creek	D	3.02-1	NC	HStr	NC+HStr
1001	Tankeeah	E	3.03-1	HecLow	HStr	HecLow+HStr
1086	Quaal River	E	3.03-1	NC	HStr	NC+HStr
1796	Bella Bella	E	3.03-1	HecLow	HStr	HecLow+HStr
1796	Hooknose	E	3.03-1	HecLow	HStr	HecLow+HStr
1804	Sally Creek	E	3.03-1	HecLow	HStr	HecLow+HStr
1809	McLoughlin	E	3.03-1	HecLow	HStr	HecLow+HStr
1820	Kitasoo	E	3.03-1	HecLow	HStr	HecLow+HStr
1838	Canoona River	E	3.03-1	NC	HStr	NC+HStr
1850	Arnoup	E	3.03-1	NC	HStr	NC+HStr
1854	Tyler	E	3.03-1	HecLow	HStr	HecLow+HStr
1906	Evelyn Creek	E	3.03-1	NC	HStr	NC+HStr
1090	Hartley Bay	E	3.03-2	HecLow	HStr	HecLow+HStr
1870	Drake Creek	E	3.03-2	NC	HStr	NC+HStr
916	Long Lake	F	3.05.01-1	RSI	HStr	RSI+HStr
918	Nekite	F	3.05.01-1	RSI	HStr	RSI+HStr
1548	Mercer	G	3.05.03-1	QCI	WQCI	QCI+WQCI
1552	Coates	G	3.05.03-1	QCI	WQCI	QCI+WQCI
1656	Tasu	G	3.05.03-1	QCI	WQCI	QCI+WQCI
1369	Conuma	G	3.05.04-2	WVI	WVI	WVI+WVI
1370	Canton	G	3.05.04-2	WVI	WVI	WVI+WVI
1371	Sucwoa	G	3.05.04-2	WVI	WVI	WVI+WVI
1290	Maggie	G	3.05.05-3	WVI	WVI	WVI+WVI

GFE_ID	sites	cluster	genetic class	FAZ	MAZ	JAZ
1297	Thorton	G	3.05.06-4	WVI	WVI	WVI+WVI
2003416	Robertson Creek	G	3.05.06-4	WVI	WVI	WVI+WVI
1511	Honna	H	3.05.02-1	QCI	HStr	QCI+HStr
1512	Tarundl	H	3.05.02-1	QCI	HStr	QCI+HStr
1683	Deena	H	3.05.02-1	QCI	HStr	QCI+HStr
1584	Pallant	H	3.05.02-2	QCI	HStr	QCI+HStr
1579	Copper	H	3.05.02-3	QCI	HStr	QCI+HStr
1580	Sheldons Bay	H	3.05.02-4	QCI	HStr	QCI+HStr
1581	Gray Bay	H	3.05.02-4	QCI	HStr	QCI+HStr
691	Seymour (ma)	I	3.04.01-	SC	GStr	SC+GStr
697	Capilano	I	3.04.01-	SC	GStr	SC+GStr
709	Mamquam	I	3.04.01-	SC	GStr	SC+GStr
724	Tenderfoot	I	3.04.01-	SC	GStr	SC+GStr
728	Ashlu	I	3.04.01-	SC	GStr	SC+GStr
760	Chapman	I	3.04.01-	SC	GStr	SC+GStr
824	Phillips	I	3.04.01-	SC	SFj	SC+SFj
831	Heydon	I	3.04.01-	SC	SFj	SC+SFj
847	Glendale	I	3.04.01-	SC	SFj	SC+SFj
853	Kwalate	I	3.04.01-	SC	SFj	SC+SFj
860	Kakweiken	I	3.04.01-	SC	SFj	SC+SFj
1112	Nimpkish	J	3.04.02-1	EVI	SFj	EVI+SFj
1217	Craigflower	J	3.04.02-1	EVI	GStr	EVI+GStr
1221	Sooke	J	3.04.02-1	WVI	WVI	WVI+WVI
1227	Kirby	J	3.04.02-1	WVI	WVI	WVI+WVI
1132	Village Bay	J	3.04.02-2	SC	SFj	SC+SFj
1146	Willow Creek	J	3.04.02-2	EVI	GStr	EVI+GStr
1144	Quinsam	J	3.04.02-3	EVI	GStr	EVI+GStr
1151	Black	J	3.04.02-3	EVI	GStr	EVI+GStr
1156	Puntledge	J	3.04.02-3	EVI	GStr	EVI+GStr
1172	Rosewall	J	3.04.02-3	EVI	GStr	EVI+GStr
1179	Big Qualicum	J	3.04.02-4	EVI	GStr	EVI+GStr
1192	Chase	J	3.04.02-4	EVI	GStr	EVI+GStr
1194	Nanaimo	J	3.04.02-4	EVI	GStr	EVI+GStr
1204	Chemainus	J	3.04.02-4	EVI	GStr	EVI+GStr
1208	Cowichan	J	3.04.02-4	EVI	GStr	EVI+GStr
1211	Goldstream	J	3.04.02-4	EVI	GStr	EVI+GStr
?	Lang Channel S	K	3.04.03-1	?	?	?
795	Myrtle	K	3.04.03-1	SC	GStr	SC+GStr
798	Sliammon	K	3.04.03-1	SC	GStr	SC+GStr
?	Salmon Creek	K	3.04.03-2	?	?	?
?	Upper Birk	K	3.04.03-3	?	?	?
13	Upper Pitt	L	3.04.04-	LFR	GStr	LFR+GStr
14	Alouette	L	3.04.04-	LFR	GStr	LFR+GStr
27	Kanaka	L	3.04.04-	LFR	GStr	LFR+GStr
28	Salmon	L	3.04.04-	LFR	GStr	LFR+GStr
29	Coghlan	L	3.04.04-	LFR	GStr	LFR+GStr
31	Nathan	L	3.04.04-	LFR	GStr	LFR+GStr
33	Whonnock	L	3.04.04-	LFR	GStr	LFR+GStr
34	Stave	L	3.04.04-	LFR	GStr	LFR+GStr

GFE_ID	sites	cluster	genetic class	FAZ	MAZ	JAZ
50	Nicomen	L	3.04.04-	LFR	GStr	LFR+GStr
51	Norrish	L	3.04.04-	LFR	GStr	LFR+GStr
52	Inch	L	3.04.04-	LFR	GStr	LFR+GStr
53	Worth Creek	L	3.04.04-	LFR	GStr	LFR+GStr
60	Siddle Creek	L	3.04.04-	LFR	GStr	LFR+GStr
62	Chilliwack	L	3.04.04-	LFR	GStr	LFR+GStr
181	Chehalis	L	3.04.04-	LFR	GStr	LFR+GStr
43	Chilqua	M	3.04.05-1	LFR	GStr	LFR+GStr
5	Booth Creek	M	3.04.05-2	LFR	GStr	LFR+GStr
30	West Creek	M	3.04.05-3	LFR	GStr	LFR+GStr
3	Brunette River	M	3.04.05-4	LFR	GStr	LFR+GStr
113	Kawkawa Creek	N	3.04.06-	FRCany	GStr	FRCany+GStr
2442	Nahatlatch	N	3.04.07-	FRCany	GStr	FRCany+GStr
2469	Lindquist	O	3.04.08-1	NTh	GStr	NTh+GStr
2746	Saskum Creek	O	3.04.08-1	NTh	GStr	NTh+GStr
279	Finn	O	3.04.08-2.1	NTh	GStr	NTh+GStr
282	Cedar	O	3.04.08-2.1	NTh	GStr	NTh+GStr
283	Cook	O	3.04.08-2.1	NTh	GStr	NTh+GStr
269	Raft	O	3.04.08-2.2	NTh	GStr	NTh+GStr
271	Reg Christie	O	3.04.08-2.2	NTh	GStr	NTh+GStr
274	Avola	O	3.04.08-2.2	NTh	GStr	NTh+GStr
277	Tumtum Creek	O	3.04.08-2.2	NTh	GStr	NTh+GStr
278	Lyon	O	3.04.08-2.2	NTh	GStr	NTh+GStr
281	Blue River	O	3.04.08-2.2	NTh	GStr	NTh+GStr
33045	Birch Island	O	3.04.08-2.2	NTh	GStr	NTh+GStr
719256264	Pig Channel	O	3.04.08-2.2	NTh	GStr	NTh+GStr
257	Louis	O	3.04.08-3	NTh	GStr	NTh+GStr
258	Barriere	O	3.04.08-3	NTh	GStr	NTh+GStr
259	East Barriere	O	3.04.08-3	NTh	GStr	NTh+GStr
262	Lemieux	O	3.04.08-3	NTh	GStr	NTh+GStr
263	Dunn	O	3.04.08-3	NTh	GStr	NTh+GStr
265	Mann	O	3.04.08-3	NTh	GStr	NTh+GStr
2746	Fennell	O	3.04.08-3	NTh	GStr	NTh+GStr
132	Gates	P	3.04.09-1	MFR	GStr	MFR+GStr
133	Bridge	P	3.04.09-1	MFR	GStr	MFR+GStr
2401	McKinley	P	3.04.09-1	MFR	GStr	MFR+GStr
2476	Seton	P	3.04.09-1	MFR	GStr	MFR+GStr
231	Anstey	P	3.04.09-2	STh	GStr	STh+GStr
2373	Hiuihill	P	3.04.09-2	STh	GStr	STh+GStr
214	Spius	P	3.04.09-3	LTh	GStr	LTh+GStr
215	Coldwater	P	3.04.09-3	LTh	GStr	LTh+GStr
216	Bonaparte	P	3.04.09-3	LTh	GStr	LTh+GStr
217	Deadman	P	3.04.09-3	LTh	GStr	LTh+GStr
2369	Guichon	P	3.04.09-3	LTh	GStr	LTh+GStr
237	Salmon SA	P	3.04.09-4	STh	GStr	STh+GStr
222	Sinmax	P	3.04.09-5	STh	GStr	STh+GStr
223	Momich	P	3.04.09-5	STh	GStr	STh+GStr
2744	Harbour Creek	P	3.04.09-5	STh	GStr	STh+GStr
243	Blurton Creek	P	3.04.09-6	STh	GStr	STh+GStr

GFE_ID	sites	cluster	genetic class	FAZ	MAZ	JAZ
253	Creighton	P	3.04.09-6	STh	GStr	STh+GStr
379	Shuswap Lake	P	3.04.09-6	STh	GStr	STh+GStr
2376	Paul Creek	P	3.04.09-6	NTh	GStr	NTh+GStr
232	Eagle	P	3.04.09-7	STh	GStr	STh+GStr
241	Middle Shuswap River	P	3.04.09-7	STh	GStr	STh+GStr
247	Danforth	P	3.04.09-7	STh	GStr	STh+GStr
249	Wap	P	3.04.09-7	STh	GStr	STh+GStr
251	Lang Channel S	P	3.04.09-7	STh	GStr	STh+GStr
251	Ireland	P	3.04.09-7	STh	GStr	STh+GStr
252	Bessette	P	3.04.09-7	STh	GStr	STh+GStr
254	Duteau	P	3.04.09-7	STh	GStr	STh+GStr
255	Harris	P	3.04.09-7	STh	GStr	STh+GStr
2392	McMomee	P	3.04.09-7	STh	GStr	STh+GStr
3542	Senn	P	3.04.09-7	STh	GStr	STh+GStr
1302	Kootowis	Q	3.06-	WVI	WVI	WVI+WVI
1306	Kennedy	Q	3.06-	WVI	WVI	WVI+WVI
1317	Tranquil	Q	3.06-	WVI	WVI	WVI+WVI
1329	Cypre	Q	3.06-	WVI	WVI	WVI+WVI
1107	Quatsese River	R	3.07-1	EVI	SFj	EVI+SFj
1457	Waukwaas	R	3.07-1	WVI	WQCI	WVI+WQCI
1459	Washlawlis	R	3.07-1	WVI	WQCI	WVI+WQCI
1460	Stephens	R	3.07-1	WVI	WQCI	WVI+WQCI
1466	Goodspeed	R	3.07-1	WVI	WQCI	WVI+WQCI
1101	Nahwitti	R	3.07-2	EVI	SFj	EVI+SFj
1105	Tsulquate	R	3.07-3	EVI	SFj	EVI+SFj
1108	Keogh River	R	3.07-3	EVI	SFj	EVI+SFj
1109	Cluxewe	R	3.07-3	EVI	SFj	EVI+SFj
1148	Storie	R	3.07-4	EVI	GStr	EVI+GStr
1106	Quatse	R	3.07-5	EVI	SFj	EVI+SFj
2001106	Glenlion	R	3.07-5	EVI	SFj	EVI+SFj
1231	San Juan	S	3.08-	WVI	WVI	WVI+WVI
1242	Nitinat	S	3.08-	WVI	WVI	WVI+WVI
1249	Pachena	S	3.08-	WVI	WVI	WVI+WVI
1252	Sarita	S	3.08-	WVI	WVI	WVI+WVI
1021	Khutze	T	3.01.01-1	NC	HStr	NC+HStr
1023	Aaltanhash	T	3.01.01-1	NC	HStr	NC+HStr
1087	Kiskosh	T	3.01.01-1	HecLow	HStr	HecLow+HStr
961	Quatlena	T	3.01.01-2.1	NC	HStr	NC+HStr
1034	Kemano River	T	3.01.01-2.1	NC	HStr	NC+HStr
1029	Paril River	T	3.01.01-2.2	NC	HStr	NC+HStr
1030	Kiltuish River	T	3.01.01-2.2	NC	HStr	NC+HStr
1041	Hugh Creek	T	3.01.01-2.2	NC	HStr	NC+HStr
986	Martin River	T	3.01.01-3	NC	HStr	NC+HStr
1798	Jenny Inlet	T	3.01.01-4	NC	HStr	NC+HStr
991	Roscoe	T	3.01.01-5	NC	HStr	NC+HStr
993	Quartcha	T	3.01.01-5	NC	HStr	NC+HStr
1901	Turn Creek	T	3.01.01-6.2	HecLow	HStr	HecLow+HStr
SEAK	Reflection	T	SEAK	foreign	foreign	foreign
943	Sheemahant	U	3.01.02-1	RSI	HStr	RSI+HStr

GFE_ID	sites	cluster	genetic class	FAZ	MAZ	JAZ
1748	Lachmach	U	3.01.02-1	LNR-P	NSKEst	LNR-P+NSKEst
1082	Gilttoyees	V	3.01.03-1	NC	HStr	NC+HStr
1050	Kitimat	V	3.01.03-2	NC	HStr	NC+HStr
850	Klinaklini	V	3.01.03-3	HK	SFj	HK+SFj
2000850	Devereux	V	3.01.03-3	HK	SFj	HK+SFj
?	Paisla	V	3.01.03-4	?	?	?
819	Homathko	V	3.01.03-4	HK	SFj	HK+SFj
968	Bella Coola	V	3.01.03-5	BCD	HStr	BCD+HStr
970	Atnarko	V	3.01.03-5	BCD	HStr	BCD+HStr
969	Snootli	V	3.01.03-6	BCD	HStr	BCD+HStr
971	Necleetsconnay	V	3.01.03-6	BCD	HStr	BCD+HStr
2242	Thorsen	V	3.01.03-6	BCD	HStr	BCD+HStr
3403	Salloomt	V	3.01.03-6	BCD	HStr	BCD+HStr
3455	Hagensborg	V	3.01.03-6	BCD	HStr	BCD+HStr
446	Green	W	3.01.04-	LSK	NSKEst	LSK+NSKEst
447	Ecstall	W	3.01.04-	LSK	NSKEst	LSK+NSKEst
2148	Scud	X	3.01.06-1	LStk	TBFj	LStk+TBFj
2138	Porcupine	X	3.01.06-2	LStk	TBFj	LStk+TBFj
2193	Verrett River	X	3.01.06-3	LStk	TBFj	LStk+TBFj
212203	Tulsequah	X	3.01.06-4	Taku	TBFj	Taku+TBFj
647	Zolzap	Y	3.01.07-	LNR-P	NSKEst	LNR-P+NSKEst
651	Tseax	Y	3.01.07-	LNR-P	NSKEst	LNR-P+NSKEst
459	Kasiks	Y	3.01.08-	LSK	NSKEst	LSK+NSKEst
460	Gitnadoix	Y	3.01.08-	LSK	NSKEst	LSK+NSKEst
473	Zymagotitz	Y	3.01.08-	LSK	NSKEst	LSK+NSKEst
504	Exchamsiks	Y	3.01.08-	LSK	NSKEst	LSK+NSKEst
521	Kalum	Y	3.01.09-	LSK	NSKEst	LSK+NSKEst
530	Clear	Y	3.01.09-	LSK	NSKEst	LSK+NSKEst
2104	Hadenschild	Y	3.01.09-	LSK	NSKEst	LSK+NSKEst
215	Coldwater	Y	3.01.10-	LTh	GStr	LTh+GStr
510	Clearwater	Y	3.01.10-	LSK	NSKEst	LSK+NSKEst
511	Schulbuckhand	Y	3.01.10-	LSK	NSKEst	LSK+NSKEst
518	Sockeye	Y	3.01.10-	LSK	NSKEst	LSK+NSKEst
523	Deep	Y	3.01.11-	LSK	NSKEst	LSK+NSKEst
478	Singlehurst	Z	3.01.12-1	LSK	NSKEst	LSK+NSKEst
7990598	Meziadin	Z	3.01.12-2	UNR	NSKEst	UNR+NSKEst
2107	Babine fence	Z	3.01.12-3.1	MSK	NSKEst	MSK+NSKEst
2107	Upper Babine	Z	3.01.12-3.2	MSK	NSKEst	MSK+NSKEst
596	Boucher	Z	3.01.12-3.3	MSK	NSKEst	MSK+NSKEst
498	Slamgeesh	Z	3.01.12-4.1	USK	NSKEst	USK+NSKEst
499	Damshilgwit	Z	3.01.12-4.2	USK	NSKEst	USK+NSKEst
501	Kluatantan	Z	3.01.12-4.3	USK	NSKEst	USK+NSKEst
7990593	Motase	Z	3.01.12-4.3	USK	NSKEst	USK+NSKEst
620	Sustut	Z	3.01.12-4.4	USK	NSKEst	USK+NSKEst
488	Kitwanga	Z	3.01.12-5	MSK	NSKEst	MSK+NSKEst
566	Kispiox	Z	3.01.12-5	MSK	NSKEst	MSK+NSKEst
541	Bulkley	Z	3.01.12-6	MSK	NSKEst	MSK+NSKEst
550	Toboggan	Z	3.01.12-6	MSK	NSKEst	MSK+NSKEst
556	Morice	Z	3.01.12-6	MSK	NSKEst	MSK+NSKEst

GFE_ID	sites	cluster	genetic class	FAZ	MAZ	JAZ
558	Owen	Z	3.01.12-6	MSK	NSKEst	MSK+NSKEst
remaining sites in the Russian Federation, Alaska and the southern USA were not classified						

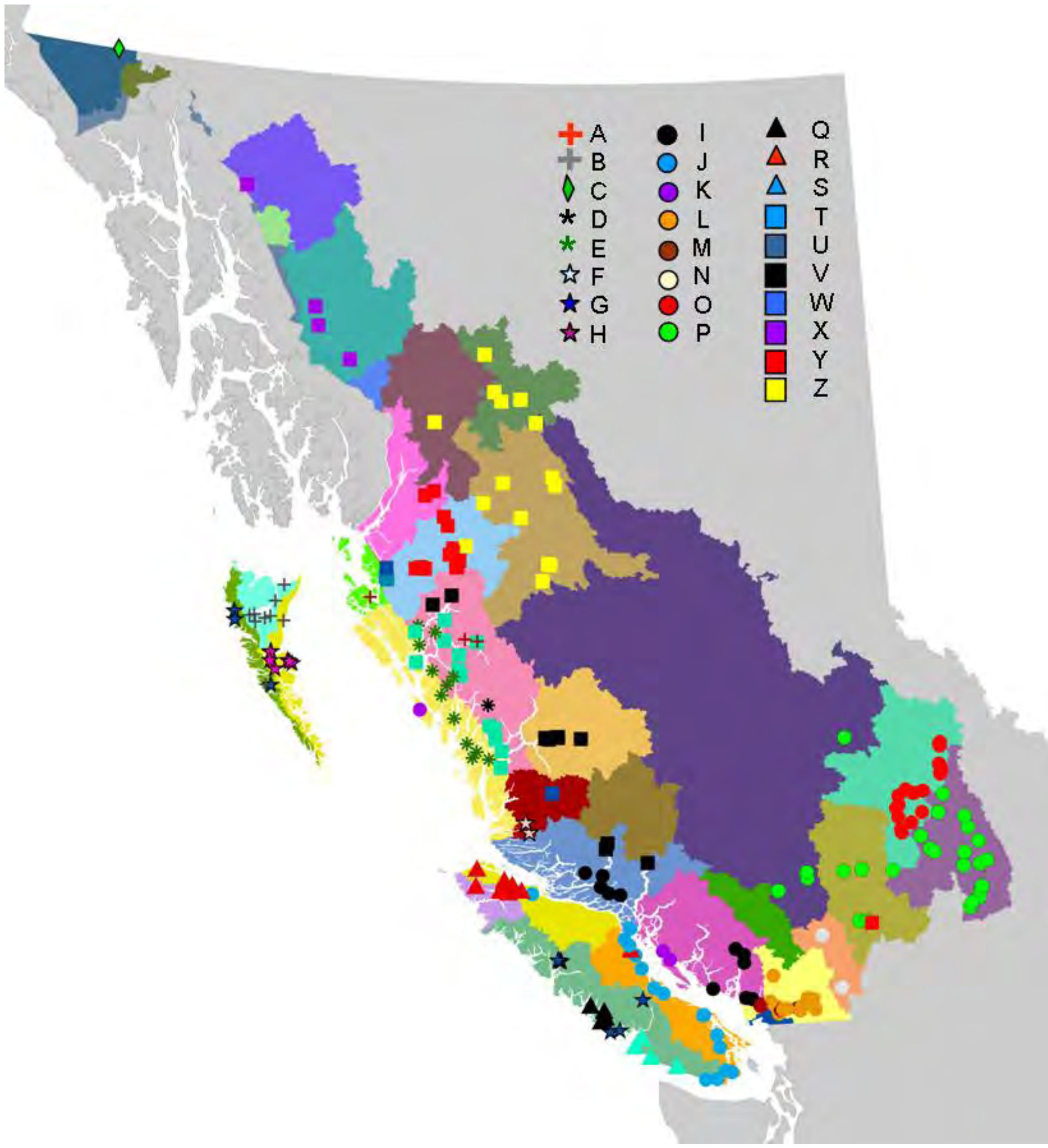


Figure 32. A map showing the relationship between the genetic clusters and JAZ ecotypic CUs of coho salmon.

Table 21. The initial crosswalk of the ecotypic CUs with the genetic classification at the cluster level for coho salmon. The table is divided into northern and southern parts. There is some overlap in the genetic structure north to south (i.e., southern representatives in predominantly northern clusters) but no overlap in the converse direction.

Northern JAZ

genetic classification		JAZ acronym																	
cluster	class†	HK+ SFj	RSI+ HStr	BCD+ HStr	QCI+ HStr	QCI+ WQCI	QCI+ NQCI	HecLow+ HStr	NC+ HStr	HecLow+ NSKEst	LSK+ NSKEst	MSK+ NSKEst	USK+ NSKEst	LNR-P+ NSKEst	UNR+ NSKEst	LStk+ TBFj	Taku+ TBFj	Alsek+ AKCst	row total
A	1.1								2	1									3
B	1.2				1		8												9
C	2.1																	1	1
T	3.1.1							2	11										13
U	3.1.2		1											1					2
V	3.1.3	3		7					2										12
W	3.1.4										2								2
X	3.1.5															3	1		4
Y	3.1.6										12			2					14
Z	3.1.7										1	8	5		1				15
D	3.2								1										1
E	3.3							7	5										12
F	3.5.1		2																2
H	3.5.2				7														7
G	3.5.3					3													9

† This is a partial code that corresponds to the cluster only.

Table 21 continued

Southern JAZ

genetic classification		JAZ acronym														
cluster	class†	BB+ GStr	LFR+ GStr	LILL + GStr	FRCany + GStr	MFR + GStr	LTh+ GStr	STh+ GStr	NTh+ GStr	SC+ GStr	SC+ SFj	EVI+ GStr	EVI+ SFj	WVI+ WVI	WVI+ WQCI	sites in cluster
I	3.4.1									6	5					11
J	3.4.2										1	12	1	2		16
K	3.4.3									2						2
L	3.4.4		15													15
M	3.4.5		4													4
N	3.4.6				2											2
O	3.4.7								19							19
P	3.4.8					4	5	19	1							29
G	3.5.3													6		9
Q	3.6													4		4
R	3.7											1	7		4	12
S	3.8													4		4

† This is a partial code that corresponds to the cluster only.

Table 22. The crosswalk of the CUs following step 2 with the genetic classification at the cluster level for coho salmon. The table is divided into northern and southern parts. Three ecotypic CUs were partitioned resulting in the addition of four CUs. Two large boundary changes resulted in the renaming of two ecotypic CUs.

Northern CUs

genetic classification		Conservation Unit after step 2																
cluster	class	HK+ SFj	Smith	Rivers	BCD+ HStr	QCI+ HStr	QCI+ WQCI	NQCI	HecLow+ HStr	NC+ HStr	HecLow+ NSKEst	LSK+ NSKEst	MSK+ NSKEst	USK+ NSKEst	LNR-P+ NSKEst	UNR+ NSKEst	LStk+ TBFj	Taku+ TBFj	Alsek+ AKCst
A	1.1									2	1								
B	1.2						1	8											
C	2.1																		1
T	3.1.1									13									
U	3.1.2			1											1				
V	3.1.3	3			7					2									
W	3.1.4											2							
X	3.1.5																3	1	
Y	3.1.6											12			2				
Z	3.1.7											1	8	5		1			
D	3.2									1									
E	3.3								10	2									
F	3.5.1		2																
H	3.5.2					7													
G	3.5.3						3												

Table 22 continued

<u>Southern CUs</u>

genetic classification		Conservation Unit after step 2																
cluster	class	BB+ GStr	LFR + GStr	LILL + GStr	FRCany + GStr	MFR+ GStr	LTh+ GStr	STh+ GStr	NTh+ GStr	Howe-Burrard	SC+ GStr	SC+ SFj	EVI+ GStr	EVI+ SFj	Nahwitti	JdF	WVI + WVI	CLAY
I	3.4.1									6		5						
J	3.4.2												15	1				
K	3.4.3										2							
L	3.4.4		15															
M	3.4.5		4															
N	3.4.6				2													
O	3.4.7								19									
P	3.4.8					4	5	19	1									
G	3.5.3																6	
Q	3.6																	4
R	3.7												1		11			
S	3.8															4		

Table 23. Summary statistics of dates of peak spawning for the coho spawning locations in British Columbia. The 1532 sites are categorized by the provisional CUs established in step 2.

		Day-of-year and season of peak spawning						
		Minimum		Mean		Maximum		range
CU after step 2	N sites	DOY	season	DOY	season	DOY	season	(d)
BB+GStr	1			299.0	MFALL			-
LFR+GStr	90	306.5	MFALL	339.6	LFALL	394.0	MWIN	87.5
LILL+GStr	13	301.5	MFALL	322.6	MFALL	333.7	LFALL	32.2
FRCany+GStr	8	301.0	MFALL	324.5	LFALL	339.3	LFALL	38.3
MFR+GStr	12	310.0	MFALL	320.8	MFALL	328.5	LFALL	18.5
LTh+GStr	6	312.1	MFALL	319.2	MFALL	330.5	LFALL	18.4
STh+GStr	38	309.0	MFALL	317.3	MFALL	330.0	LFALL	21.0
NTh+GStr	37	311.4	MFALL	319.2	MFALL	327.0	LFALL	15.6
Howe-Burrard	51	262.5	LSUM	324.2	LFALL	370.6	EWIN	108.1
SC+GStr	47	268.9	EFALL	312.1	MFALL	344.3	LFALL	75.5
SC+SFj	93	258.0	LSUM	289.0	EFALL	321.0	MFALL	63.0
EVI+GStr	98	289.9	EFALL	325.8	LFALL	359.0	EWIN	69.1
EVI+SFj	13	256.0	LSUM	291.1	EFALL	313.5	MFALL	57.5
Nahwitti	65	258.0	LSUM	292.6	EFALL	334.0	LFALL	76.0
JdF	25	295.9	MFALL	314.7	MFALL	347.0	LFALL	51.1
WVI+WVI	105	261.7	LSUM	306.3	MFALL	331.5	LFALL	69.9
CLAY	43	288.3	EFALL	315.1	MFALL	327.0	LFALL	38.8
HK+SFj	3	276.1	EFALL	282.9	EFALL	288.9	EFALL	12.7
Smith	10	258.0	LSUM	287.8	EFALL	324.0	LFALL	66.0
Rivers	23	278.5	EFALL	295.6	MFALL	313.3	MFALL	34.8
BCD+HStr	22	283.1	EFALL	313.6	MFALL	354.8	EWIN	71.7
QCI+HStr	117	270.0	EFALL	290.9	EFALL	307.7	MFALL	37.7
QCI+WQCI	51	258.0	LSUM	287.5	EFALL	305.0	MFALL	47.0
NQCI	27	279.8	EFALL	290.4	EFALL	305.8	MFALL	26.0
HecLow+HStr	156	248.8	LSUM	273.6	EFALL	319.5	MFALL	70.7
NC+HStr	100	227.0	MSUM	284.3	EFALL	329.0	LFALL	102.0
HecLow+NSKEst	29	254.3	LSUM	281.7	EFALL	298.8	MFALL	44.5
LSK+NSKEst	71	281.5	EFALL	309.0	MFALL	324.0	LFALL	42.5
MSK+NSKEst	68	253.3	LSUM	291.4	EFALL	313.6	MFALL	60.3
USK+NSKEst	12	258.0	LSUM	279.2	EFALL	292.7	EFALL	34.7
LNR-P+NSKEst	46	227.0	MSUM	290.5	EFALL	326.8	LFALL	99.8
UNR+NSKEst	13	273.4	EFALL	287.1	EFALL	310.8	MFALL	37.4
Overall	1532	227.0	MSUM	301.3	MFALL	394.0	MWIN	167.0

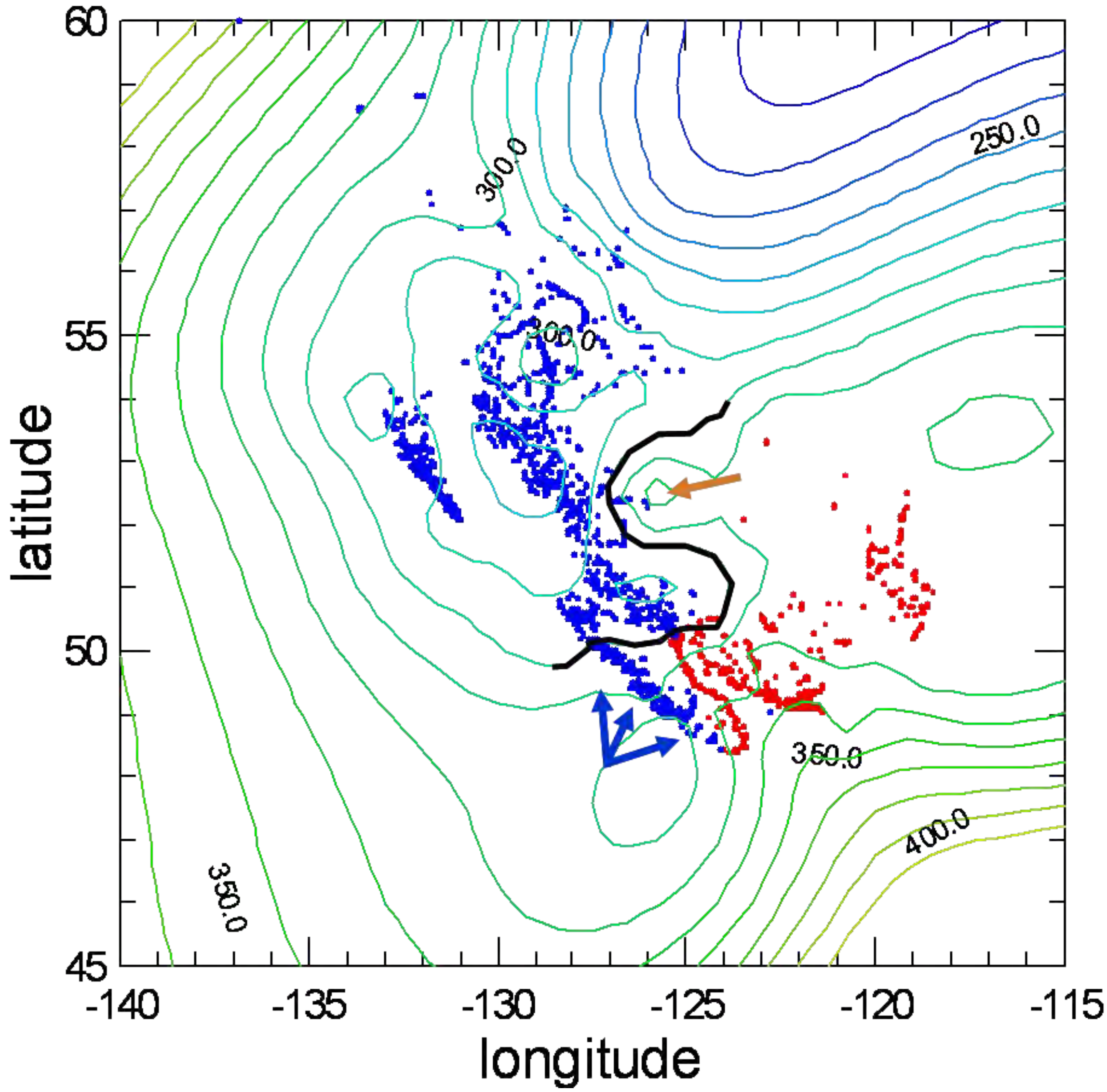


Figure 33. A geographic contour plot of the DOY of peak spawning for coho salmon in British Columbia. A slight tendency for spawning to be later in the south and the southern interior can be discerned. The red dots are from JAZ predominated by sites in genetic clusters I to P inclusive. The black line identifies the approximate criterion for separating the blue and red dots established by a simple discriminant function. The arrows indicate the two areas where sites were misclassified (blue: WVI and gold: BCD).

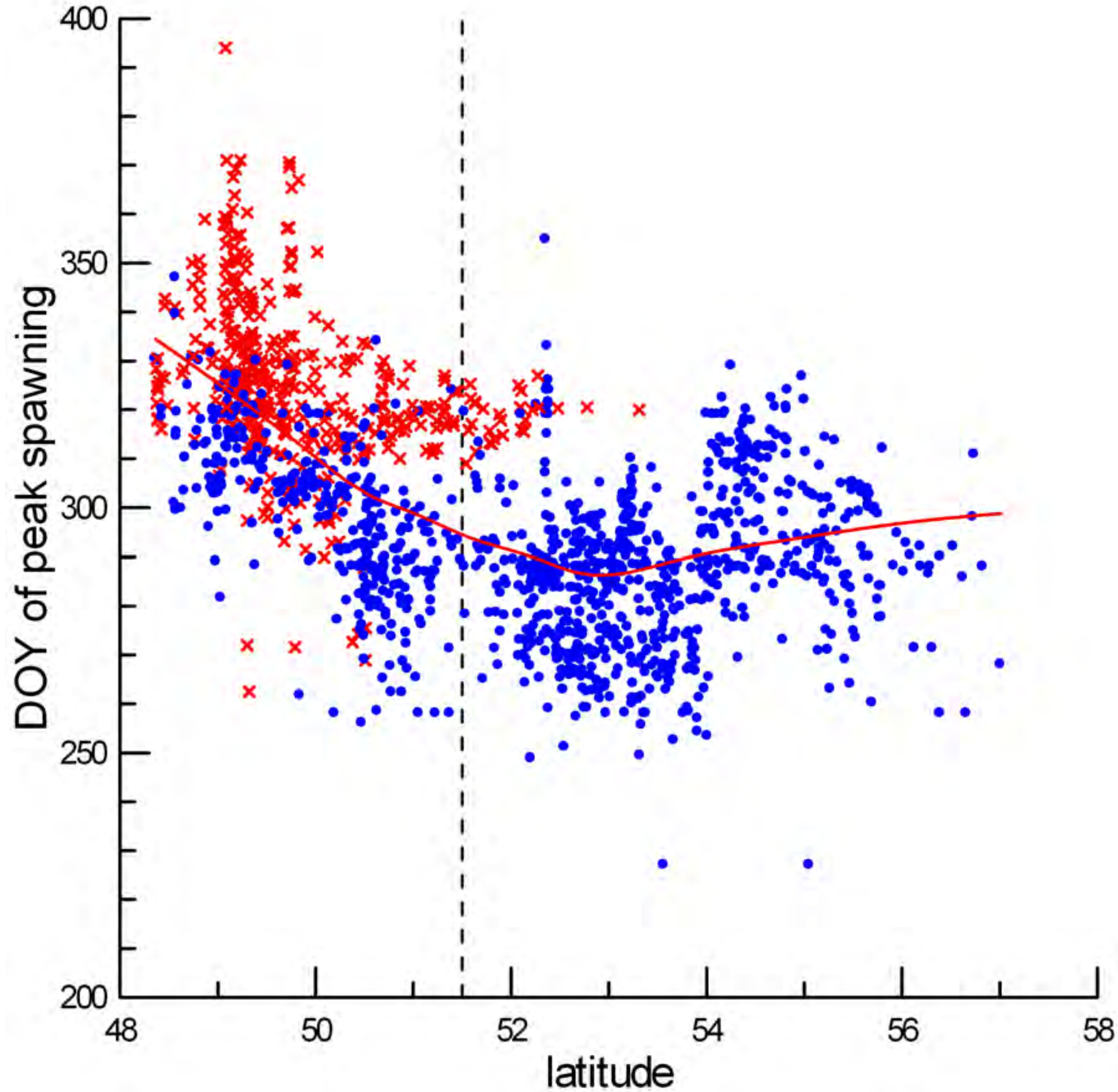


Figure 34. For coho salmon, a plot of the DOY of peak spawning against latitude. The red crosses are sites that drain into the Strait of Georgia. The vertical dashed line marks the discontinuity in the DOY of peak spawning observed in chum salmon at 51.5°N. A similar discontinuity is apparent in coho salmon. The solid red line is a LOWESS smoothing function applied to all of the sites.

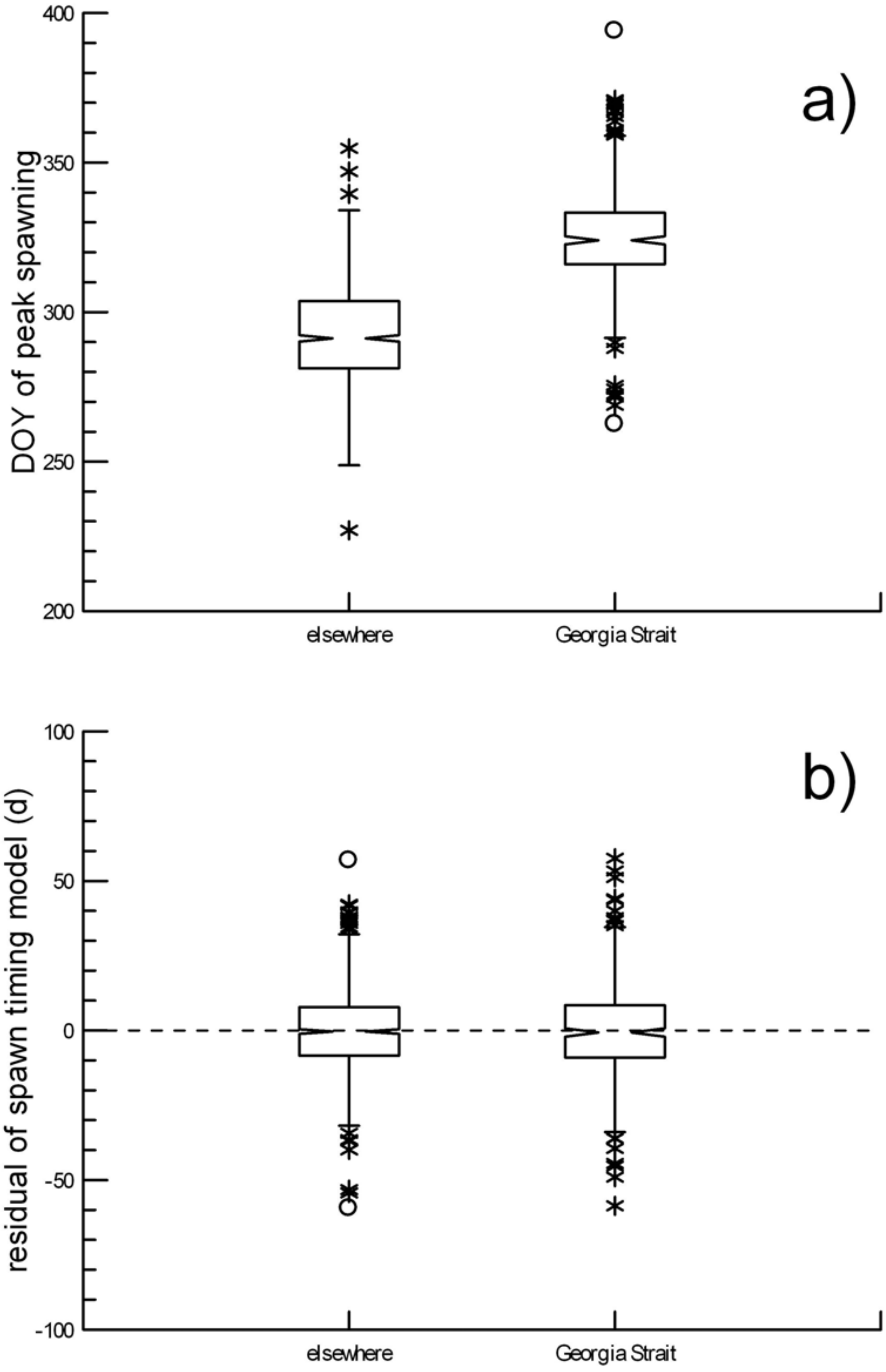


Figure 35. Box plots of a) the mean DOY of peak spawning for coho populations sites draining into the Strait of Georgia or elsewhere and b) the residual of the spawn timing model. The difference in mean spawning date is highly significant (*P*<<0.0001) but there is no difference in the mean residuals.

Table 24. GLM for mean day of peak spawning for coho salmon in British Columbia.

Variables	Levels and associated genetic clusters	
GRPI2P$	elsewhere	genetic clusters A to H, Q to Z, inclusive
	GStr	genetic clusters I, J, K, L, M, O, P

Dependent Variable	day of peak spawning (DOY) [variable: DOY_PK_SPAWN]
N	1493
Multiple R	0.784
Squared Multiple R	0.614

Model

Effect	Coefficient	StdErr	df	F	p-value	
TRIB_GRAD	0.451	0.0585	1	59.4	<<0.001	mean gradient of all tributaries (°)
PPT_AUG	-0.251	0.0139	1	326.90	<<0.001	mean precipitation in August (mm)
PPT_DEC	0.0410	0.00440	1	86.7	<<0.001	mean precipitation in December (mm)
AT_AUG	1.844	0.38	1	23.1	<<0.001	mean air temperature in August (°C)
MAX_P_MAG	0.000243	0.000024	1	103.6	<<0.001	a measure of hydrological stability
GRPI2P$	-7.56	0.634	1	142.0	<<0.001	genetic cluster, see above

Analysis of Variance

Source	Type III SS	df	Mean Squares	F-ratio	p-value
TRIB_GRAD	11635.8	1	11635.8	59. 4	<<0.001
PPT_AUG	64081.2	1	64081.2	326.9	<<0.001
PPT_DEC	16999.8	1	16999.8	86.7	<<0.001
MAX_P_MAG	20301.3	1	203013	103.6	<<0.001
GRPI2P$	27839. 1	1	278391	142.	<<0.001
AT_AUG	4527. 9	1	4527.9	23.1	<<0.001
Error	2.913E+005	1486	196.0		

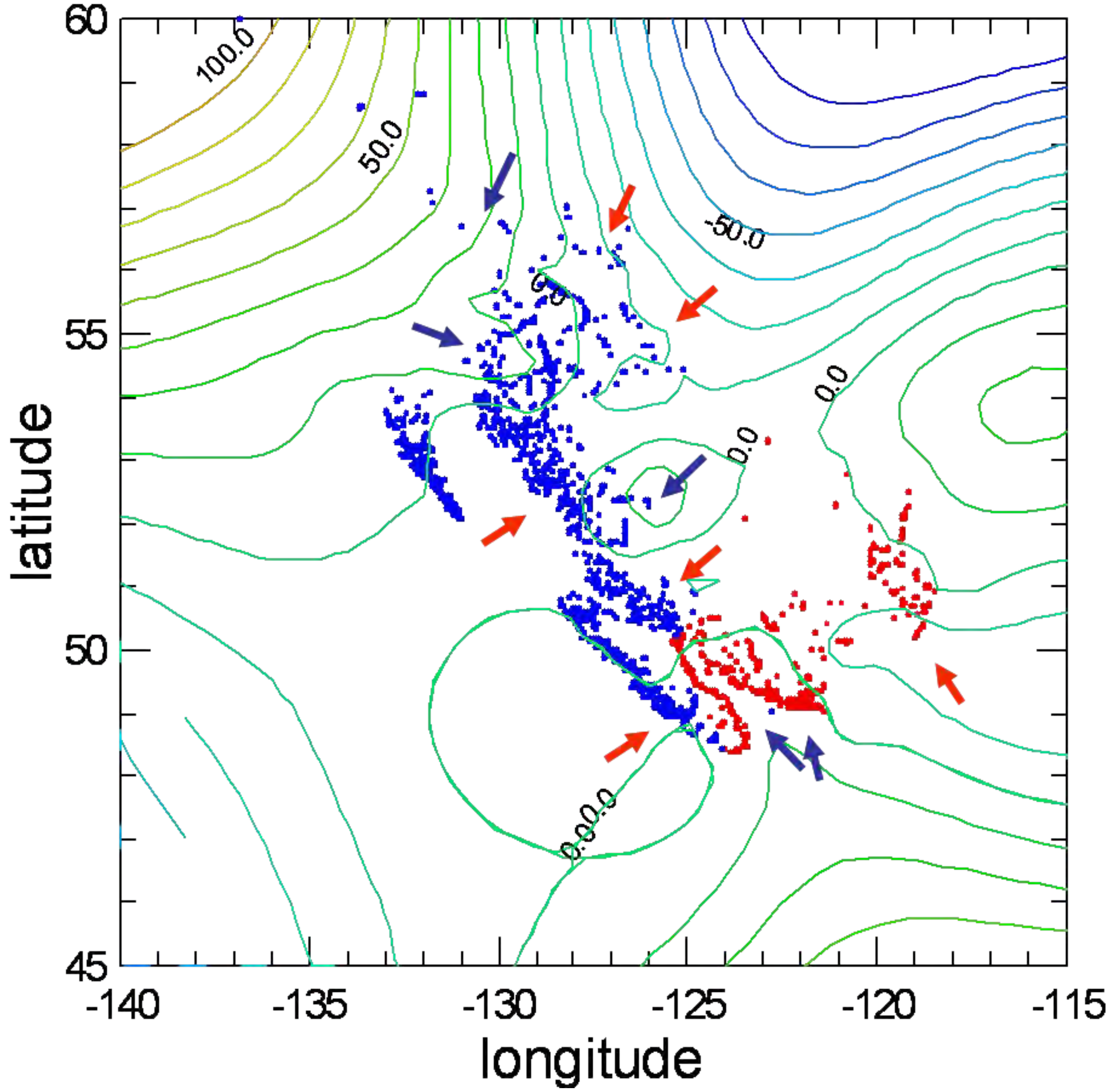


Figure 36. A contour map of the residuals from the spawning time model for coho salmon in British Columbia. The blue arrows indicate areas where the model predicted earlier spawning than was observed (i.e., positive residuals). The red arrows indicate areas where spawning was consistently earlier than predicted.

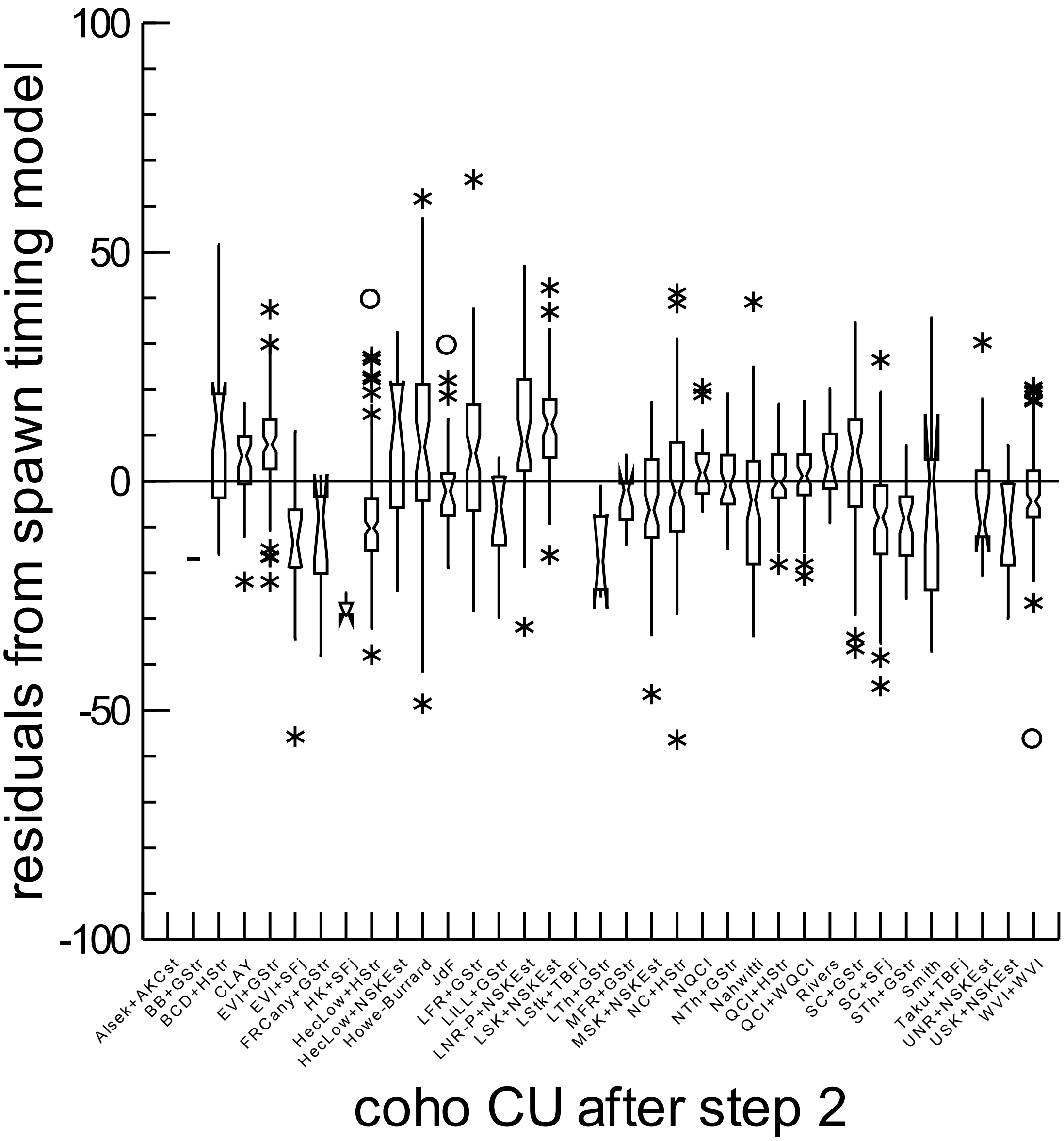


Figure 37. Box plots of the residuals for the coho spawn timing model categorized by the provisional CUs after step 2. The CUs are arranged alphabetically.

Table 25. A habitat discrimination for genetic clusters L and M of coho salmon in the lower Fraser River.

Group Frequencies

Cluster L: 32	Cluster M: 9

Group Means

variable	Cluster L	Cluster M	variable description
MS_GRAD	1.4	2.3	mean mainstem gradient (°)
MS_GR_8_12	1.6	1.0	percent of mainstem or tributaries with
T_GR_2_8	16.4	29.9	indicated gradient
TUNDRA_PC	5.7	0.3	percent of watershed as high elevation tundra
LAKE_PC	4.6	2.8	percent of watershed as lake
AT_AUG	16.6	17.3	
AT_OCT	8.9	10.0	mean air temperature in indicated moth (°C)
AT_DEC	1.1	2.6	
VFW_MEAN	2.7	7.4	mean width of the valley floor (km)
KFAC_LOG	4.169	4.196	an index of the flashiness of the stream

Stepping Summary

	F(+ent,-rem)	Approx. F-ratio	p-value
VFW_MEAN	11.6	11.6	0.0015
AT_DEC	10.8	12.6	<0.001
KFAC_LOG	9.4	13.4	<0.001
T_GR_2_8	5.1	12.5	<0.001
TUNDRA_PC	3.1	11.2	<0.001
MS_GR_8_12	3.7	10.7	<0.001
VFW_MEAN	-1.5	12.3	<0.001
AT_OCT	3.4	11.5	<0.001
AT_AUG	8.0	13.1	<0.001

Jackknifed Classification Matrix

	Cluster L	Cluster M	%correct
Cluster L	31	1	97
Cluster M	0	9	100
Total	31	10	98

Canonical Discriminant Functions : Standardized by Within Variances

	1		1
MS_GR_8_12	0.493	AT_OCT	13.051
T_GR_2_8	-0.602	AT_DEC	-9.344
TUNDRA_PC	-1.547	KFAC_LOG	-1.996
AT_AUG	-6.626		

Canonical Scores of Group Means

Cluster L	0.861	**Cluster M**	-3.063

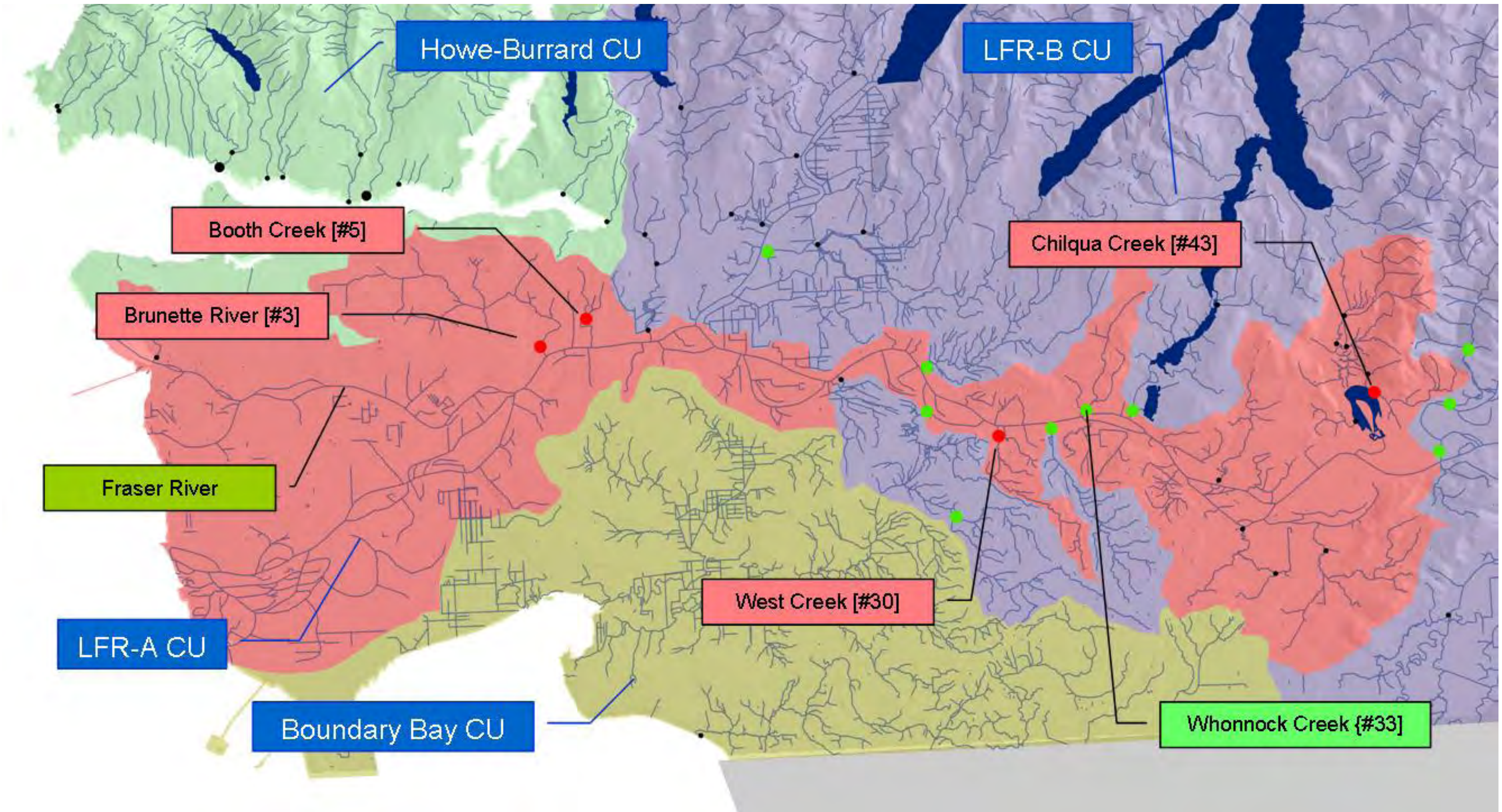


Figure 38. A map showing the two CUs in the lower Fraser River. The small black dots are coho sites in our database. The larger red and green dots are sites where genetic sample were available. The pink polygon with solid red dots is the new lower Fraser-B CU. The light blue polygon with solid green dots is the lower Fraser-A CU. One of the green dots (Whonnock Creek) appears misclassified due to a limitation of the map.

Table 26. A summary of the 43 Conservation Units for coho salmon in index order, which is roughly geographical from south to north. The number of sites indicated is the total in our database and is not to be interpreted as the number of sites where coho salmon are persistently found. The short names are suggestions only.

Conservation Unit	acronym	index	number of sites	classification step	comments
Boundary Bay	BB	1	1	ecotypic	
Lower Fraser	LFR-A	2	77	habitat	suggested by genetics
Lower Fraser-B	LFR-B	3	15	habitat	suggested by genetics
Lillooet	LILL	4	13	ecotypic	confirmed by genetics
Fraser Canyon	FRCany	5	9	ecotypic	confirmed by genetics
Middle Fraser	MFR	6	12	timing	
Lower Thompson	LTHOM	7	7	habitat	three CUs in the same genetic cluster
South Thompson	STHOM	8	40	habitat	
North Thompson	NTHOM	9	38	ecotypic	
Howe Sound-Burrard Inlet	Howe-Burrard	10	51	genetic	
Georgia Strait Mainland	SC+GStr	11	47	ecotypic	
S Coastal Streams| QCStr-JStr-SFjords	SC+SFj	12	95	ecotypic	confirmed by genetics
Georgia Strait-E Vancouver Island	EVI+GStr	13	100	ecotypic	confirmed by genetics
E Vancouver Island |JStr-SFjords	EVI+SFj	14	13	ecotypic	confirmed by timing
Nahwitti Lowland	Nahwitti	15	67	genetic	
Juan de Fuca-Pachena	JdF	16	25	genetic	
W Vancouver Island	WVI	17	108	genetic	
Clayoquot	CLAY	18	45	genetic	
Homathko - Klinaklini Rivers	HK	19	4	ecotypic	confirmed by genetics
Smith Inlet	Smith	20	11	genetic	
Rivers Inlet	Rivers	21	23	genetic	
Bella Coola - Dean Rivers	BCD	22	23	ecotypic	confirmed by genetics
Queen Charlottes | Hecate Strait - Q.C. Sound	EQCI	23	117	ecotypic	confirmed by genetics
Queen Charlottes | Outer Graham Island	WQCI	24	56	ecotypic	confirmed by genetics
QCI-Graham Island Lowlands	NQCI	25	28	genetic	

Conservation Unit	acronym	index	number of sites	classification step	comments
Mussel-Kynoch	MusKyn	26	12	genetic	
Hecate Strait Mainland	HecLow+HStr	27	165	ecotypic	confirmed by genetics
Brim-Wahoo	BRIM	28	2	genetic/habitat	suggested by genetics
Douglas Channel-Kitimat Arm	DOUG	29	31	genetic/habitat	suggested by genetics
N Coastal Streams	NCS	30	57	ecotypic	
Skeena Estuary	SKEst	31	21	ecotypic	confirmed by genetics
Lower Skeena	LSKNA	32	74	ecotypic	confirmed by genetics
Middle Skeena	MSKNA	33	76	ecotypic	confirmed by genetics
Upper Skeena	USKNA	34	12	ecotypic	confirmed by genetics
Lower Nass	LNASS	35	22	habitat	suggested by genetics
Upper Nass	UNASS	36	13	ecotypic	confirmed by genetics
Portland Sound-Observatory Inlet-Portland Canal	PORT	37	24	habitat	suggested by genetics
Unuk River	UNUK	38	0	ecotypic	
Lower Stikine	LSTK	39	3	ecotypic	
Whiting River	Whiting	40	0	ecotypic	
Taku	Taku	41	4	ecotypic	
Lynn Canal	LYNN	42	0	ecotypic	
Alsek	Alsek	43	1	ecotypic	confirmed by genetics

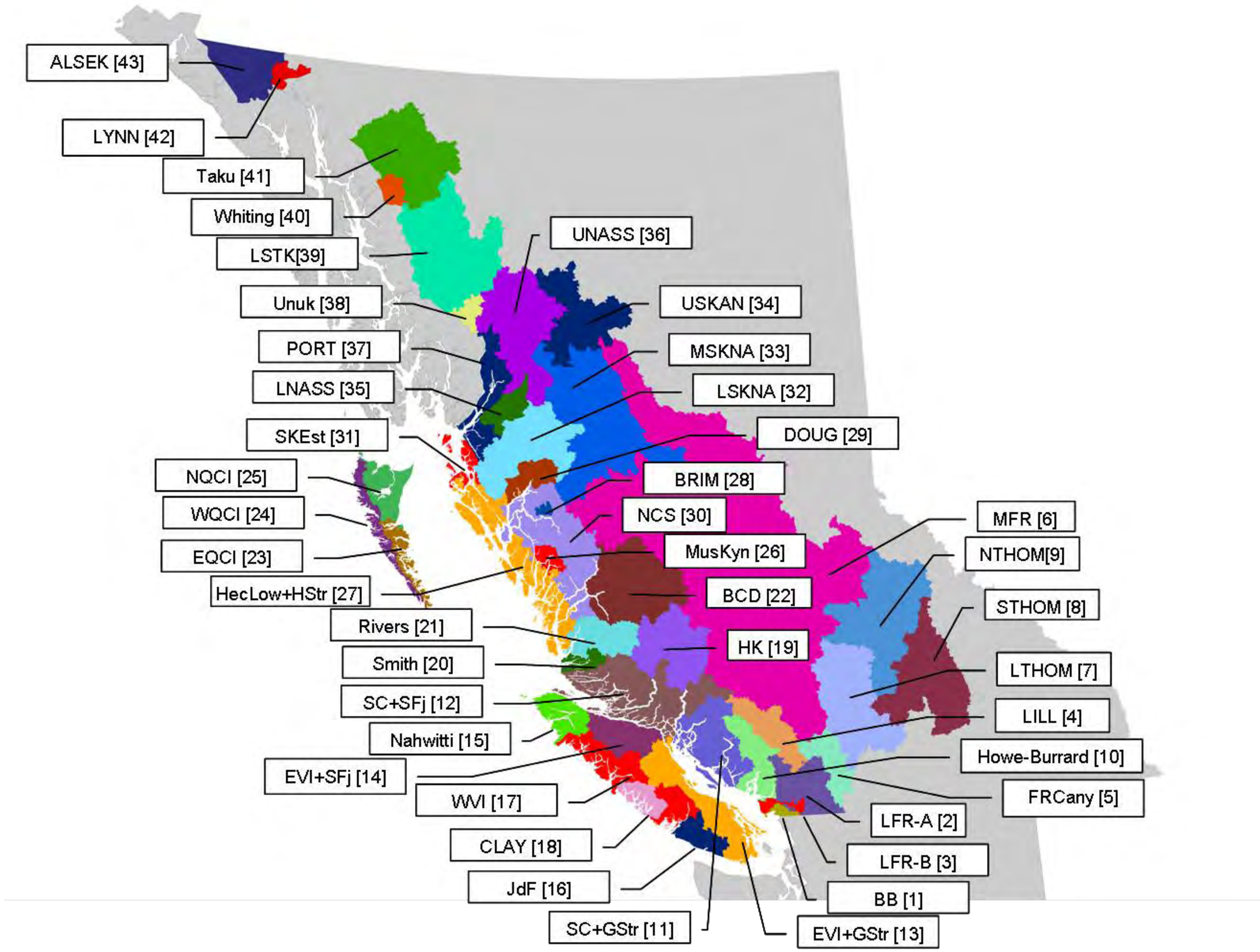


Figure 39. A map showing the 43 CUs of coho salmon in British Columbia.

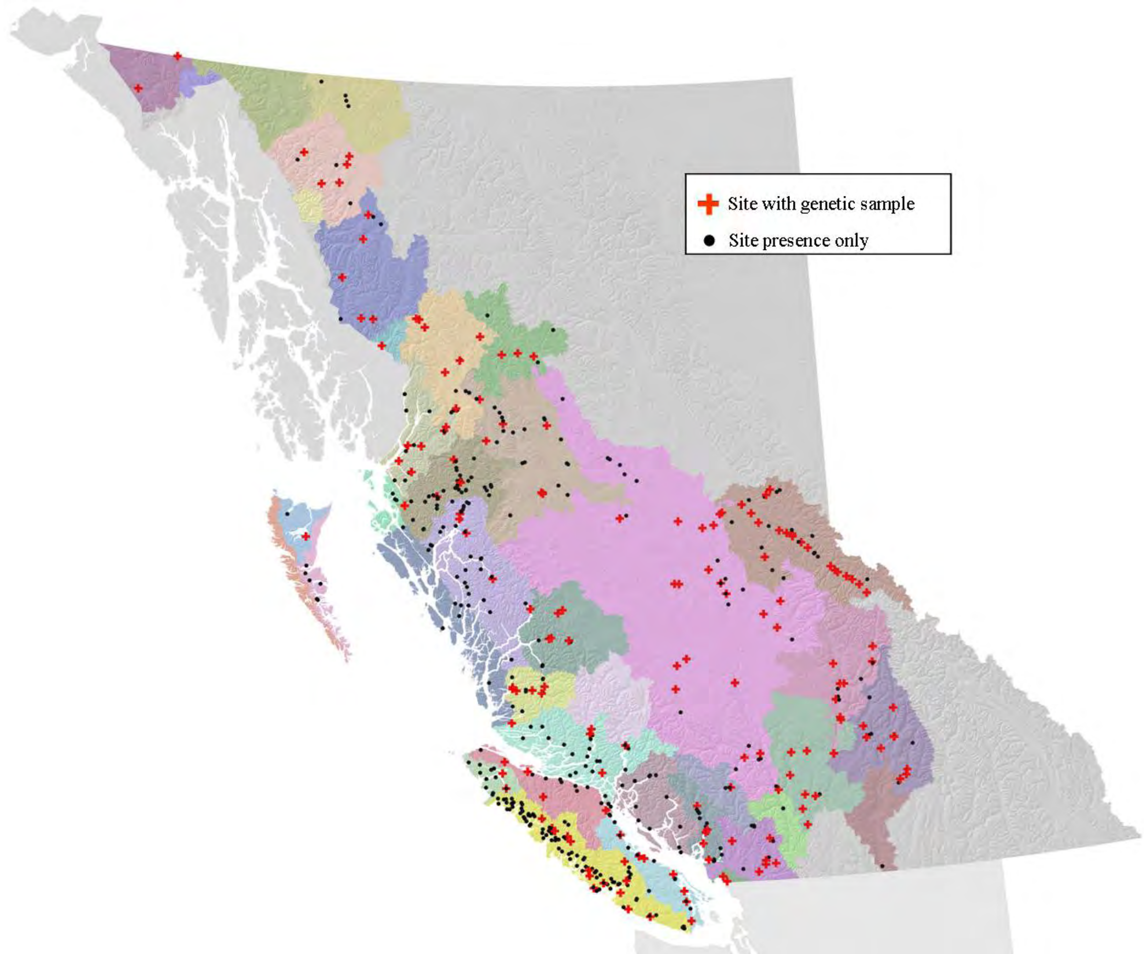


Figure 40. A map showing the location of the 559 sites within British Columbia with chinook salmon. The red crosses are sites where genetic samples were available. The colored polygons are the JAZ ecotypic CUs either where chinook salmon was documented or where the species is probably present.

Table 27. A summary of the 37 ecotypic Conservation Units of chinook salmon in British Columbia.

JAZ	JAZ Acronym	JAZ code	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic clusters
Okanagan | OR-WA Coastal	OK+ORWA	1	1	1	100%	documented	01.04.02	D
Boundary Bay | Georgia Strait	BB+GStr	2	2	8	25%	documented	01.02.01-02.04; 01.02.01-02.05;	A
Lower Fraser | Georgia Strait	LFR+GStr	3	9	133	7%	documented	03.01.01; 03.01.02-01; 03.01.02-02; 04.01.03; 04-11	G; H; J
Lillooet | Georgia Strait	LILL+GStr	4	7	16	44%	documented	03.01.02-03	G
Fraser Canyon | Georgia Strait	FRCany+GStr	5	1	20	5%	documented	-	-
Middle Fraser | Georgia Strait	MFR+GStr	6	42	176	24%	documented	04.01.01; 04-01; 04-02; 04-03; 04-04; 04-05.01; 04-05.02; 04-06; 04-07.02; 04-08; 04-09	H; J
Upper Fraser | Georgia Strait	UFR+GStr	7	38	45	84%	documented	04-07.01; 04-10; 04-11; 04-12.01; 04-12.02; 04-13; 04-14.01;	J

JAZ	JAZ Acronym	JAZ code	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic clusters
							04-14.02; 04-14.03; 04-14.04; 04-14.05; 04-14.06	
Lower Thompson | Georgia Strait	LTh+GStr	8	9	20	45%	documented	04.01.02; 04.02.02-02; 04.02.02-03.01; 04.02.02-03.02	H; I
South Thompson | Georgia Strait	STh+GStr	9	15	66	23%	documented	04.01.02; 04.01.04; 04.01.05-01.01; 04.01.05-01.02; 04.01.05-02.01; 04.01.05-02.02; 04.01.05-02.03	H
North Thompson | Georgia Strait	NTh+GStr	10	14	47	30%	documented	04.02.01-01.01; 04.02.01-01.02; 04.02.01-01.03; 04.02.01-02.01; 04.02.01-02.02; 04.02.02-01	I
S Coastal Streams | Georgia Strait	SC+GStr	11	35	131	27%	documented	03.01.01; 03.02.03-01; 03.02.03-02; 03.02.03-03	G
S Coastal Streams | QCStr-JStr-SFjords	SC+SFj	12	22	109	20%	documented	01.02.03-01	C
E Vancouver Island | Georgia Strait	EVI+GStr	13	23	90	26%	documented	01.02.02-01; 01.02.02-02; 01.02.02-03; 01.02.02-04; 01.02.02-05; 01.02.02-06;	B; C

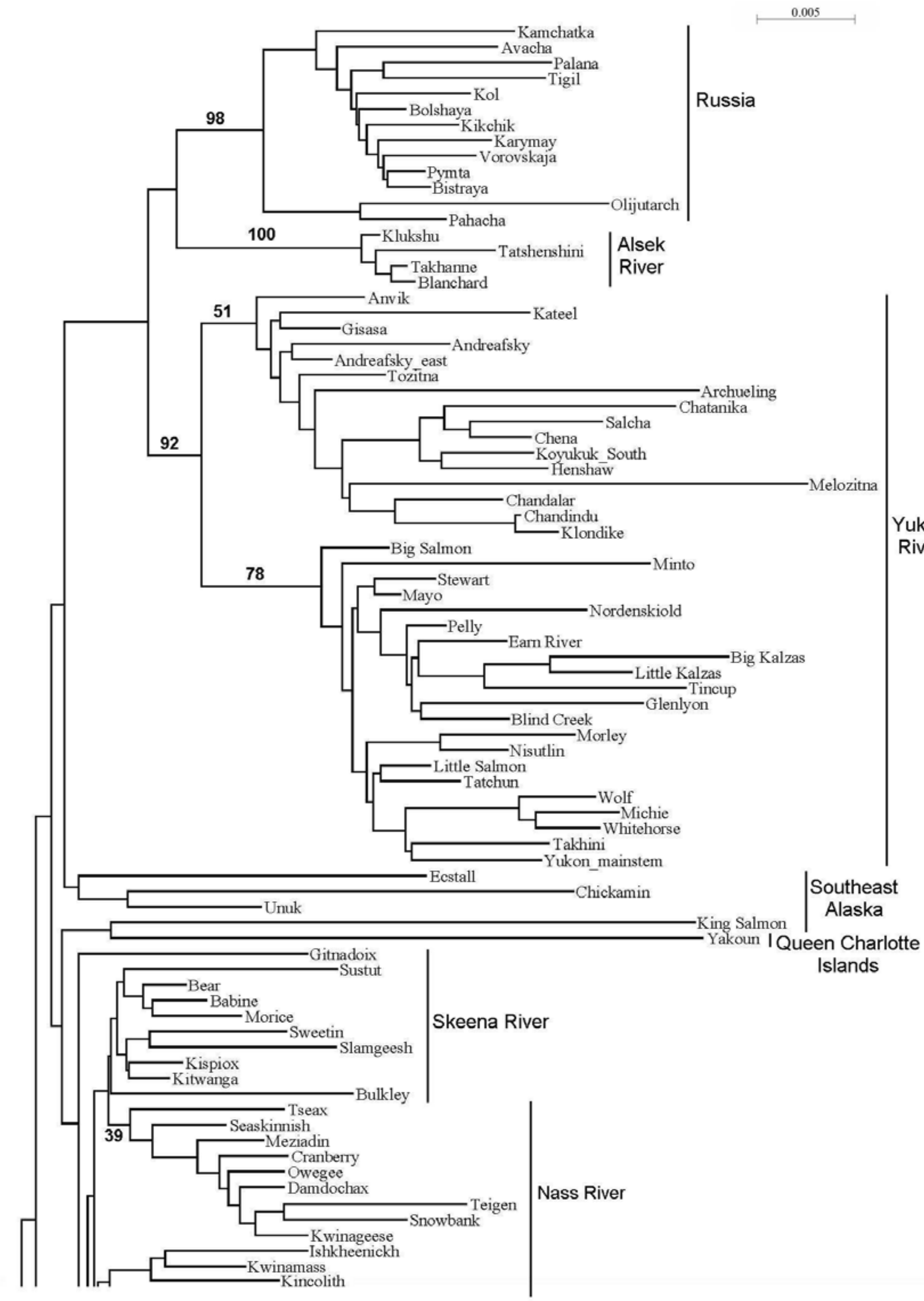
JAZ	JAZ Acronym	JAZ code	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic clusters
E Vancouver Island | QCStr-JStr-SFjords	EVI+SFj	14	11	33	33%	documented	01.02.02-07; 01.02.03-02.01 01.02.03-02.02; 01.02.03-03	C
W Vancouver Island | Vancouver Island Coastal Current	WVI+WVI	15	105	249	42%	documented	02.02-01.01; 02.02-01.02; 02.02-01.03; 02.02-02.01; 02.02-02.02; 02.02-02.03; 02.02-02.04; 02.03-03	F
W Vancouver Island | Outer Graham Island	WVI+WQCI	16	14	64	22%	documented	2.01	F
Homathko - Klinaklini Rivers | QCStr-JStr-SFjords	HK+SFj	17	4	4	100%	documented	03.02.01; 03.02.02	G
Rivers-Smith Inlets | Hecate Strait - Q.C. Sound	RSI+HStr	18	15	30	50%	documented	01.05; 06; 07.02.02-01; 07.02.02-02.01; 07.02.02-02.02; 07.02.02-02.03	E; K; L
Bella Coola - Dean Rivers | Hecate Strait - Q.C. Sound	BCD+HStr	19	10	40	25%	documented	07.01-01.01; 07.01-01.02; 07.01-01.03; 07.01-02.01; 07.01-02.02	L
Queen Charlottes | Hecate Strait - Q.C. Sound	QCI+HStr	20	6	142	4%	probable†	-	-
Queen Charlottes | Outer Graham Island	QCI+WQCI	21	-	83	-	possible	-	-
Queen Charlottes | North Graham Island	QCI+NQCI	22	2	18	11%	documented	8.02	N
Hecate Lowlands |	HecLow+HStr	23	6	174	3%	documented	-	-

JAZ	JAZ Acronym	JAZ code	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic clusters
Hecate Strait - Q.C. Sound								
N Coastal Streams | Hecate Strait - Q.C. Sound	NC+HStr	24	35	118	30%	documented	07.02.01-01; 07.02.01-03; 07.02.01-04	L
Hecate Lowlands | Nass - Skeena Estuary	HecLow+NSKEs t	25	3	67	4%	documented	-	-
Lower Skeena | Nass - Skeena Estuary	LSK+NSKEst	26	39	107	36%	documented	08.03; 08.05-01; 08.05-02; 09.01	O; Q; S
Middle Skeena | Nass - Skeena Estuary	MSK+NSKEst	27	32	113	28%	documented	08.07; 08.08-01; 08.08-02; 08.09-02	R
Upper Skeena | Nass - Skeena Estuary	USK+NSKEst	28	6	19	32%	documented	08.08-02; 08.09-01; 08.09-02	R
Lower Nass - Portland | Nass - Skeena Estuary	LNR-P+NSKEst	29	18	75	24%	documented	07.02.01-02; 08.05-03; 08.06-01; 08.06-02	L; Q; R
Upper Nass | Nass - Skeena Estuary	UNR+NSKEst	30	12	23	52%	documented	08.06-03.01; 08.06-03.02	R
Unuk River | Transboundary Fjords	Unuk+TBFj	31	1	2	50%	documented	09.02	T
Lower Stikine | Transboundary Fjords	LStk+TBFj	32	8	16	50%	documented	08.04-01.02; 08.04-02; 08.04-03	P
Whiting River | Transboundary Fjords	Whtng+TBFj	33	-	1	-	probable	-	-
Taku | Transboundary Fjords	Taku+TBFj	34	8	18	44%	documented	08.04-04.01; 08.04-04.02; 08.04-05.01; 08.04-05.02	P
Lynn Canal |	LYNN+TBFj	35	-	4	-	probable	-	-

JAZ	JAZ Acronym	JAZ code	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic clusters
Transboundary Fjords								
Alsek | Alaska Coastal Downwelling	Alsek+AKCst	36	2	6	33%	documented	10.02-01; 10.02-02; 10.02-03	U
Teslin Headwaters | Bering Sea	TesHW+Ber	37	4	4	100%	documented	11-03.03; 12.01; 12.02; 12.03-01; 12.03-02; 12.03-03; 12.03-04; 12.04-01; 12.04-02; 12.04-03.01; 12.04-03.02; 12.04-04; 12.04-05	V; W
Lower Liard | Arctic Ocean	Liard+AO	38	-	1	-	possible	-	-
Yukon River | Bering Sea	Yuk+Ber	37	23	?	-	documented	11-03.03; 12.01; 12.02; 12.03-01; 12.03-02; 12.03-03; 12.03-04; 12.04-01; 12.04-02; 12.04-03.01; 12.04-03.02; 12.04-04; 12.04-05	V; W
Mackenzie River | Arctic Ocean	MacR+AO	39	-	1	-	possible	-	-

† There are very limited timing information for 6 sites in this JAZ. One site is a naturalized transplant from the Quinsam River and was excluded from further consideration. The escapement data are also very limited and do not confirm persistence of chinook in this JAZ. We have included this JAZ as an ecotypic CU for analysis and later consideration as a Conservation Unit.

Figure 39…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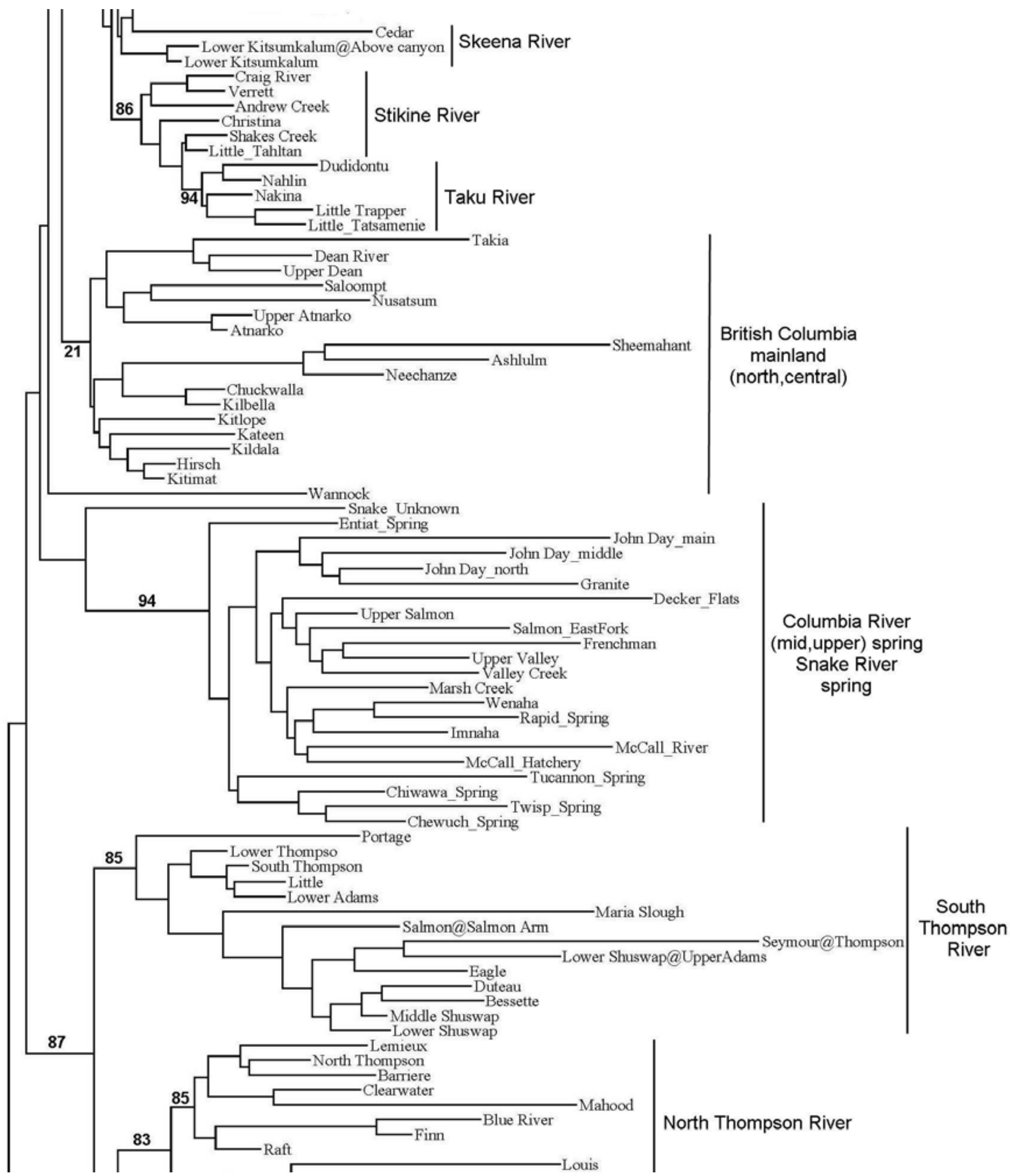
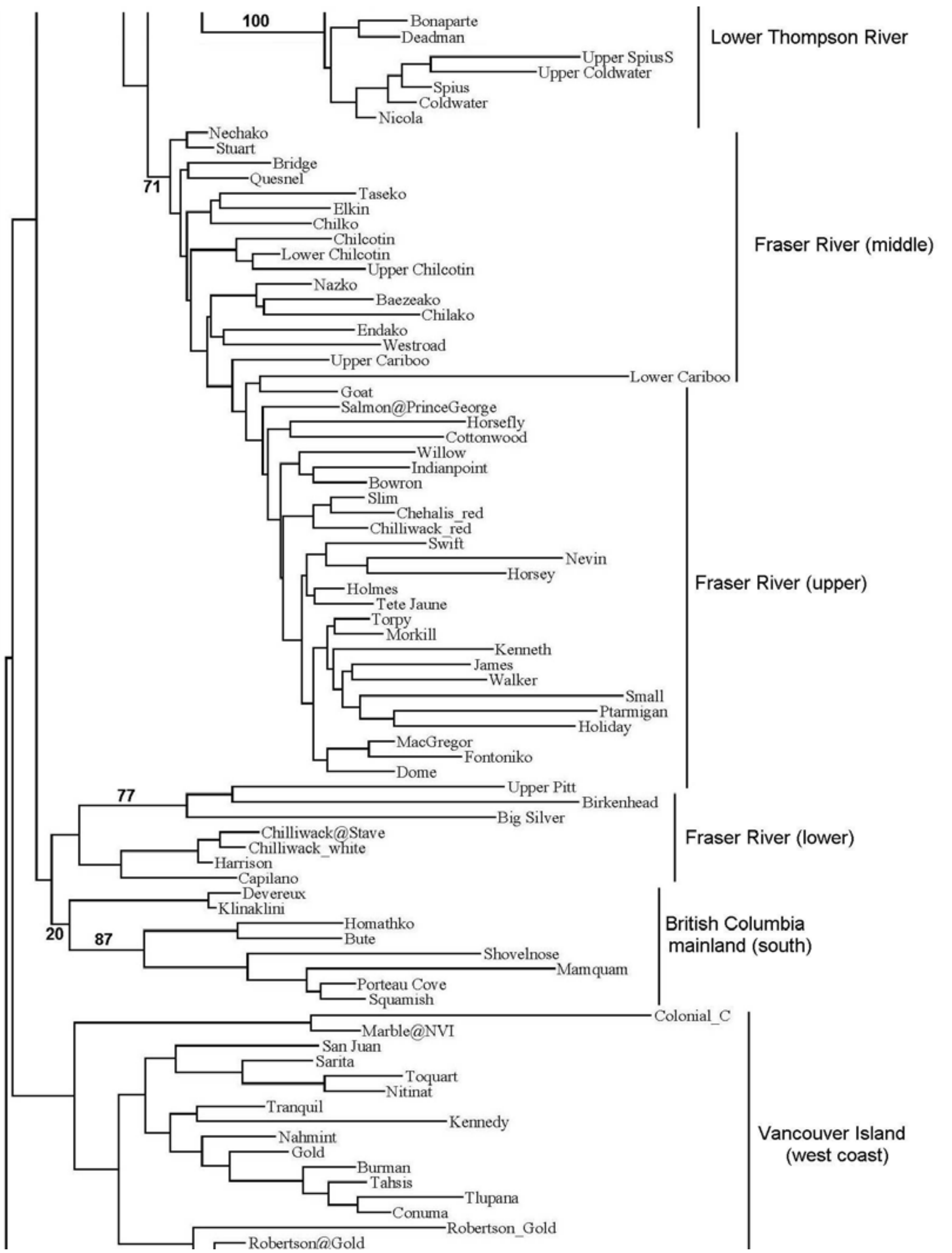
Kamchatka
Avacha
Palana
Tigil
Kol
Bolshaya
Kikchik
Karymay
Vorovskaja
Pymta
Bistraya
Olijutarch
Pahacha
Russia
98
100
Klukshu
Tatshenshini
Takhanne
Blanchard
Alsek River
Anvik
51
Kateel
Gisasa
Andreafsky
Andreafsky_east
Tozitna
Archueling
Chatanika
Salcha
Chena
Koyukuk_South
Henshaw
92
Melozitna
Chandalar
Chandindu
Klondike
Big Salmon
78
Minto
Stewart
Mayo
Nordenskiold
Pelly
Earn River
Big Kalzas
Little Kalzas
Tincup
Glenlyon
Blind Creek
Morley
Nisutlin
Little Salmon
Tatchun
Wolf
Michie
Whitehorse
Takhini
Yukon_mainstem
Yukon River
Ecstall
Chickamin
Unuk
Southeast Alaska
King Salmon
Yakoun
Queen Charlotte Islands
Gitnadoix
Sustut
Bear
Babine
Morice
Sweetin
Slamgeesh
Kispiox
Kitwanga
Bulkley
Skeena River
Tseax
39
Seaskinnish
Meziadin
Cranberry
Owegee
Damdochax
Teigen
Snowbank
Kwinageese
Ishkheenickh
Kwinamass
Kincolith
Nass River

Figure 39…



Cedar
Lower Kitsumkalum@Above canyon
Lower Kitsumkalum
Skeena River
Craig River
Verrett
Andrew Creek
Christina
Shakes Creek
Little_Tahltan
Stikine River
86
Dudidontu
Nahlin
Nakina
Little Trapper
Little_Tatsamenie
94
Taku River
Takia
Dean River
Upper Dean
Saloompt
Nusatsum
Upper Atnarko
Atnarko
Sheemahant
Ashlulm
Neechanze
Chuckwalla
Kilbella
Kitlope
Kateen
Kildala
Hirsch
Kitimat
21
Wannock
British Columbia mainland (north,central)
Snake_Unknown
Entiat_Spring
John Day_main
John Day_middle
John Day_north
Granite
Decker_Flats
Upper Salmon
Salmon_EastFork
Frenchman
Upper Valley
Valley Creek
Marsh Creek
Wenaha
Rapid_Spring
Imnaha
McCall_River
McCall_Hatchery
Tucannon_Spring
Chiwawa_Spring
Twisp_Spring
Chewuch_Spring
94
Columbia River (mid,upper) spring Snake River spring
Portage
Lower Thompso
South Thompson
Little
Lower Adams
Maria Slough
Salmon@Salmon Arm
Seymour@Thompson
Lower Shuswap@UpperAdams
Eagle
Duteau
Bessette
Middle Shuswap
Lower Shuswap
85
South Thompson River
87
Lemieux
North Thompson
Barriere
Clearwater
Mahood
Blue River
Finn
Raft
Louis
85
83
North Thompson River

Figure 39…



100
Bonaparte
Deadman
Upper SpiusS
Upper Coldwater
Spius
Coldwater
Nicola
Lower Thompson River
Nechako
Stuart
Bridge
Quesnel
71
Taseko
Elkin
Chilko
Chilcotin
Lower Chilcotin
Upper Chilcotin
Nazko
Baezeako
Chilako
Endako
Westroad
Upper Cariboo
Lower Cariboo
Fraser River (middle)
Goat
Salmon@PrinceGeorge
Horsefly
Cottonwood
Willow
Indianpoint
Bowron
Slim
Chehalis_red
Chilliwack_red
Swift
Nevin
Horsey
Holmes
Tete Jaune
Torpy
Morkill
Kenneth
James
Walker
Small
Ptarmigan
Holiday
MacGregor
Fontoniko
Dome
Fraser River (upper)
77
Upper Pitt
Birkenhead
Big Silver
Chilliwack@Stave
Chilliwack_white
Harrison
Capilano
Fraser River (lower)
Devereux
Klinaklini
20
87
Homathko
Bute
Shovelnose
Mamquam
Porteau Cove
Squamish
British Columbia mainland (south)
Colonial_C
Marble@NVI
San Juan
Sarita
Toquart
Nitinat
Tranquil
Kennedy
Nahmint
Gold
Burman
Tahsis
Tlupana
Conuma
Robertson_Gold
Robertson@Gold
Vancouver Island (west coast)

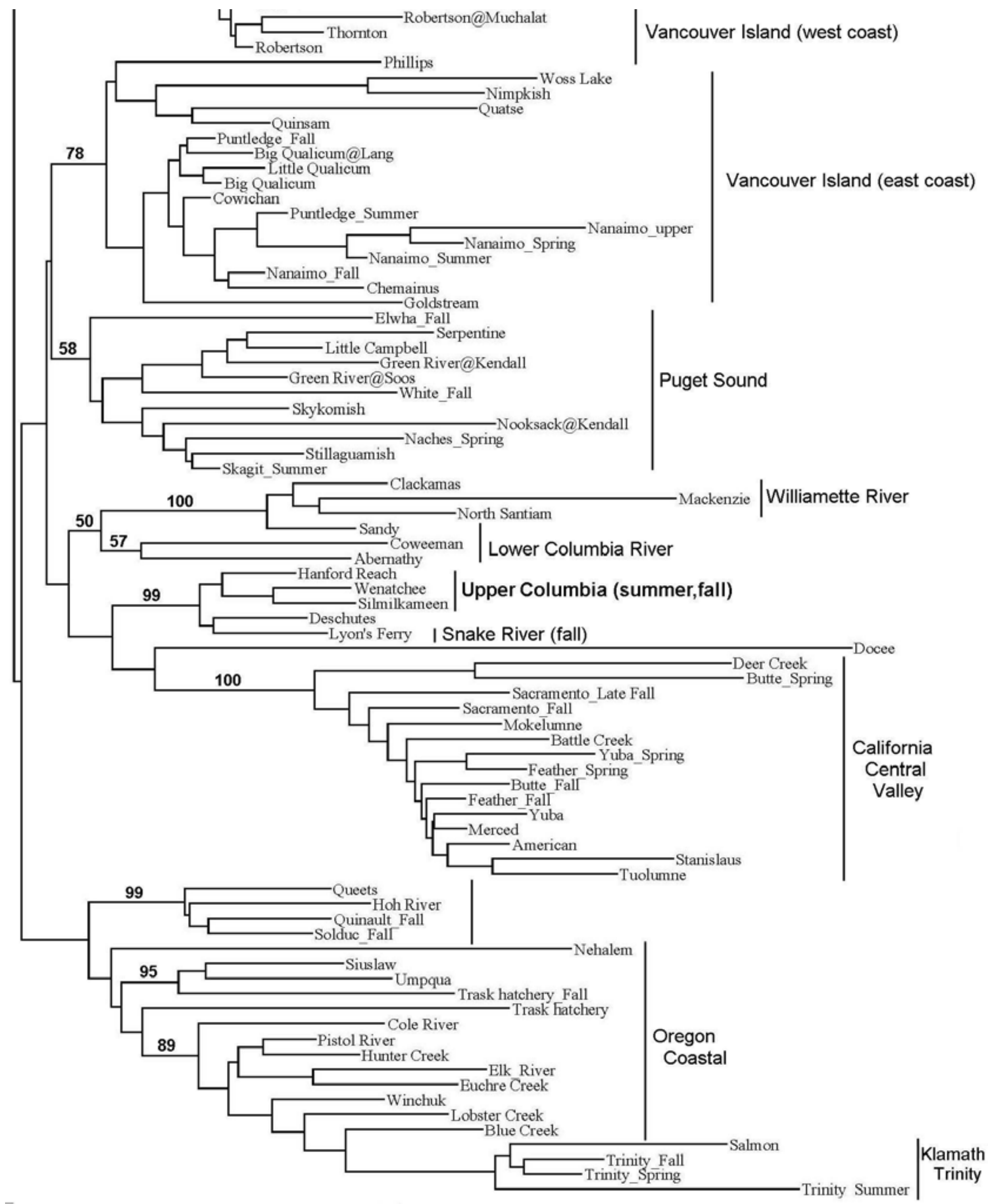


Figure 41. Neighbor-joining dendrogram of Cavalli-Sforza and Edwards chord distance for chinook salmon populations surveyed at 12 microsatellite loci (from Beacham et al. (2006b).

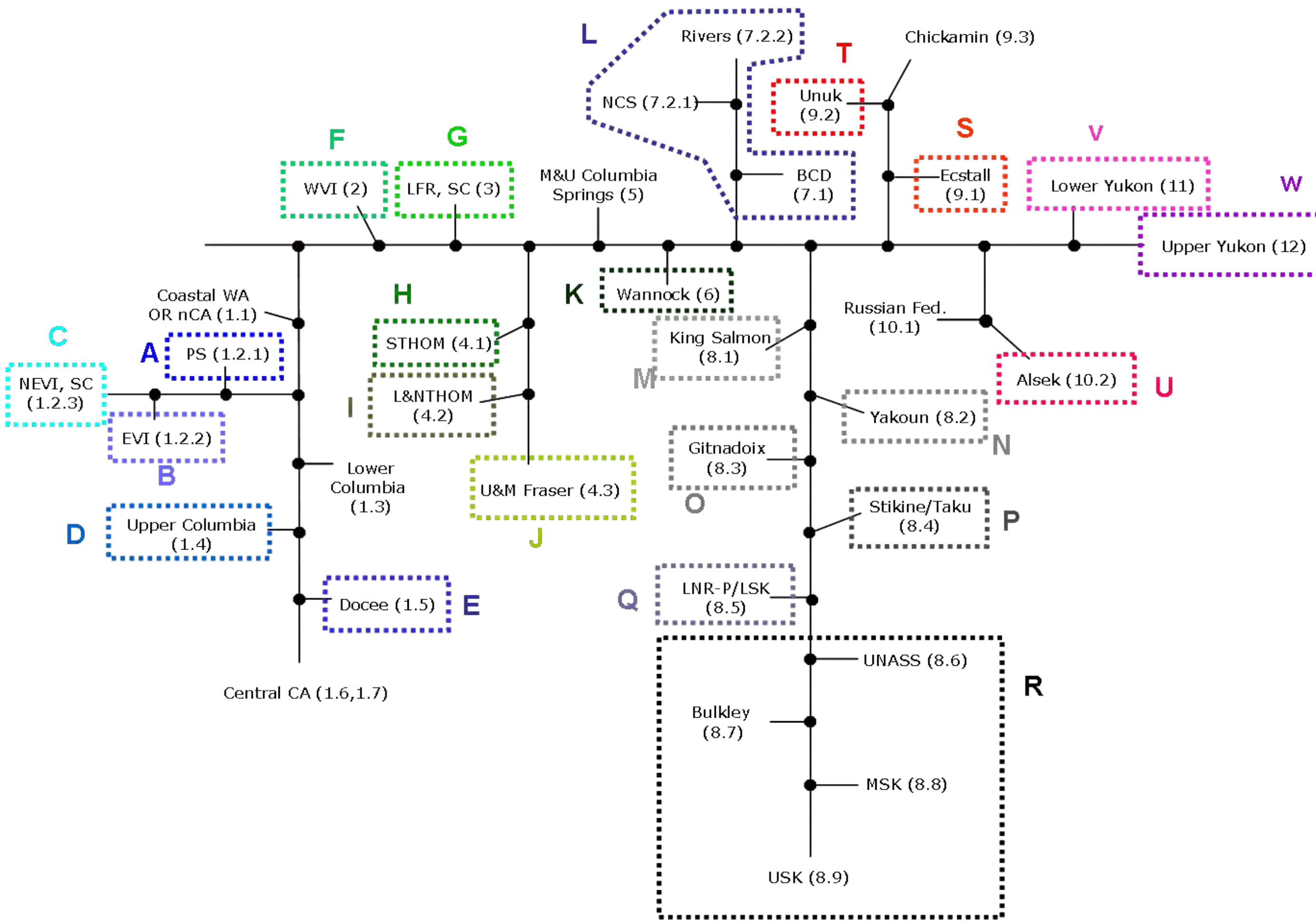


Figure 42. A diagrammatic depiction of the dendrogram for chinook salmon. The dotted boxes and corresponding letters indicate the genetic clusters identified. The numbers in parentheses following the nominal cluster names are that part of the genetic class sufficient to identify the cluster.

Table 28. The genetic and ecotypic classification of all sites in the genetic dendrogram (Figure 41). In most instances the genetic class of foreign sites was not fully enumerated and where possible, foreign branches have been compressed.

GFE_ID	sites	class	cluster	FAZ	MAZ	JAZ
coastal WA-OR-north Calif.	Queets to Trinity summer	01.01				
PS	Elwhat fall	01.02.01-01				
PS	White fall	01.02.01-02.01				
PS	Green River@Soos	01.02.01-02.02				
PS	Green River@Kendall	01.02.01-02.03				
681	Little Campbell	01.02.01-02.04	A	BB	GStr	BB+GStr
677	Serpentine	01.02.01-02.05	A	BB	GStr	BB+GStr
PS	Skykomish	01.02.01-03.01				
PS	Nooksack@Kendall	01.02.01-03.02				
PS	Naches spring	01.02.01-03.03				
PS	Skagit summer	01.02.01-03.04				
PS	Stillaguamish	01.02.01-03.05				
1211	Goldstream	01.02.02-01	B	EVI	GStr	EVI+GStr
1181	Little Qualicum	01.02.02-02	B	EVI	GStr	EVI+GStr
1179	Big Qualicum	01.02.02-02	B	EVI	GStr	EVI+GStr
1156	Puntledge Fall	01.02.02-02	B	EVI	GStr	EVI+GStr
1208	Cowichan	01.02.02-03	B	EVI	GStr	EVI+GStr
1204	Chemainus	01.02.02-03	B	EVI	GStr	EVI+GStr
1194	Nanaimo fall	01.02.02-03	B	EVI	GStr	EVI+GStr
1156	Puntledge Summer	01.02.02-04	B	EVI	GStr	EVI+GStr
1194	Nanaimo summer	01.02.02-05	B	EVI	GStr	EVI+GStr
1194	Nanaimo spring	01.02.02-06	B	EVI	GStr	EVI+GStr
1194	Nanaimo upper	01.02.02-07	B	EVI	GStr	EVI+GStr
824	Phillips	01.02.03-01	C	SC	SFj	SC+SFj
1144	Quinsam	01.02.03-02.01	C	EVI	GStr	EVI+GStr
1106	Quatse	01.02.03-02.02	C	EVI	SFj	EVI+SFj
300041	Woss Lake	01.02.03-03	C	EVI	SFj	EVI+SFj
1112	Nimpkish	01.02.03-03	C	EVI	SFj	EVI+SFj
lower Columbia	Coweeman	01.03.01-				
lower Columbia	Abernathy	01.03.01-				
lower Columbia	Clackamas	01.03.02-				
lower Columbia	Mackenzie	01.03.02-				
lower Columbia	North Santiam	01.03.02-				
lower Columbia	Sandy	01.03.02-				
upper Columbia-summer&fall	Deschutes	01.04.01-				
upper Columbia-summer&fall	Lyons Ferry	01.04.01-				
442†	Okanagan	01.04.02-	D	OK	ORWA	OK+ORWA
upper Columbia-summer&fall	Hanford Reach	01.04.02-				
upper Columbia-summer&fall	Wenatchee	01.04.02-				
upper Columbia-summer&fall	Similkameen	01.04.02-				

GFE_ID	sites	class	cluster	FAZ	MAZ	JAZ
914	Docee	01.05-	E	RSI	HStr	RSI+HStr
California-Central Valley	Sacramento late fall to Tuolumne	01.06-				
California-Central Valley	Deer Creek & Butte spring	01.07-				
1451	Colonial	02.01-	F	WVI	WQCI	WVI+WQCI
1455	Marble@NVI	02.01-	F	WVI	WQCI	WVI+WQCI
1231	San Juan	02.02-01.01	F	WVI	WVI	WVI+WVI
1252	Sarita	02.02-01.02	F	WVI	WVI	WVI+WVI
1242	Nitinat	02.02-01.03	F	WVI	WVI	WVI+WVI
1288	Toquart	02.02-01.03	F	WVI	WVI	WVI+WVI
1306	Kennedy	02.02-02.01	F	WVI	WVI	WVI+WVI
1317	Tranquil	02.02-02.01	F	WVI	WVI	WVI+WVI
1270	Nahmint	02.02-02.02	F	WVI	WVI	WVI+WVI
1358	Gold	02.02-02.03	F	WVI	WVI	WVI+WVI
1356	Burman	02.02-02.04	F	WVI	WVI	WVI+WVI
1367	Tlupana	02.02-02.04	F	WVI	WVI	WVI+WVI
1369	Conuma	02.02-02.04	F	WVI	WVI	WVI+WVI
1377	Tahsis	02.02-02.04	F	WVI	WVI	WVI+WVI
1297	Thorton	02.03-03	F	WVI	WVI	WVI+WVI
11486	Robertson	02.03-03	F	WVI	WVI	WVI+WVI
179	Harrison	03.01.01-	G	LFR	GStr	LFR+GStr
697	Capilano	03.01.01-	G	SC	GStr	SC+GStr
192	Big Silver	03.01.02-01	G	LFR	GStr	LFR+GStr
13	Upper Pitt	03.01.02-02	G	LFR	GStr	LFR+GStr
198	Birkenhead	03.01.02-03	G	LILL	GStr	LILL+GStr
2000850	Devereux	03.02.01-	G	HK	SFj	HK+SFj
850	Klinaklini	03.02.01-	G	HK	SFj	HK+SFj
819	Homathko	03.02.02-	G	HK	SFj	HK+SFj
819	Bute	03.02.02-	G	HK	SFj	HK+SFj
737	Shovelnose	03.02.03-01	G	SC	GStr	SC+GStr
709	Mamquam	03.02.03-02	G	SC	GStr	SC+GStr
708	Squamish	03.02.03-03	G	SC	GStr	SC+GStr
2000708	Porteau Cove	03.02.03-03	G	SC	GStr	SC+GStr
129	Portage	04.01.01-	H	MFR	GStr	MFR+GStr
211	Lower Thompson	04.01.02-	H	LTh	GStr	LTh+GStr
218	South Thompson	04.01.02-	H	STh	GStr	STh+GStr
219	Little River	04.01.02-	H	STh	GStr	STh+GStr
2432	Lower Adams	04.01.02-	H	STh	GStr	STh+GStr
104	Maria Slough	04.01.03-	H	LFR	GStr	LFR+GStr
237	Salmon River@Salmon Arm	04.01.04-	H	STh	GStr	STh+GStr
232	Eagle	04.01.05-01.01	H	STh	GStr	STh+GStr
229	Seymour@Thompson	04.01.05-01.02	H	STh	GStr	STh+GStr
240	Lower Shuswap@Upper Adams	04.01.05-01.02	H	STh	GStr	STh+GStr
240	Lower Shuswap	04.01.05-02.01	H	STh	GStr	STh+GStr
241	Middle Shuswap	04.01.05-02.02	H	STh	GStr	STh+GStr
252	Bessette	04.01.05-02.03	H	STh	GStr	STh+GStr
254	Duteau	04.01.05-02.03	H	STh	GStr	STh+GStr

GFE_ID	sites	class	cluster	FAZ	MAZ	JAZ
256	North Thompson	04.02.01-01.01	I	NTh	GStr	NTh+GStr
258	Barriere	04.02.01-01.01	I	NTh	GStr	NTh+GStr
262	Lemieux	04.02.01-01.01	I	NTh	GStr	NTh+GStr
266	Clearwater	04.02.01-01.02	I	NTh	GStr	NTh+GStr
268	Mahood	04.02.01-01.03	I	NTh	GStr	NTh+GStr
269	Raft	04.02.01-02.01	I	NTh	GStr	NTh+GStr
279	Finn	04.02.01-02.02	I	NTh	GStr	NTh+GStr
281	Blue River	04.02.01-02.02	I	NTh	GStr	NTh+GStr
257	Louis	04.02.02-01	I	NTh	GStr	NTh+GStr
216	Bonaparte	04.02.02-02	I	LTh	GStr	LTh+GStr
217	Deadman	04.02.02-02	I	LTh	GStr	LTh+GStr
213	Nicola	04.02.02-03.01	I	LTh	GStr	LTh+GStr
214	Spius	04.02.02-03.01	I	LTh	GStr	LTh+GStr
215	Coldwater	04.02.02-03.01	I	LTh	GStr	LTh+GStr
2000214	Upper Spius	04.02.02-03.02	I	LTh	GStr	LTh+GStr
2000215	Upper Coldwater	04.02.02-03.02	I	LTh	GStr	LTh+GStr
295	Nechako	04-01	J	MFR	GStr	MFR+GStr
305	Stuart	04-01	J	MFR	GStr	MFR+GStr
133	Bridge	04-02	J	MFR	GStr	MFR+GStr
289	Quesnel	04-02	J	MFR	GStr	MFR+GStr
286	Chilko	04-03	J	MFR	GStr	MFR+GStr
288	Elkin	04-03	J	MFR	GStr	MFR+GStr
2636	Taseko	04-03	J	MFR	GStr	MFR+GStr
285	Chilcotin	04-04	J	MFR	GStr	MFR+GStr
2463	Lower Chilcotin	04-04	J	MFR	GStr	MFR+GStr
285	Upper Chilcotin	04-04	J	MFR	GStr	MFR+GStr
294	West Road	04-05.01	J	MFR	GStr	MFR+GStr
299	Endako	04-05.01	J	MFR	GStr	MFR+GStr
296	Chilako	04-05.02	J	MFR	GStr	MFR+GStr
2455	Baezeako	04-05.02	J	MFR	GStr	MFR+GStr
2456	Nazko	04-05.02	J	MFR	GStr	MFR+GStr
2000290	Upper Cariboo	04-06	J	MFR	GStr	MFR+GStr
169	Goat	04-07.01	J	UFR	GStr	UFR+GStr
290	Lower Cariboo	04-07.02	J	MFR	GStr	MFR+GStr
146	Salmon@PrinceGeorge	04-08	J	MFR	GStr	MFR+GStr
291	Horsefly	04-09	J	MFR	GStr	MFR+GStr
2457	Cottonwood	04-09	J	MFR	GStr	MFR+GStr
147	Willow	04-10	J	UFR	GStr	UFR+GStr
157	Bowron	04-10	J	UFR	GStr	UFR+GStr
159	Indianpoint	04-10	J	UFR	GStr	UFR+GStr
62	Chilliwack (red)	04-11	J	LFR	GStr	LFR+GStr
162	Slim	04-11	J	UFR	GStr	UFR+GStr
181	Chehalis (red)	04-11	J	LFR	GStr	LFR+GStr
173	Holmes	04-12.01	J	UFR	GStr	UFR+GStr
2477	Tete Jaune	04-12.01	J	UFR	GStr	UFR+GStr
174	Nevin	04-12.02	J	UFR	GStr	UFR+GStr
175	Horsey	04-12.02	J	UFR	GStr	UFR+GStr
176	Swift	04-12.02	J	UFR	GStr	UFR+GStr
149	Macgregor	04-13	J	UFR	GStr	UFR+GStr

GFE_ID	sites	class	cluster	FAZ	MAZ	JAZ
155	Fontoniko	04-13	J	UFR	GStr	UFR+GStr
163	Dome	04-13	J	UFR	GStr	UFR+GStr
164	Torpy	04-14.01	J	UFR	GStr	UFR+GStr
168	Morkill	04-14.01	J	UFR	GStr	UFR+GStr
161	Kenneth	04-14.02	J	UFR	GStr	UFR+GStr
154	James	04-14.03	J	UFR	GStr	UFR+GStr
165	Walker	04-14.03	J	UFR	GStr	UFR+GStr
2043	Small	04-14.04	J	UFR	GStr	UFR+GStr
2034	Holiday	04-14.05	J	UFR	GStr	UFR+GStr
166	Ptarmigan	04-14.06	J	UFR	GStr	UFR+GStr
M&U Columbia spring	Snake	05.01-				
M&U Columbia spring	Entiat_spring	05.02-				
M&U Columbia spring	Tucannon spring to Chewuch spring	05.03-				
M&U Columbia spring	John Day main to Granite	05.04-				
M&U Columbia spring	Decker Flats to Valley Creek	05.05.01-				
M&U Columbia spring	Marsh Creek to McCall hatchery	05.05.02-				
935	Wannock	06-	K	RSI	HStr	RSI+HStr
970	Atnarko	07.01-01.01	L	BCD	HStr	BCD+HStr
970	upper Atnarko	07.01-01.01	L	BCD	HStr	BCD+HStr
3403	Saloompt	07.01-01.02	L	BCD	HStr	BCD+HStr
2250	Nusatsum	07.01-01.03	L	BCD	HStr	BCD+HStr
975	Dean	07.01-02.01	L	BCD	HStr	BCD+HStr
2000975	Upper Dean	07.01-02.01	L	BCD	HStr	BCD+HStr
300035	Takia	07.01-02.02	L	BCD	HStr	BCD+HStr
7990614	Kitlope	07.02.01-01	L	NC	HStr	NC+HStr
2001754	Kateen	07.02.01-02	L	LNR-P	NSKEst	LNR-P+NSKEst
1044	Kildala	07.02.01-03	L	NC	HStr	NC+HStr
1050	Kitimat	07.02.01-04	L	NC	HStr	NC+HStr
1054	Hirsch	07.02.01-04	L	NC	HStr	NC+HStr
947	Kilbella	07.02.02-01	L	RSI	HStr	RSI+HStr
948	Chuckwalla	07.02.02-01	L	RSI	HStr	RSI+HStr
941	Neechanze	07.02.02-02.01	L	RSI	HStr	RSI+HStr
939	Ashlulm	07.02.02-02.02	L	RSI	HStr	RSI+HStr
943	Sheemahant	07.02.02-02.03	L	RSI	HStr	RSI+HStr
SEAK	King Salmon	08.01-	M			
1571	Yakoun	08.02-	N	QCI	NQCI	QCI+NQCI
460	Gitnadoix	08.03-	O	LSK	NSKEst	LSK+NSKEst
SEAK	Andrew Creek	08.04-01.01	P			
2186	Craig	08.04-01.02	P	LStk	TBFj	LStk+TBFj
2193	Verrett	08.04-01.02	P	LStk	TBFj	LStk+TBFj
2145	Christina	08.04-02	P	LStk	TBFj	LStk+TBFj
2201	Little Tahltan	08.04-03	P	LStk	TBFj	LStk+TBFj
200010	Shakes Creek	08.04-03	P	LStk	TBFj	LStk+TBFj
2216	Nakina	08.04-04.01	P	Taku	TBFj	Taku+TBFj

GFE_ID	sites	class	cluster	FAZ	MAZ	JAZ
2212	Little Tatsamenie	08.04-04.02	P	Taku	TBFj	Taku+TBFj
2222	Little Trapper	08.04-04.02	P	Taku	TBFj	Taku+TBFj
2224	Nahlin	08.04-05.01	P	Taku	TBFj	Taku+TBFj
2225	Dudidontu	08.04-05.02	P	Taku	TBFj	Taku+TBFj
521	Lower Kalum	08.05-01	Q	LSK	NSKEst	LSK+NSKEst
521	Lower Kalum above Canyon	08.05-01	Q	LSK	NSKEst	LSK+NSKEst
531	Cedar	08.05-02	Q	LSK	NSKEst	LSK+NSKEst
630	Kincolith	08.05-03	Q	LNR-P	NSKEst	LNR-P+NSKEst
661	Ishkheenickh	08.05-03	Q	LNR-P	NSKEst	LNR-P+NSKEst
1756	Kwinamass	08.05-03	Q	LNR-P	NSKEst	LNR-P+NSKEst
651	Tseax	08.06-01	R	LNR-P	NSKEst	LNR-P+NSKEst
655	Seaskinnish	08.06-02	R	LNR-P	NSKEst	LNR-P+NSKEst
663	Cranberry	08.06-03.01	R	UNR	NSKEst	UNR+NSKEst
7990598	Meziadin	08.06-03.01	R	UNR	NSKEst	UNR+NSKEst
7990602	Owegee	08.06-03.01	R	UNR	NSKEst	UNR+NSKEst
7990604	Damdochax	08.06-03.01	R	UNR	NSKEst	UNR+NSKEst
659	Kwinageese	08.06-03.02	R	UNR	NSKEst	UNR+NSKEst
670	Teigen	08.06-03.02	R	UNR	NSKEst	UNR+NSKEst
671	Snowbank	08.06-03.02	R	UNR	NSKEst	UNR+NSKEst
541	Bulkley	08.07-	R	MSK	NSKEst	MSK+NSKEst
488	Kitwanga	08.08-01	R	MSK	NSKEst	MSK+NSKEst
566	Kispiox	08.08-01	R	MSK	NSKEst	MSK+NSKEst
498	Slamgeesh	08.08-02	R	USK	NSKEst	USK+NSKEst
579	Sweetin	08.08-02	R	MSK	NSKEst	MSK+NSKEst
620	Sustut	08.09-01	R	USK	NSKEst	USK+NSKEst
556	Morice	08.09-02	R	MSK	NSKEst	MSK+NSKEst
592	Babine	08.09-02	R	MSK	NSKEst	MSK+NSKEst
621	Bear	08.09-02	R	USK	NSKEst	USK+NSKEst
447	Ecstall	09.01-	S	LSK	NSKEst	LSK+NSKEst
2002118	Unuk	09.02-	T	Unuk	TBFj	Unuk+TBFj
SEAK	Chickamin	09.03-				
Russian Fed.	Kamchatka to Pahacha	10.01-				
2332	Klukshu	10.02-01	U	Alsek	AKCst	Alsek+AKCst
2325	Tatshenshini	10.02-02	U	Alsek	AKCst	Alsek+AKCst
2333	Takhanne	10.02-03	U	Alsek	AKCst	Alsek+AKCst
2334	Blanchard	10.02-03	U	Alsek	AKCst	Alsek+AKCst
Lyuk	Anvik to Tozitna	11-01	V			
Lyuk	Archueling	11-02	V			
Lyuk	Chandalar	11-03.02	V			
CdnYukRiv	Chandindu	11-03.03	V	Yuk	Ber	Yuk+Ber
CdnYukRiv	Klondike	11-03.03	V	Yuk	Ber	Yuk+Ber
Lyuk	Koyukuk_S to Melozitna	11-04.01	V			
Lyuk	Chatanika	11-04.02	V			
Lyuk	Salcha	11-04.03	V			
Lyuk	Chena	11-04.03	V			
2516	Big Salmon	12.01-	W	Yuk	Ber	Yuk+Ber
CdnYukRiv‡	Minto	12.02-	W	Yuk	Ber	Yuk+Ber
2517	Nisutlin	12.03-01	W	Yuk	Ber	Yuk+Ber

GFE_ID	sites	class	cluster	FAZ	MAZ	JAZ
2520	Morley	12.03-01	W	Yuk	Ber	Yuk+Ber
2493	Tatchun	12.03-02	W	Yuk	Ber	Yuk+Ber
2495	Little Salmon	12.03-02	W	Yuk	Ber	Yuk+Ber
2521	Takhini	12.03-03	W	Yuk	Ber	Yuk+Ber
2569	Yukon mainstem	12.03-03	W	Yuk	Ber	Yuk+Ber
2498	Michie	12.03-04	W	Yuk	Ber	Yuk+Ber
2518	Wolf	12.03-04	W	Yuk	Ber	Yuk+Ber
2568	Whitehorse	12.03-04	W	Yuk	Ber	Yuk+Ber
CdnYukRiv	Stewart	12.04-01	W	Yuk	Ber	Yuk+Ber
CdnYukRiv	Mayo	12.04-01	W	Yuk	Ber	Yuk+Ber
CdnYukRiv	Nordenskiold	12.04-02	W	Yuk	Ber	Yuk+Ber
CdnYukRiv	Pelly	12.04-03.01	W	Yuk	Ber	Yuk+Ber
2508	Tincup	12.04-03.02	W	Yuk	Ber	Yuk+Ber
2543	Big Kalzas	12.04-03.02	W	Yuk	Ber	Yuk+Ber
2544	Earn River	12.04-03.02	W	Yuk	Ber	Yuk+Ber
2552	Little Kalzas	12.04-03.02	W	Yuk	Ber	Yuk+Ber
2514	Blind	12.04-04	W	Yuk	Ber	Yuk+Ber
2545	Glenlyon	12.04-05	W	Yuk	Ber	Yuk+Ber

† Okanagan was not sampled by Beacham et al. ((2006b). We have included it in this table based on our understanding of the material presented in the COSEWIC status report (COSEWIC 2006).
‡ Not all of the Canadian sites in the Yukon Territory have been assigned GFE_ID.

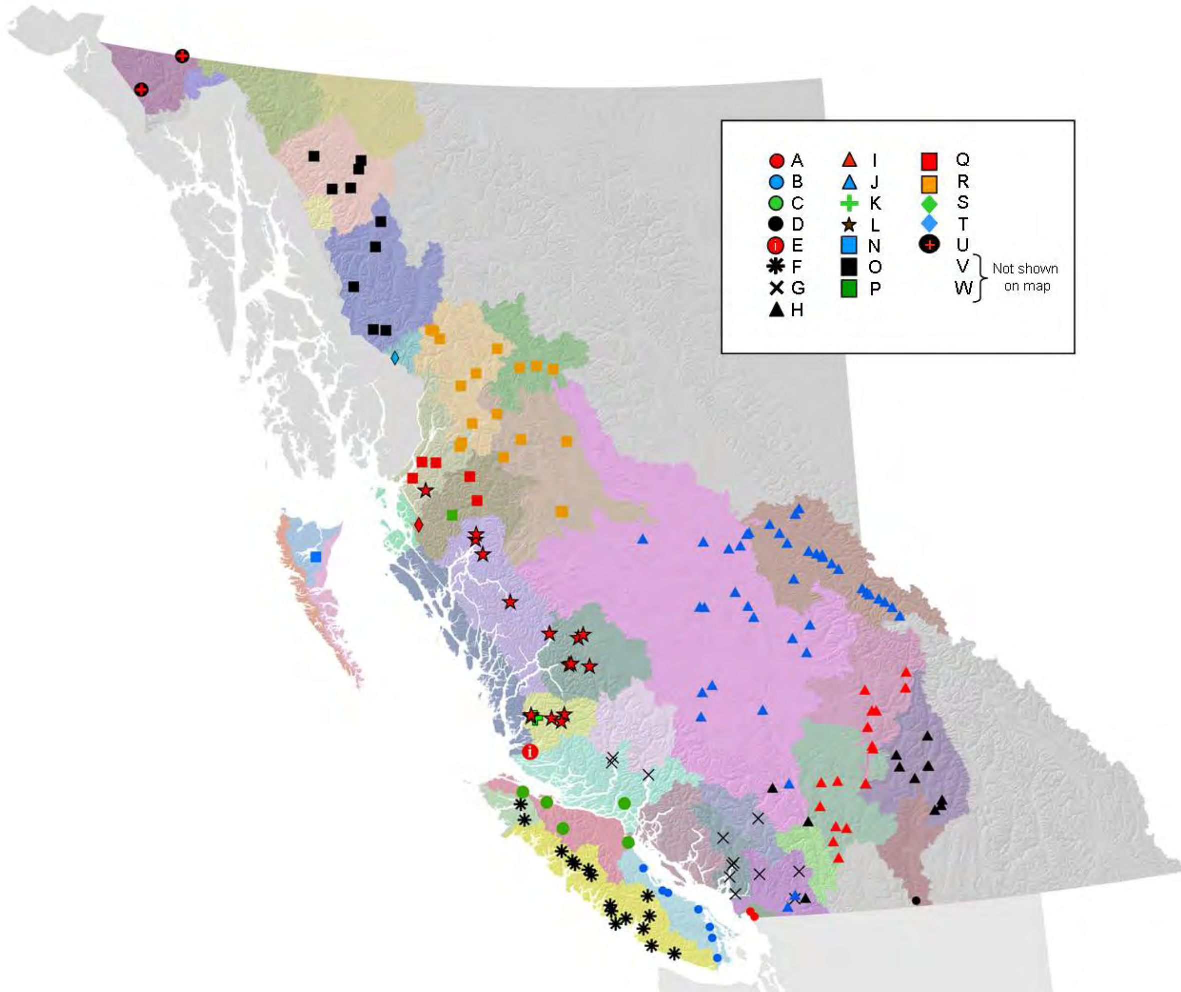


Figure 43. The 20 genetic clusters of chinook salmon in British Columbia. An additional two clusters (V & W) are located in the Yukon River and are not shown. The colored polygons of the map are the ecotypic JAZ CUs following step 2.

Table 29. A tabulated summary of the crosswalk between the ecotypic JAZ CUs and the genetic clusters for chinook salmon. Some of the JAZ that have been diverse in other species either have few chinook (HecLow+HStr) or are monotypic (NC+HStr) while others remain diverse (e.g. LNR-P+NSKEst). A majority of the JAZ are monotypic (19 of 28, excluding those in the Yukon Territory).

		cluster																							
index	JAZ	A	B	C	D	E	F	G	H	I	J	K	L	N	O	P	Q	R	S	T	U	V	W	sites	clusters in JAZ
1	OK+ORWA				1																			1	1
2	BB+GStr	2																						2	1
3	LFR+GStr							3	1		2													6	3
4	LILL+GStr							1																1	1
6	MFR+GStr								1		20													21	2
7	UFR+GStr										21													21	1
8	LTh+GStr								1	7														8	2
9	STh+GStr								11															11	1
10	NTh+GStr									9														9	1
11	SC+GStr							5																5	1
12	SC+SFj			1																				1	1
13	EVI+GStr		11	1																				12	2
14	EVI+SFj			3																				3	1
15	WVI+WVI						14																	14	1
16	WVI+WQCI						2																	2	1
17	HK+SFj							4																4	1
18	RSI+HStr					1						1	5											7	3
19	BCD+HStr												7											7	1
22	QCI+NQCI													1										1	1
24	NC+HStr												4											4	1
26	LSK+NSKEst														1		3		1					5	3
27	MSK+NSKEst																	6						6	1
28	USK+NSKEst																	3						3	1
29	LNR-P+NSKEst												1				3	2						6	3

index	JAZ	cluster																						sites	clusters in JAZ
		A	B	C	D	E	F	G	H	I	J	K	L	N	O	P	Q	R	S	T	U	V	W		
30	UNR+NSKEst																	7						7	1
32	LStk+TBFj															5								1	1
33	Unuk+TBFj																			1				5	1
34	Taku+TBFj															5								5	1
36	Alsek+AKCst																				4			4	1
37	Yuk+Ber																					2	21	23	2
	sites	2	11	5	1	1	16	13	14	16	43	1	17	1	1	11	6	18	1	1	4	16	21	205	
	JAZ in cluster	1	1	3	1	1	2	4	4	2	3	1	4	1	1	2	2	4	1	1	1	1	1		

Table 30. A tabular summary of step 2 for chinook salmon in British Columbia. The bracketed numbers (#) are the GFE_IDs of the corresponding site. In many cases, additional factors were considered in defining the CUs. Those factors are identified in the table and more fully discussed in the text.

cluster	genetic class(es)	ecotypic or geographical descriptors	other factors considered	comments	number of sites	decision
G	03.01.01	LFR-Harrison (#179)	- ocean-type - fall run-timing - white flesh	Capilano (#697) is a hatchery stock of Harrison origin	3	LFR-fall white is a CU
	03.01.02	remaining sites in LFR and LILL	- stream-type - summer run-timing	Lower Fraser springs	13	LFR-spring is a CU
	03.02.01	Klinaklini River	- Homathko-Klinaklini FAZ does not include other tributaries to either Bute or Knight Inlet.	Klinaklini is genetically distinct at the third level from related Homathko.	2	Split the JAZ into two CUs: Klinaklini and Bute Inlet
	03.02.02	Homathko River			2	
	03.02.03	Howe Sound & Burrard Inlet	- population structures in coho and chum	Genetic samples are only from Howe Sound but based on patterns in coho and chum.	19	SC+GStr CU

cluster	genetic class(es)	ecotypic or geographical descriptors	other factors considered	comments	number of sites	decision
H	04.04.01	Portage Creek (#129)	- stream-type (possible) - fall run-timing	As recommended by Fraser Area biologists. Characteristics perhaps due to the geological origins of Seton and Anderson Lakes	1	CU
	04.04.02	S Thompson River (#218); Thomspon River (#211), Little River (#219) and Lower Adams (#2432)	- ocean type - age 0.3 - spawning location at outflows of large lakes	The Thompson River (#211) is included in this cluster. The location(s) of spawning for this site were not specified	4	CU
	04.04.03	Maria Slough (#104)	- ocean type - age 0.3	Related to S Thompson, ocean type, MSUM migration populations	1	CU
	04.04.04	Salmon River (#237)	- stream-type - MSUM run-timing	Extensive hatchery program and is non-wild	1	excluded
	04.04.05-01 04.01.05-02.01 04.01.05-02.02	tributaries of the S Thompson River & Shuswap Lake	- stream-type - age 1.3 - ESUM run-timing	Unknown if age is fixed trait or habitat dependent	5	CU
	04.01.05-02.03	upper Bessette (#252); Duteau (#254)	- stream type - age 1.2 - probable ESUM migration timing	Spawning time estimates available for Duteau suggest earlier migration timing than age 1.3 stream type fish in STHOM	3	CU
L	07.01	Bella-Coola Dean	- genetic class corresponds to ecotypic CU	Consideration of separation of Bella Coola and Dean Rivers deferred to timing and habitat	BC-7 Dean-3	CU
	07.02.01	NC+HStr		One population in LNR-P (Kateen #2001754, a tributary of the Khutzeymateen), considered an outlier	38	CU
	07.02.02	Rivers Inlet		Single site in Smith Inlet is in different and unrelated cluster	12	Rivers Inlet CU

cluster	genetic class(es)	ecotypic or geographical descriptors	other factors considered	comments	number of sites	decision
R	08.06	LNR-P & UNR		The fourth level genetic class indicates relatedness by distance up the Nass River	35	inconclusive, deferred to timing
	08.07 to 08.09	MSK & USK		The three third-level classes are distributed in both ecotypic CUs	MSK-32 USK-6	inconclusive, deferred to timing
C	01.02.03	SC+SFj (1 site), EVI+GStr (1 site), EVI+SFj (3 sites)		The site in EVI+GStr (Quinsam #1144) is at northern border, warranting a small border shift south of the EVI+SFj CU	EVI+SFj-1 4 SC+SFj-22	inconclusive, possible merger of EVI+SFj and SC+SFj, deferred to timing
J	04-n	MFR & UFR		If cluster is partitioned at 04-10, conforms to ecotypic CUs with only 2 exceptions (Goat River #169, class 04-07.01 is in UFR with MFR genetic class; Walker Creek #165 is in MFR with UFR genetic class)	MFR-40 UFR-38	confirm ecotypic CUs with no boundary change
	04	LFR	- stream-type - summer run-timing	Two sites (Chehalis #181 & Chilliwack #62) are hatchery stocks of interior origin	4	non-wild, not part of any CU
F	02.01	WVI+WQCI		2 sites – ecotypic CU confirmed	14	ecotypic CU confirmed
	02.02	WVI+WVI		14 sites – ecotypic CU confirmed; extensive enhancement excludes some sites (e.g. Robertson Creek)	≈95	ecotypic CU confirmed
I	04.02.01	NTH	- MSUM migration - age 1.3	1 exception (Louis #257) is a lower end of N Thompson and was resolved by small boundary change.	13	ecotypic CU confirmed
	04.02.02	LTH	- ESUM migration - age 1.2	ecotypic CU confirmed	10	ecotypic CU confirmed
K	06	Wannock (#935)	- ocean type - outlet spawners	Life history and genetics distinct from other sits in Rivers Inlet	1	CU
E	01.05	Docee River (#914)	- ocean type	Only site in Smith Inlet; very distinctive from all other sites in Canada	1	CU

cluster	genetic class(es)	ecotypic or geographical descriptors	other factors considered	comments	number of sites	decision
N	08.02	Yakoun (#1571)	- timing	Earlier spawning from other sites on QCI (except Mathers #1695). Possibly a distinct CU.	6	inconclusive habitat
O	08.03	Gitnadoix (#460)		Genetically distinct from other Lower Skeena sites	5	CU
P	08.04	LStk and Taku	- no information available	The two ecotypic CUs can be separated at the fourth level of genetic hierarchy, a weak confirmation of ecotypic CUs	Taku-8 LStk-8	2 CUs corresponding to the ecotypic CUs
Q	08.05	LSK and LNR-P		Sites can be distinguished in timing and river system at the fourth level of the genetic hierarchy.	LSK-31 LNR-P-16	inconclusive, deferred to timing
S	09	Ecstall (#447)		Genetically distinct from other LSK sites and from the Gitnadoix CU	4	CU

Table 31. Multiple spawning times are listed for only 12 chinook populations (of approx. 553). The different spawning runs are variously reported as run 1, run 2, spring, summer, fall or unknown. Of the 12 populations with multiple spawning times, four (bold underline) have enough observations to verify that there are (Chilliwack, Nanaimo) or are not (Chilcotin, Puntledge) different spawning time components

		Run 1		Run 2		Fall		Spring		Summer		Not specified	
GFE_ID	name	mean DOY	N	mean DOY	N	mean DOY	N	mean DOY	N	mean DOY	N	mean DOY	N
290	CARIBOO RIVER	250.6	13	268.0	1								
285	**CHILCOTIN RIVER**	235.5	48	239.7	9								
62	**CHILLIWACK RIVER**					307.2	17					243.9	11
215	COLDWATER RIVER	243.6	46	259.0	1								
850	KLINAKLINI RIVER	235.2	43	279.0	1								
312	KUZKWA CREEK					258.0	1					256.0	27
1194	**NANAIMO RIVER**					275.9	8			273.4	33		
824	PHILLIPS RIVER	252.3	49	261.0	2								
1156	**PUNTLEDGE RIVER**					286.3	23	286.9	36				
167	SNOWSHOE CREEK					238.0	1					233.7	6
214	SPIUS CREEK	236.0	45	259.0	1								
142	SWIFT RIVER	235.8	47	237.0	2	239.5	4						

Table 32. Mean spawning times averaged within the JAZ ecotypes for chinook salmon spawning in British Columbia.

JAZ	N	Min. DOY		Mean DOY		Max. DOY		Range
BB+GStr	1	299.0	MFALL	299.0	MFALL	299.0	MFALL	
BCD+HStr	6	239.0	LSUM	247.7	LSUM	258.2	LSUM	19
EVI+GStr	21	273.3	EFALL	290.5	EFALL	329.0	LFALL	56
EVI+SFj	10	217.6	MSUM	269.3	EFALL	299.0	MFALL	81
FRCany+GStr	1	264.4	EFALL	264.4	EFALL	264.4	EFALL	
HecLow+HStr	5	227.5	MSUM	252.0	LSUM	258.4	LSUM	31
HecLow+NSKEst	4	233.1	LSUM	258.8	LSUM	278.0	EFALL	45
HK+SFj	3	235.2	LSUM	245.6	LSUM	257.7	LSUM	23
LFR+GStr	9	162.7	LSPR	253.5	LSUM	313.6	MFALL	151
LILL+GStr	6	184.7	ESUM	262.7	LSUM	312.3	MFALL	128
LNR-P+NSKEst	16	217.6	MSUM	233.8	LSUM	288.2	EFALL	71
LSK+NSKEst	37	222.7	MSUM	244.6	LSUM	260.4	LSUM	38
LTh+GStr	7	236.0	LSUM	249.4	LSUM	261.8	LSUM	26
MFR+GStr	38	227.0	MSUM	250.4	LSUM	319.0	MFALL	92
MSK+NSKEst	33	224.6	MSUM	245.5	LSUM	288.0	EFALL	63
NC+HStr	34	212.0	MSUM	234.2	LSUM	289.0	EFALL	77
NTh+GStr	14	231.9	LSUM	255.6	LSUM	298.0	MFALL	66
QCI+HStr	6	145.7	LSPR	265.6	EFALL	309.0	MFALL	163
QCI+NQCI	2	243.7	LSUM	255.9	LSUM	268.0	EFALL	24
RSI+HStr	15	238.1	LSUM	258.9	LSUM	319.0	MFALL	81
SC+GStr	27	204.0	MSUM	258.8	LSUM	302.5	MFALL	99
SC+SFj	28	169.3	LSPR	243.8	LSUM	303.5	MFALL	134
STh+GStr	14	252.7	LSUM	269.4	EFALL	285.6	EFALL	33
UFR+GStr	38	225.0	MSUM	235.1	LSUM	250.0	LSUM	25
UNR+NSKEst	12	224.0	MSUM	243.1	LSUM	274.0	EFALL	50
USK+NSKEst	1	227.0	MSUM	227.0	MSUM	227.0	MSUM	
WVI+WQCI	14	227.5	MSUM	275.1	EFALL	320.0	MFALL	93
WVI+WVI	104	258.0	LSUM	287.7	EFALL	322.5	MFALL	65
Overall	506	145.7	LSPR	258.6	LSUM	329.0	LFALL	183

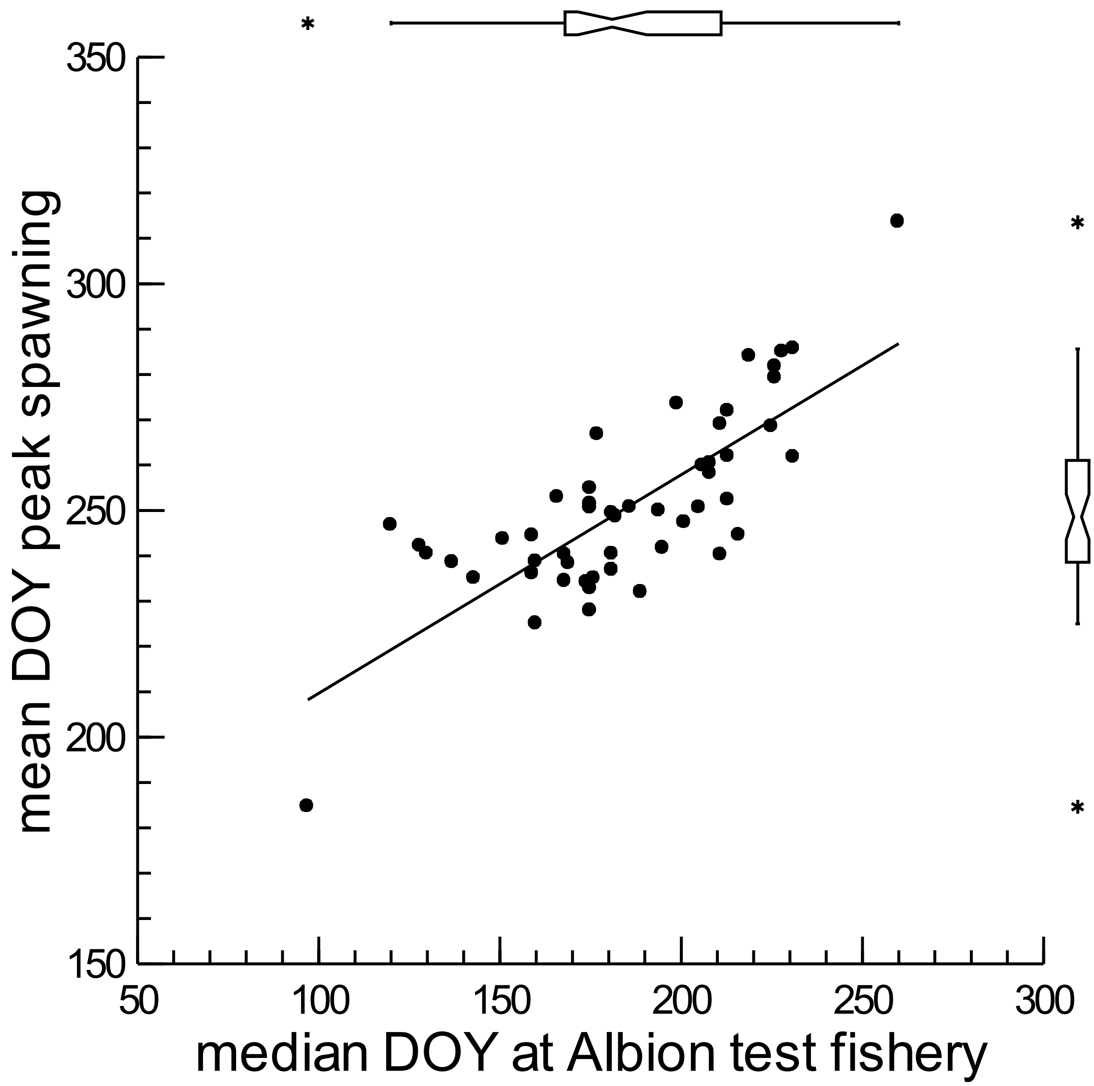


Figure 44. The date of peak spawning is related to the date of passage through the Albion (lower Fraser River) test fishery, as shown by this graph for chinook salmon in the Fraser River. Stock ID was made using microsatellite DNA.

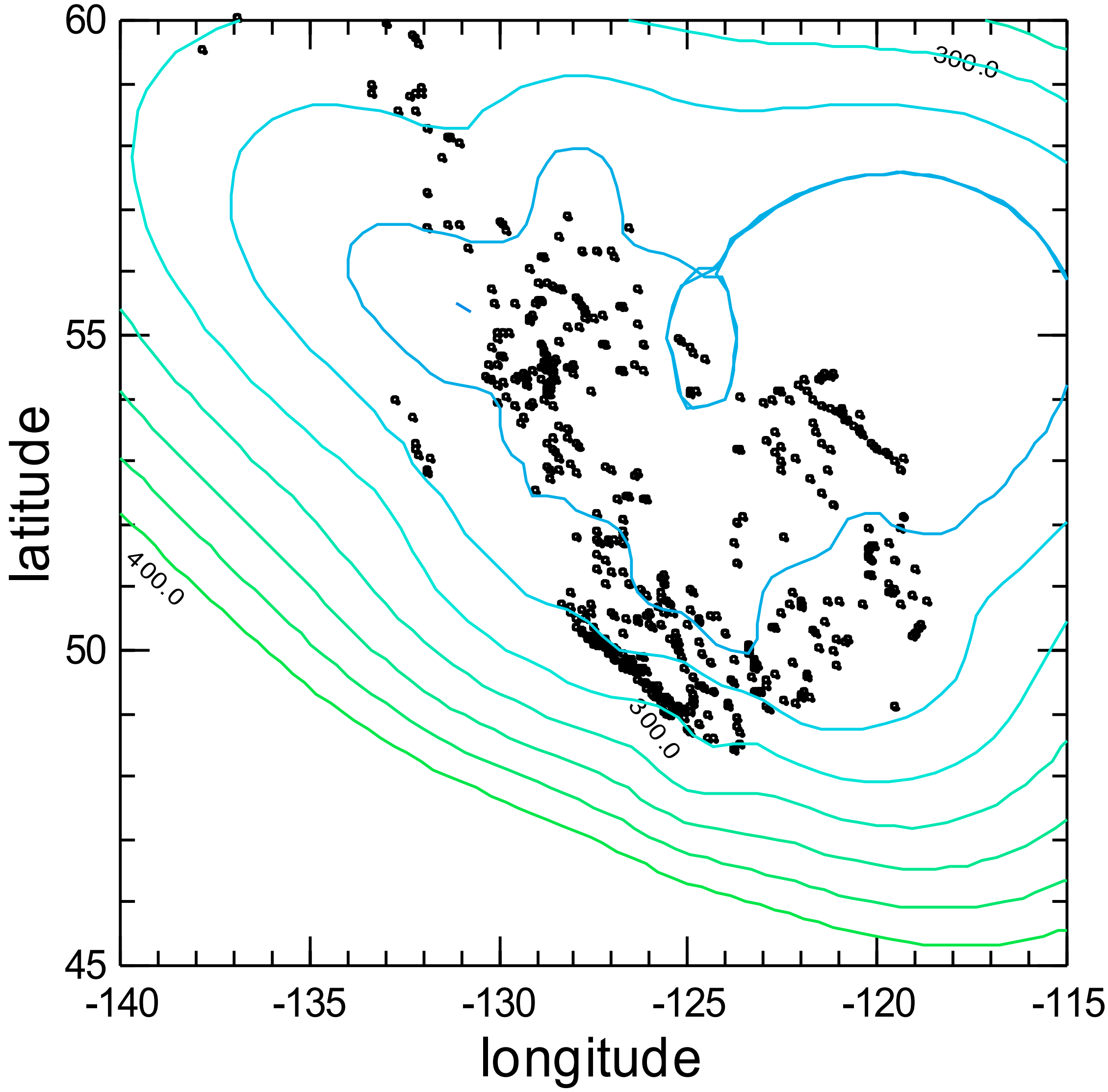


Figure 45. A geographical contour plot of mean spawning day-of-year for chinook salmon in British Columbia. Chinook spawning dates appear to be more uniform than the other species and the variation is distributed differently.

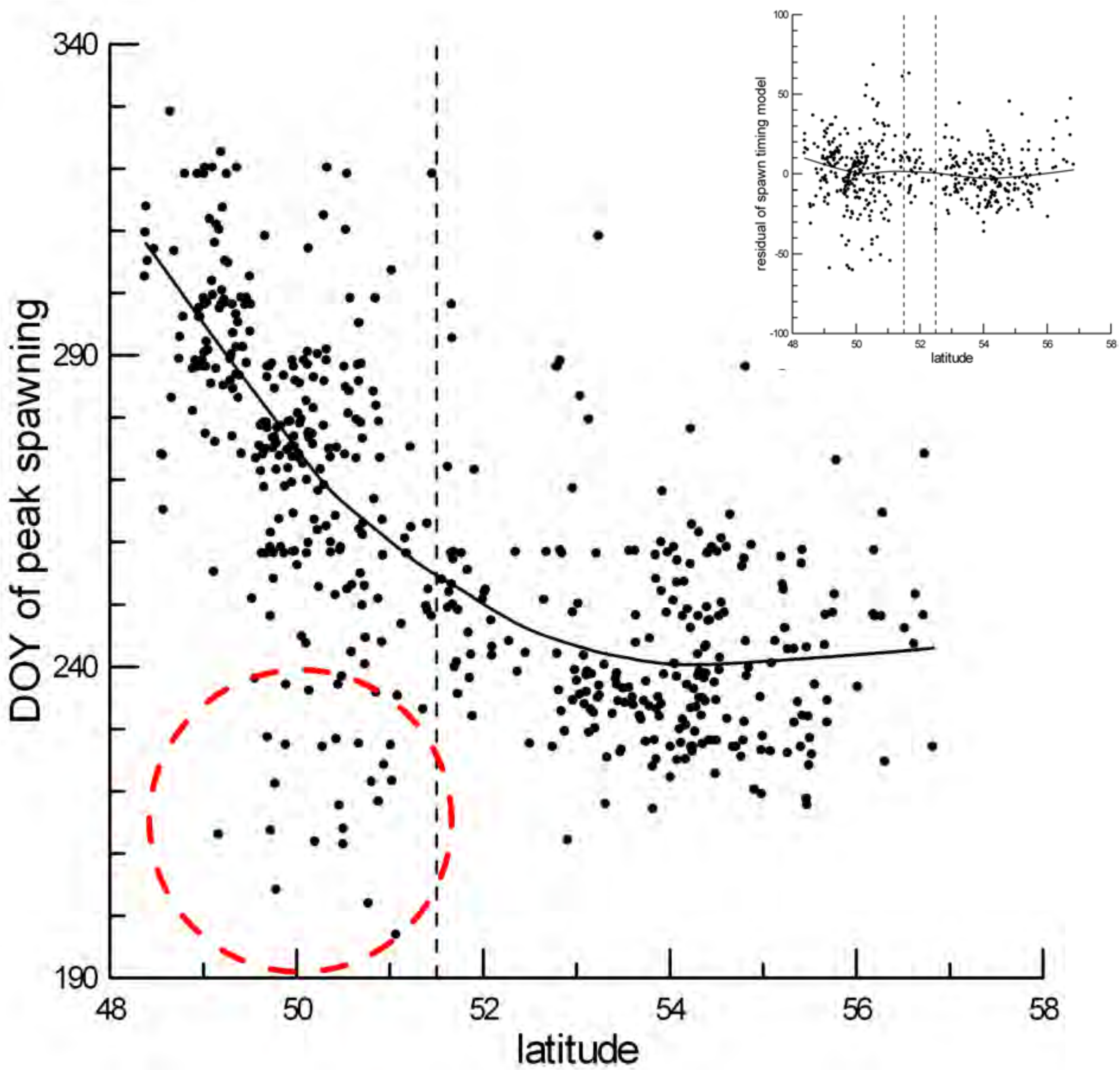


Figure 46. The relationship between the mean data of spawning (DOY) and latitude for chinook salmon in British Columbia. The solid line is a LOWESS smoothing function. The dashed vertical line indicates the latitude where a similar discontinuity in spawning time appears. For chinook salmon the discontinuity appears to be shifted about 1° northward. The populations inside the dotted circle are mostly in the SC FAZ and are thought to be predominantly stream-type. The small inset graph demonstrates how there is no discontinuity in the residuals.

Table 33. A regression model predicting DOY peak spawn for chinook salmon spawning in British Columbia.

The following populations were excluded as extreme outliers:
Chehalis River, Theodosia Creek, Fulmore River, Mathers Creek. In all four cases the date of peak spawning was exceptionally early.

Dep Var:DOY of peak spawning
N: 502
Adjusted squared multiple R: 0.531
Standard error of estimate: 18.324

Effect	Coefficient	Std Error	t	P(2 Tail)
CONSTANT	432.436	30.914	13.988	<0.001
Latitude (decimal degrees)	-3.627	0.558	-6.499	<0.001
% watershed either tundra or glaciers	-0.261	0.053	-4.888	<0.001
% watershed lake	0.774	0.175	4.418	<0.001
Annual degree days (C)	0.010	0.001	6.816	<0.001

Analysis of Variance

Source	SS	df	MSS	F-ratio	P
Regression	191588.156	4	47897.039	142.642	<0.001
Residual	166884.917	497	335.785		

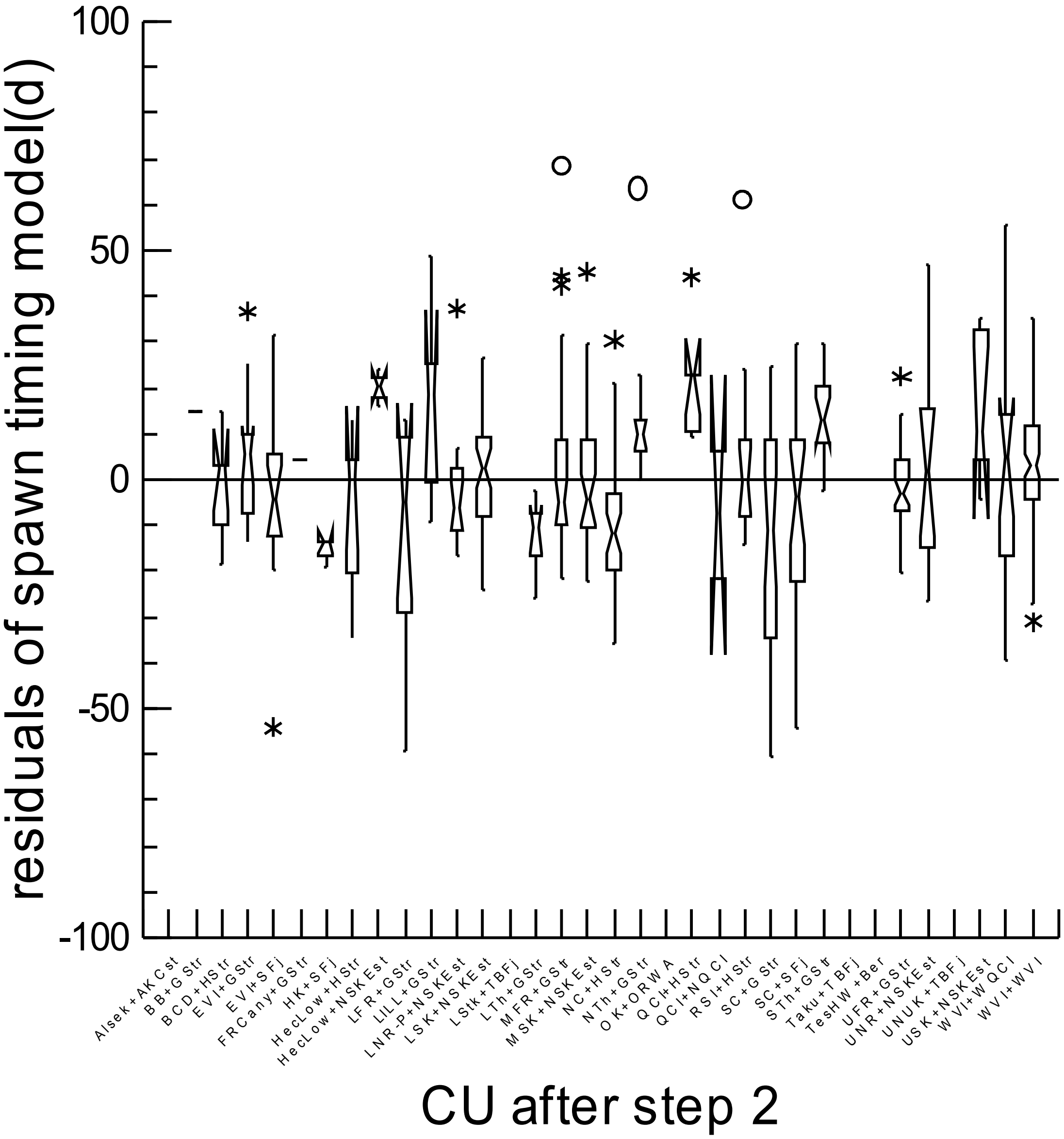


Figure 47. Box plots of the residuals from the spawn timing model for the chinook salmon of British Columbia summarized by JAZ ecotypic CU after step 2. The JAZ CUs are arranged alphabetically.

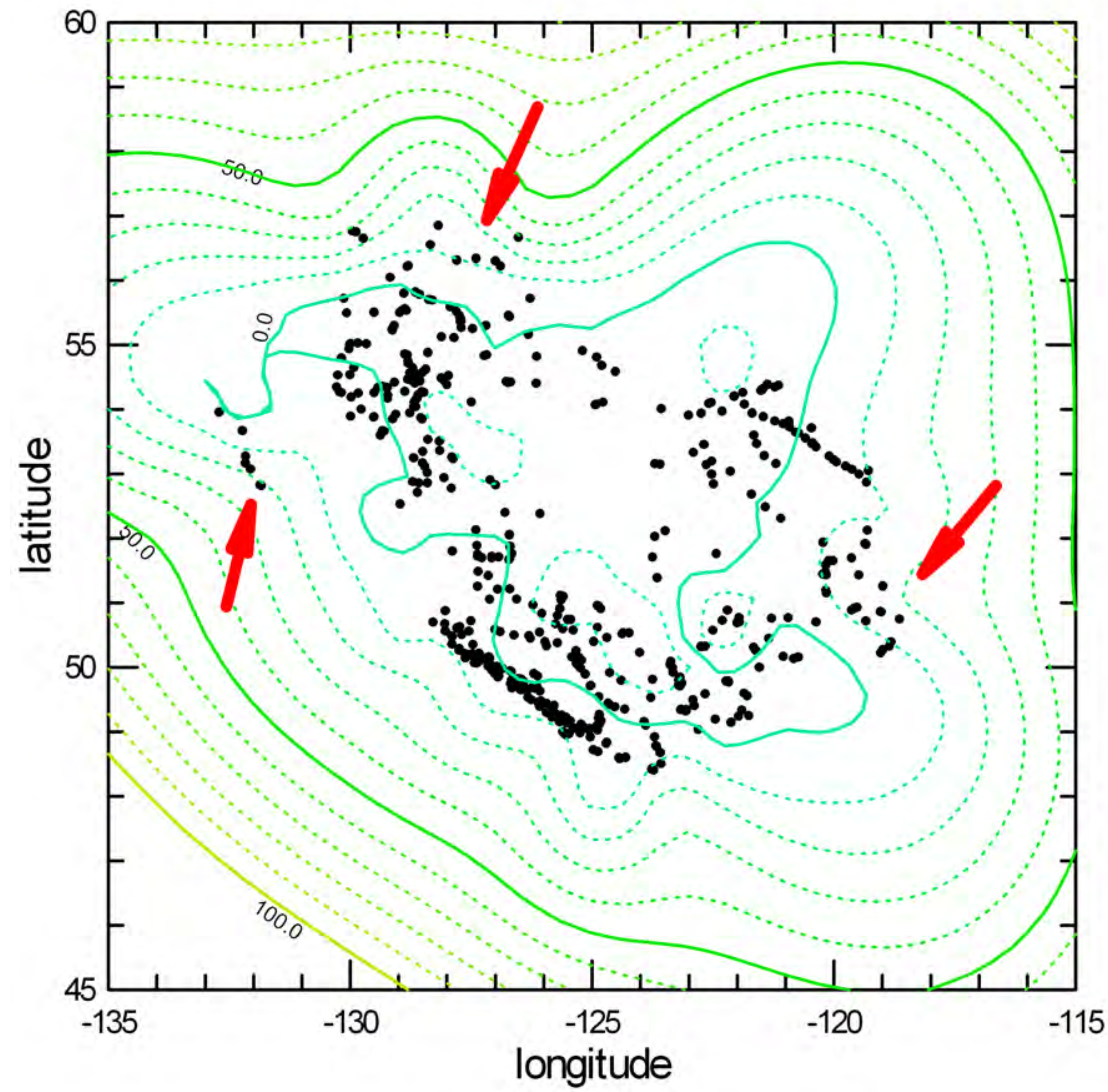


Figure 48. A geographical contour plot of the residuals from the spawn timing model for chinook salmon in British Columbia. The red arrows indicate areas where the model consistently under-predicted the observed spawning date (i.e., the residuals were positive).

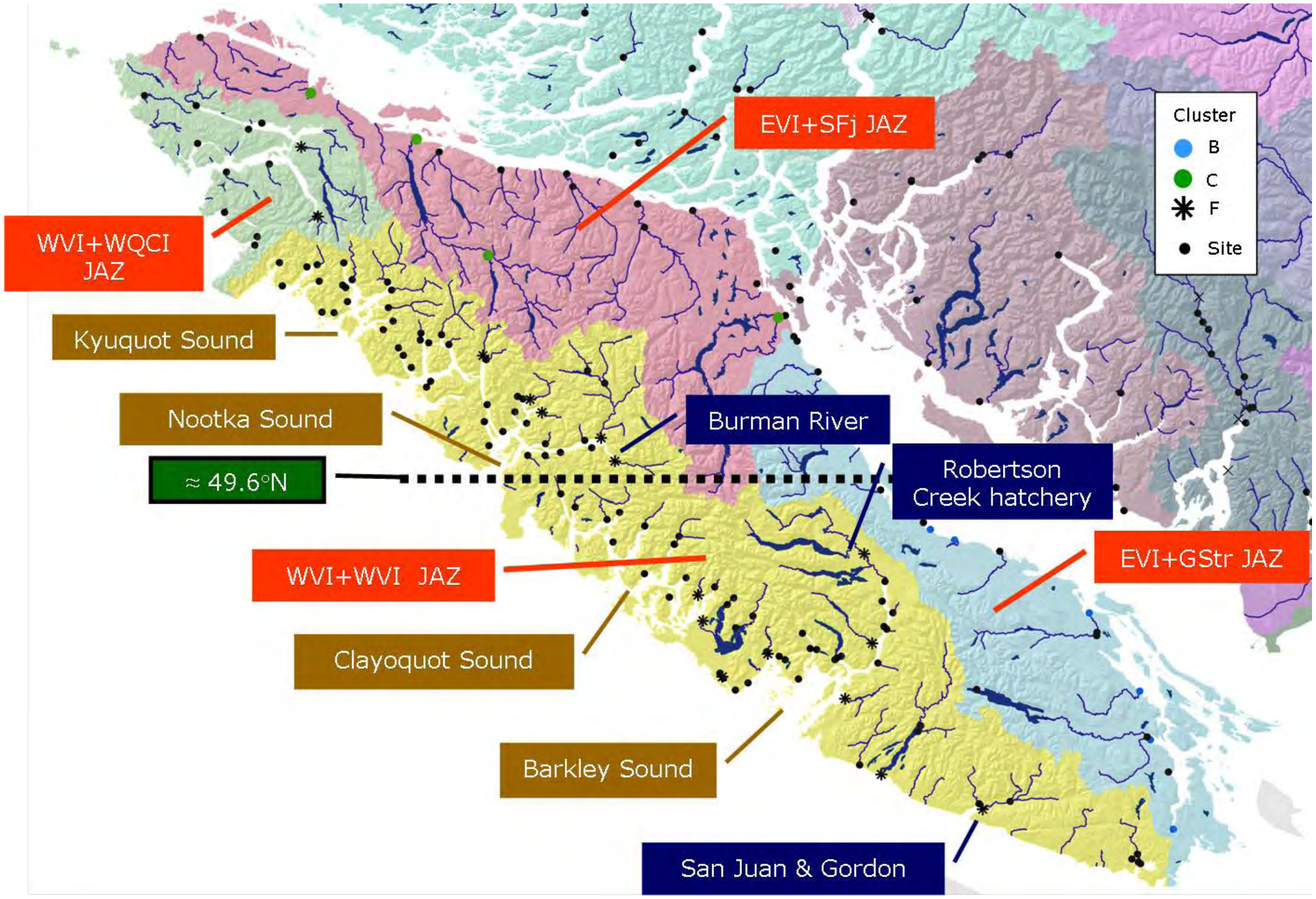


Figure 49. A map showing sites with chinook salmon on the west coast of Vancouver Island. The ecotypic CUs are labeled in red. Geographical features mentioned in the text are labeled in brown and chinook sites mentioned in the text are labeled in blue. The line of latitude that is shown (approximately) divides the two major chinook CUs in the WVI+WVI ecotypic CU.

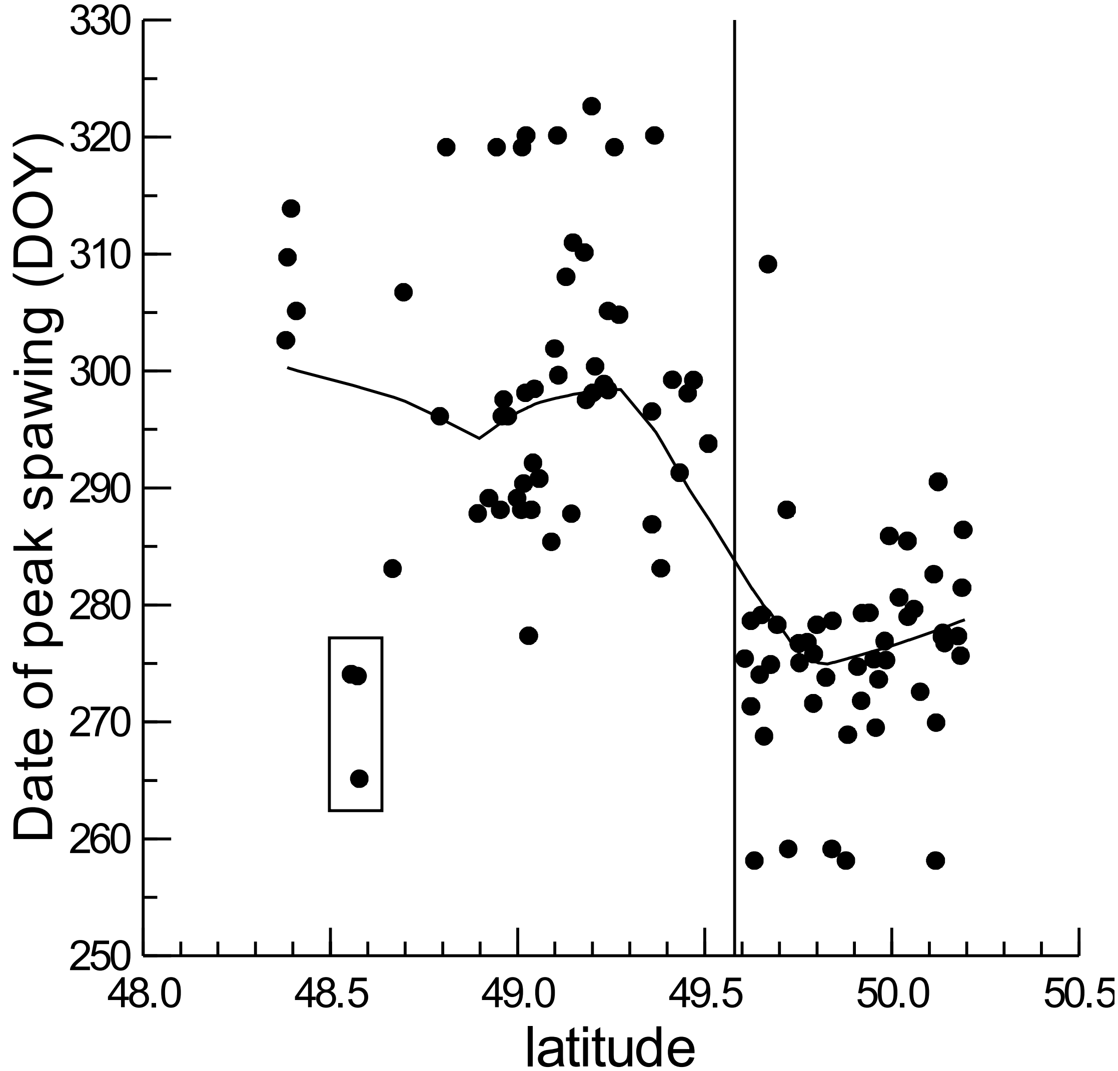


Figure 50. The date of peak spawning in chinook populations on the west coast of Vancouver Island shifts abruptly at latitude 49.58°N(the vertical dashed line), which lies to the immediate south of Kyuquot Sound. The three sites in the solid box are in the San Juan River system and spawn anomalously early for southern populations.

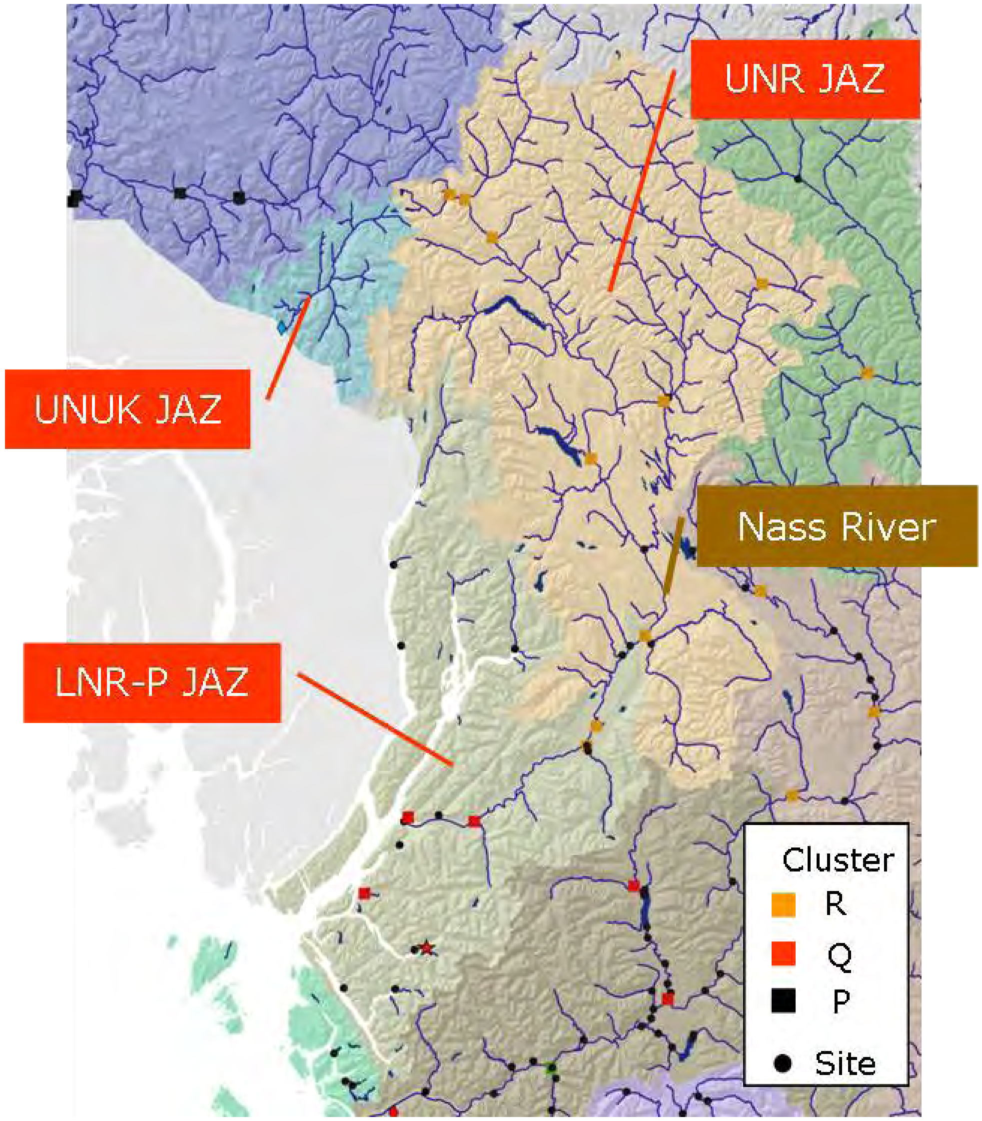


Figure 51. A map showing the location of chinook salmon sites in clusters Q and R within the LNR-P and UNR ecotypic CUs. Spawn timing data were used to expand the UNR CU to include the three sites in genetic cluster R (KSI SII AKS #651 & KSI SGASGINIST #655) that lie in the LNR-P ecotypic CU.

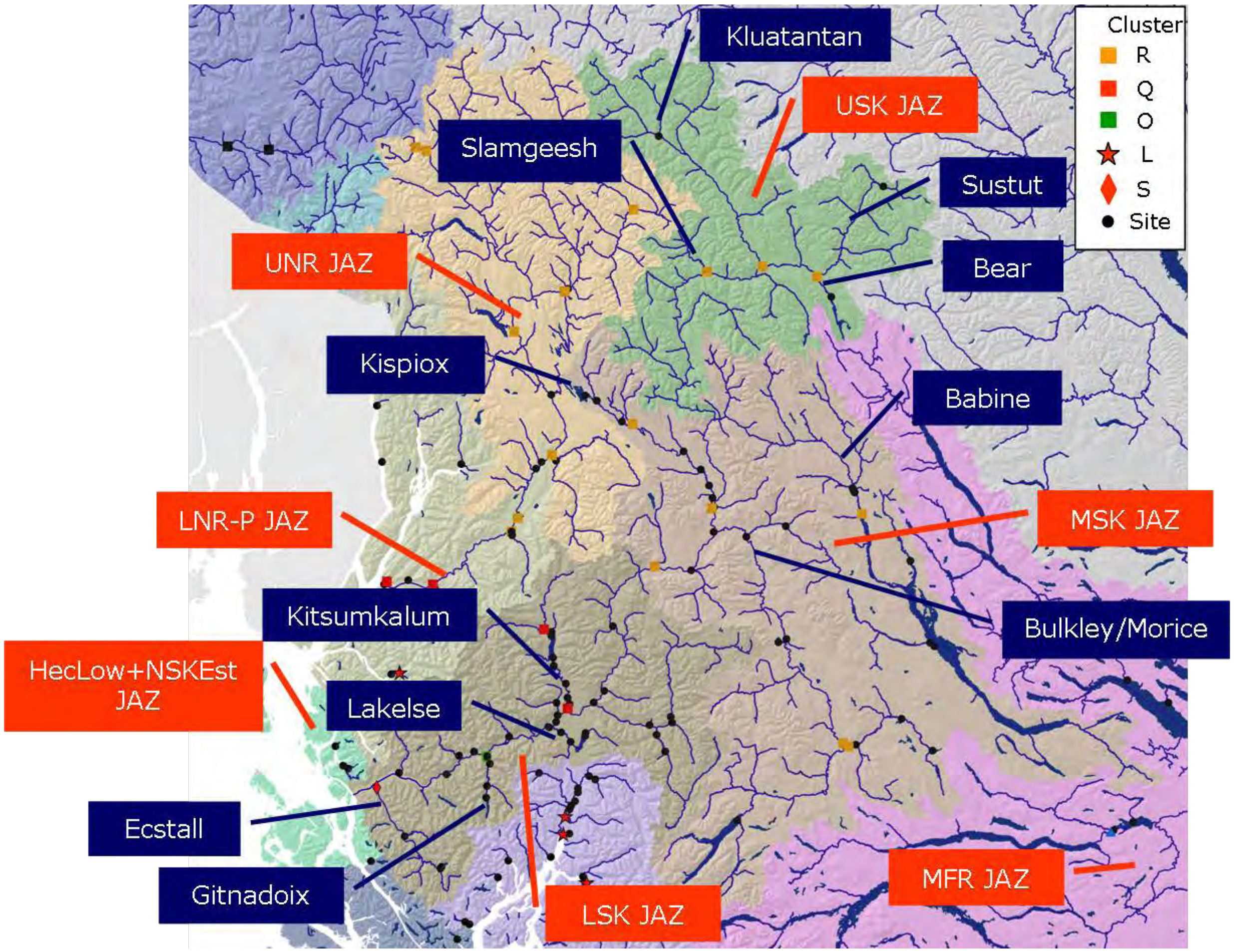


Figure 52. A map showing the locations of chinook sites in the Skeena River watershed. The genetic cluster of those sites with genetic samples is also shown. The ecotypic CUs (JAZ) are colored and labeled with red tags. Tributaries of the Skeena River mentioned in the text are labeled in blue.

Table 34. Genetic classification, peak spawning time and escapement information for chinook sites in the MSK and USK FAZ. Shaded sites had fewer than 5 observations of spawning time and were not used in the analyses. The genetic group was assigned to begin the examination of ecotypic CUs based on genetic structure (see text). The leftmost N_{obs} applies to the observations of peak spawning date and the other N_{obs} to the number of escapement observations. The residual comes from the spawn timing model for chinook and is applicable to the mean date of spawning for the site. The last two columns show the decisions concerning the Conservation Units in the two ecotypic CUs and are explained in the text.

			genetic		peak spawning				escapement (1950-2004)		Conservation Unit	
GFE_ID	site	FAZ	class	group	DOY	season	N obs	residual	mean	N obs	acronym	index
596	BOUCHER CREEK	MSK	.	1	227.0	MSUM	2	-11.1	18	4	MSK-LGLK	49
606	TACHEK CREEK	MSK	.	1	228.0	MSUM	1	-11.2	no data	-	MSK-LGLK	49
2350	SIMPSON CREEK	MSK	.	1	231.0	MSUM	4	-19.3	26	6	MSK-LGLK	49
544	HAROLD PRICE CREEK	MSK	.	1	242.7	LSUM	3	3.2	28	4	MSK-LGLK	49
601	MORRISON CREEK	MSK	.	1	244.0	LSUM	1	-2.6	no data	-	MSK-LGLK	49
540	BULKLEY RIVER-LOWER	MSK	.	1	246.1	LSUM	11	-5.6	359	26	MSK-LGLK	49
621	BEAR RIVER	USK	08.09-02	1	248.0	LSUM	40	4.1	9556	54	MSK-LGLK	49
556	MORICE RIVER	MSK	08.09-02	1	249.4	LSUM	45	-4.5	9737	54	MSK-LGLK	49
543	SUSKWA RIVER	MSK	.	1	252.2	LSUM	9	15.0	88	13	MSK-LGLK	49
593	BABINE RIVER-SECTION 4	MSK	08.09-02	1	256.4	LSUM	7	14.7	2287	55	MSK-LGLK	49
561	NANIKA RIVER	MSK	.	1	256.9	LSUM	28	9.3	220	35	MSK-LGLK	49
622	BEAR LAKE	USK	.	1	258.5	LSUM	4	14.7	1914	7	MSK-LGLK	49
595	NICHYESKWA CREEK	MSK	.	1	258.5	LSUM	13	20.2	no data	-	MSK-LGLK	49
2108	BABINE RIVER-SECTION 5	MSK	.	1	271.4	EFALL	5	-	921	44	MSK-LGLK	49
553	CANYON CREEK	MSK	.	1	288.0	EFALL	1	45.3	no data	-	MSK-LGLK	49
592	BABINE RIVER-SECTIONS 1 TO 3	MSK	08.09-02	1	no data	-	-	-	3587	3	MSK-LGLK	49
501254	FULTON RIVER	MSK	.	1	no data	-	-	-	16	17	MSK-LGLK	49
537	KITSEGUECLA RIVER	MSK	.	2a	226.3	MSUM	11	-22.5	75	13	MSK-M/S	48
496	SHEGUNIA RIVER	MSK	.	2a	230.9	MSUM	16	-6.8	155	26	MSK-M/S	48
569	MCCULLY CREEK	MSK	.	2a	231.9	LSUM	14	-7.1	46	8	MSK-M/S	48
568	HEVENOR CREEK	MSK	.	2a	232.0	LSUM	2	-16.0	35	2	MSK-M/S	48
567	DATE CREEK	MSK	.	2a	234.2	LSUM	6	-2.6	53	8	MSK-M/S	48
571	CULLON CREEK	MSK	.	2a	237.0	LSUM	1	-8.2	25	11	MSK-M/S	48

			genetic		peak spawning				escapement (1950-2004)		Conservation Unit	
GFE_ID	site	FAZ	class	group	DOY	season	N obs	residual	mean	N obs	acronym	index
488	KITWANGA RIVER	MSK	08.08-01	2	240.4	LSUM	31	-9.7	695	44	MSK	47
566	KISPIOX RIVER	MSK	08.08-01	2	242.7	LSUM	35	-0.7	3375	45	MSK	47
579	SWEETIN RIVER	MSK	08.08-02	2	243.3	LSUM	23	6.0	158	28	MSK	47
581	NANGEESE RIVER	MSK	.	2	248.2	LSUM	21	8.4	170	23	MSK	47
585	STEPHENS CREEK	MSK	.	2	248.5	LSUM	22	-9.7	no data	-	MSK	47
498	SLAMGEESH RIVER	USK	08.08-02	2	264.5	EFALL	4	32.9	380	5	MSK	47
587	CLUB CREEK-UPPER	MSK	.	2	273.0	EFALL	2	14.8	no data	-	MSK	47
3559	STEPHENS CREEK	MSK	.	2	no data	-	-	-	144	30	MSK	47
541	BULKLEY RIVER-UPPER	MSK	08.07-	3	234.3	LSUM	16	-17.4	822	52	MSK-UprBulk	50
565	MAXAN CREEK	MSK	.	3	238.0	LSUM	1	-11.7	35	2	MSK-UprBulk	50
563	BUCK CREEK	MSK	.	3	243.3	LSUM	7	-4.3	46	7	MSK-UprBulk	50
564	RICHFIELD CREEK	MSK	.	3	no data	-	-	-	51	5	MSK-UprBulk	50
620	SUSTUT RIVER	USK	08.09-01	4	224.6	MSUM	5	-4.5	489	11	USK	51
501	KLUATANTAN RIVER	USK	.	4	227.0	MSUM	1	5.7	no data	-	USK	51
627	JOHANSON CREEK	USK	.	4	251.5	LSUM	2	34.9	88	6	USK	51

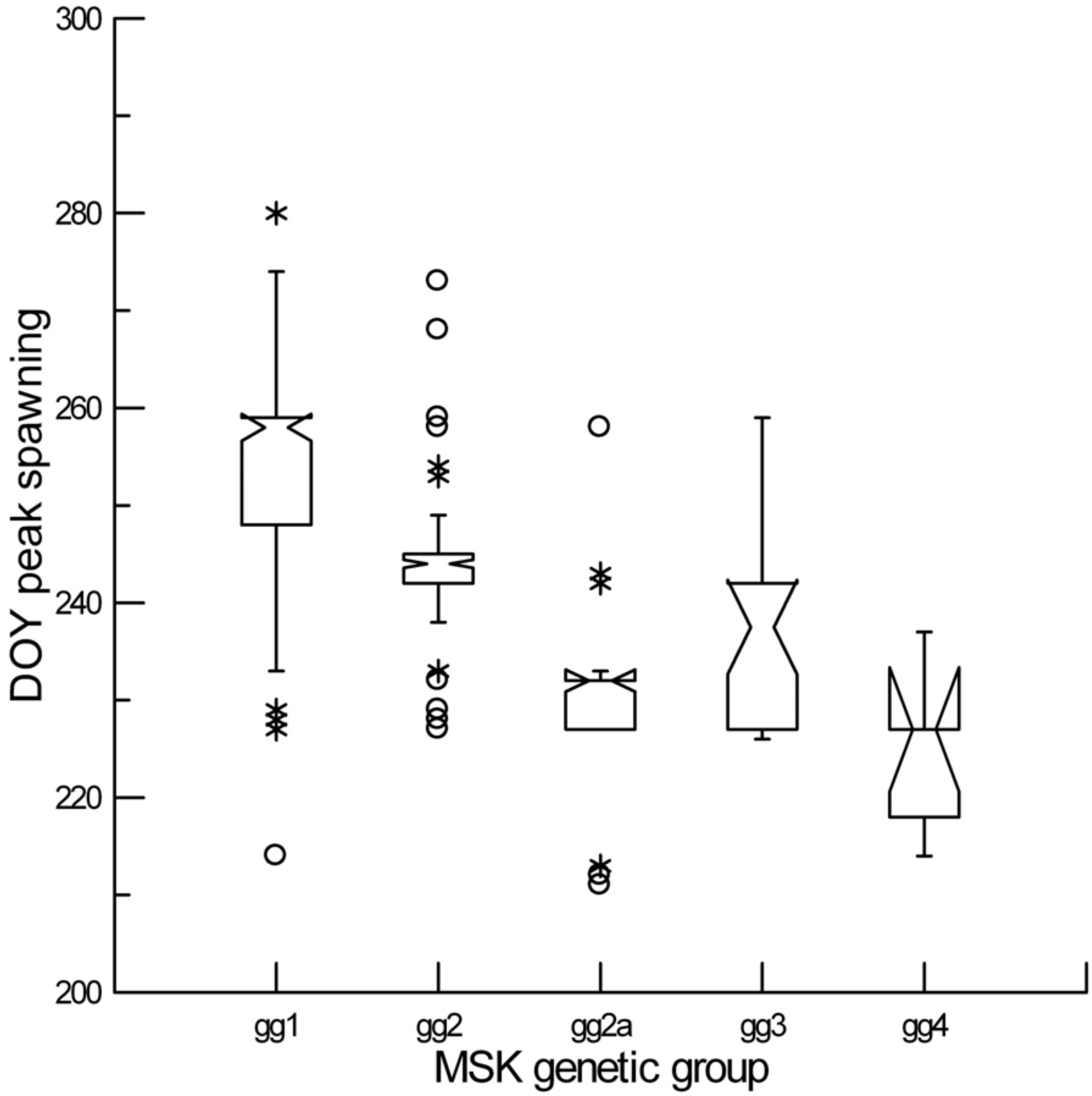


Figure 53. Box plots of the DOY of peak spawning for five genetic groups of streams in the MSK and USK ecotypic CUs. The principal systems in each group are indicated in Table 34.

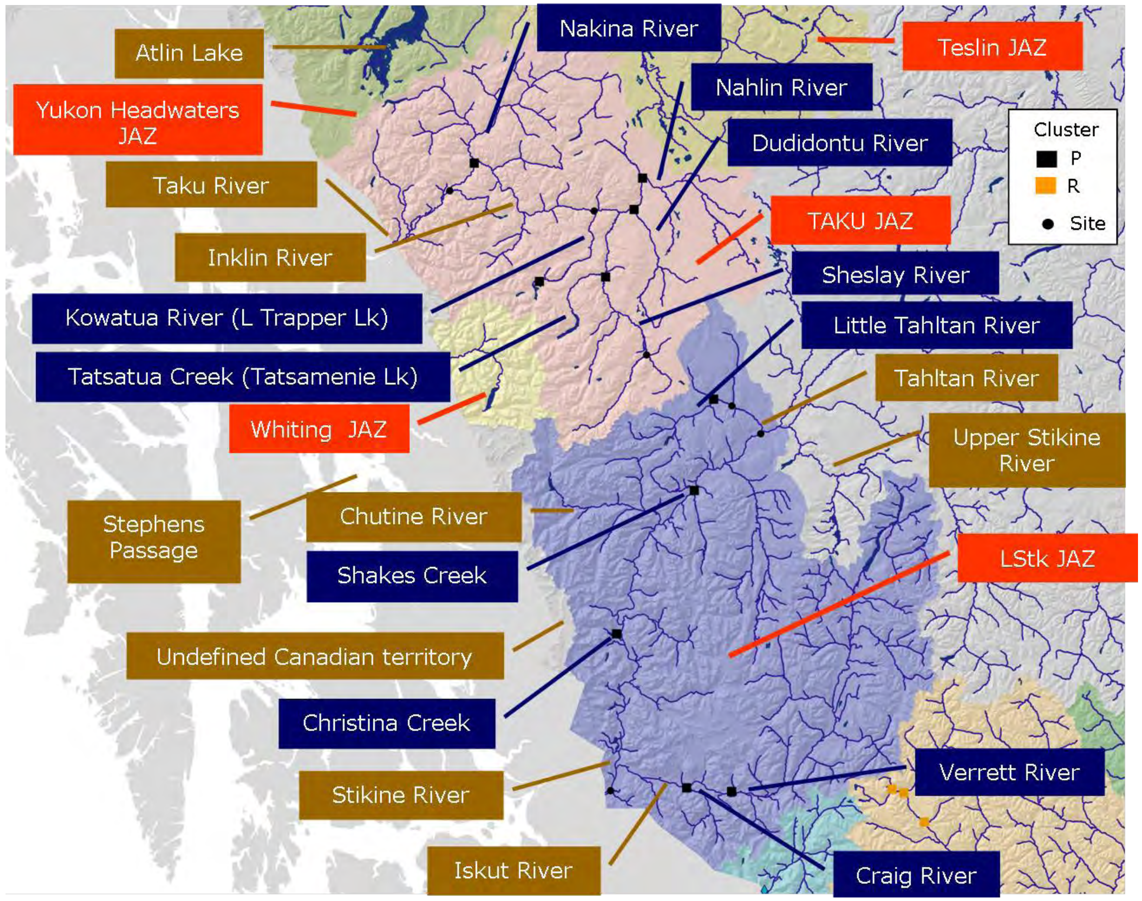


Figure 54. A map showing chinook sites in the Stikine and Taku Rivers. Ecotypic CUs (JAZ) are labeled in red and geographic features of interest in brown. Sites mentioned in the text of for which there are genetic samples are labeled in blue. The undefined Canadian territories are areas with no streams that were not included in the Ecological Drainage Units that are the basis of the JAZ.

Table 35. A discriminant function for the lower Stikine and Taku sites with chinook salmon.

Group Frequencies

Lower Stikine	Taku
8	8

Group Means

variable	Lower Stikine	Taku
MS_GR	4.97	3.92
T_GR	84.8	55.3
GLAC_PERC	6.57	1.33
PERCTUNDRA	33.0	21.4
HIGHLEVEL	39.6	22.7
LAKE_PERC	0.45	1.65
PPT_ANN_M	1496.7	571.6
TEMP_ANN_M	1.14	-0.25
ELEV_MEAN	1191.5	1086.6
KFAC_LOG	3.99	3.75
VFW_MEAN	2.46	1.69
PPT_AUG_M	95.3	45.5
PPT_SEP_M	160.4	68.8
PPT_OCT_M	231.4	75.3
PPT_NOV_M	169.5	59.9
PPT_DEC_M	160.0	56.0
TEMP_AUG_M	11.7	10.9
TEMP_SEP_M	7.68	6.44
TEMP_OCT_M	2.05	0.80
TEMP_NOV_M	-6.08	-8.52
TEMP_DEC_M	-9.28	-10.6

Stepping Summary

variable	Approx. F-ratio	p-value
T_GR	8.41	0.012
LAKE_PERC	9.14	0.003
PERCTUNDRA	8.15	0.003
ELEV_MEAN	7.87	0.003

Jackknifed Classification Matrix

	Lower Stikine	Taku	%correct
Lower Stikine	7	1	88
Taku	2	6	75
Total	9	7	81

Canonical Discriminant Functions Standardized by Within Variances

variable	component 1
T_GR	0.91
PERCTUNDRA	0.70
LAKE_PERC	-1.18
ELEV_MEAN	0.61

Canonical Scores of Group Means

population group	component 1
Lower Stikine	1.58
Taku	-1.58

Table 36. A discriminant function for the two run timing groups of chinook salmon in the lower Stikine.

Group Frequencies

first-run	second-run
5	3

Group Means

variable	first	second
MS_GR	5.80	3.59
T_GR	76.1	99.2
GLAC_PERC	3.58	11.5
PERCTUNDRA	31.9	34.8
HIGHLEVEL	35.5	46.4
LAKE_PERC	0.53	0.33
PPT_ANN_M	882.1	2520.9
TEMP_ANN_M	0.44	2.31
ELEV_MEAN	1471.8	724.3
KFAC_LOG	3.84	4.23
VFW_MEAN	1.21	4.54
PPT_AUG_M	59.2	155.5
PPT_SEP_M	96.3	267.1
PPT_OCT_M	132.1	397.0
PPT_NOV_M	95.5	292.9
PPT_DEC_M	96.6	265.6
TEMP_AUG_M	11.5	12.0
TEMP_SEP_M	7.23	8.41
TEMP_OCT_M	1.44	3.06
TEMP_NOV_M	-7.52	-3.68
TEMP_DEC_M	-10.5	-7.31

Stepping Summary

variable	Approx. F-ratio	p-value
PPT_AUG_M	18.2	0.0053
LAKE_PERC	54.9	0.0004
GLAC_PERC	61.8	0.0008

Jackknifed Classification Matrix

	Lower Stikine	Taku	%correct
first	4	1	80
second	0	3	100
Total	4	4	88

Canonical Discriminant Functions Standardized by Within Variances

variable	component 1
GLAC_PERC	1.11
LAKE_PERC	-3.51
PPT_AUG_M	3.22

Canonical Scores of Group Means

population group	component 1
first-run	-4.57
second-run	7.61

Table 37. A discriminant function for the three run timing groups of Taku River chinook.

Group Frequencies

early	late	mid
3	4	1

Group Means

variable	early	mid	late
MS_GR	6.57	0.96	7.84
T_GR	43.5	64.0	55.7
GLAC_PERC	0.00	2.65	0.00
PERCTUNDRA	11.2	30.0	17.4
HIGHLEVEL	11.2	32.7	17.4
LAKE_PERC	1.14	2.42	0.08
PPT_ANN_M	524.4	628.2	486.5
TEMP_ANN_M	-0.73	-0.30	1.41
ELEV_MEAN	1050.0	1150.8	940.0
KFAC_LOG	3.69	3.79	3.80
VFW_MEAN	1.22	2.46	0.00
PPT_AUG_M	48.2	43.2	46.7
PPT_SEP_M	59.6	79.3	54.4
PPT_OCT_M	61.9	89.7	58.1
PPT_NOV_M	51.8	69.4	46.3
PPT_DEC_M	49.8	63.6	44.3
TEMP_AUG_M	11.0	10.8	11.0
TEMP_SEP_M	6.32	6.35	7.17
TEMP_OCT_M	0.36	0.76	2.26
TEMP_NOV_M	-9.16	-8.93	-4.99
TEMP_DEC_M	-12.2	-10.32	-6.87

Stepping summary

variable	Approx. F-ratio	p-value
KFAC_LOG	32.0	0.0014
TEMP_NOV_M	15.5	0.0008
TEMP_SEP_M	141.8	<<0.0001

Jackknifed Classification Matrix

	early	late	mid	%correct
early	3	0	0	100
late	0	4	0	100
mid	0	0	1	100

Canonical Discriminant Functions : Standardized by Within Variances

variable	component 1	component 2
KFAC_LOG	3.53	1.05
TEMP_SEP_M	23.4	0.37
TEMP_NOV_M	-23.8	-0.36

Canonical Scores of Group Means

population group	component 1	component 2
early	3.56	-3.59
late	17.2	2.31

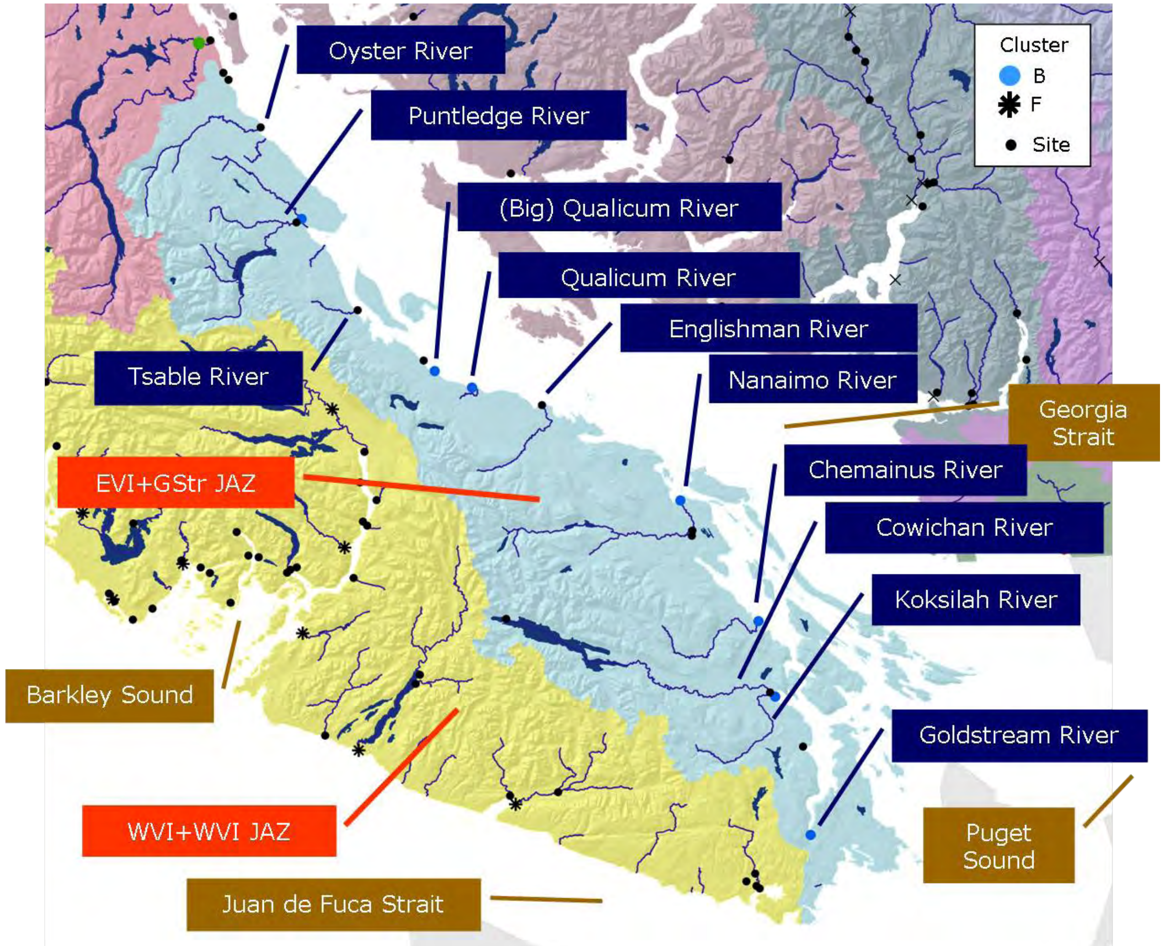


Figure 55. A map showing sites in the EVI+GStr JAZ ecotypic CU with chinook salmon. Sites mentioned in the text are labeled in blue. Other landmarks of interest are labeled in brown.

Table 38. The numbers of hatchery supplementations that occurred in EVI+GStr chinook systems between 1968 and 2005. The source of the brood stock used is noted. All releases in the tributaries and adjacent marine areas were included. Two release sites are not shown but both were marine sites not adjacent to a known wild or non-wild chinook population.

River system	number of interventions with stock of specified source						%interventions using native stock
	Native	Naturalized	Non-Native	Part Naturalized	Hybrid	Total	
Chemainus R	23				2	25	92%
Cowichan R	76					76	100%
Englishman R			14			14	0%
Goldstream R	19		21			40	48%
Koksilah R	2					2	100%
Little Qualicum R	2	34	7	2		45	4%
Nanaimo R	56		5			61	92%
Oyster R		12	2			14	0%
Puntledge R	109		18		10	137	80%
Qualicum R	59					59	100%
Shawnigan C	1		9			10	10%
Tsable R			8			8	0%
Tsolum R			1			1	0%
Menzies C			1			1	0%

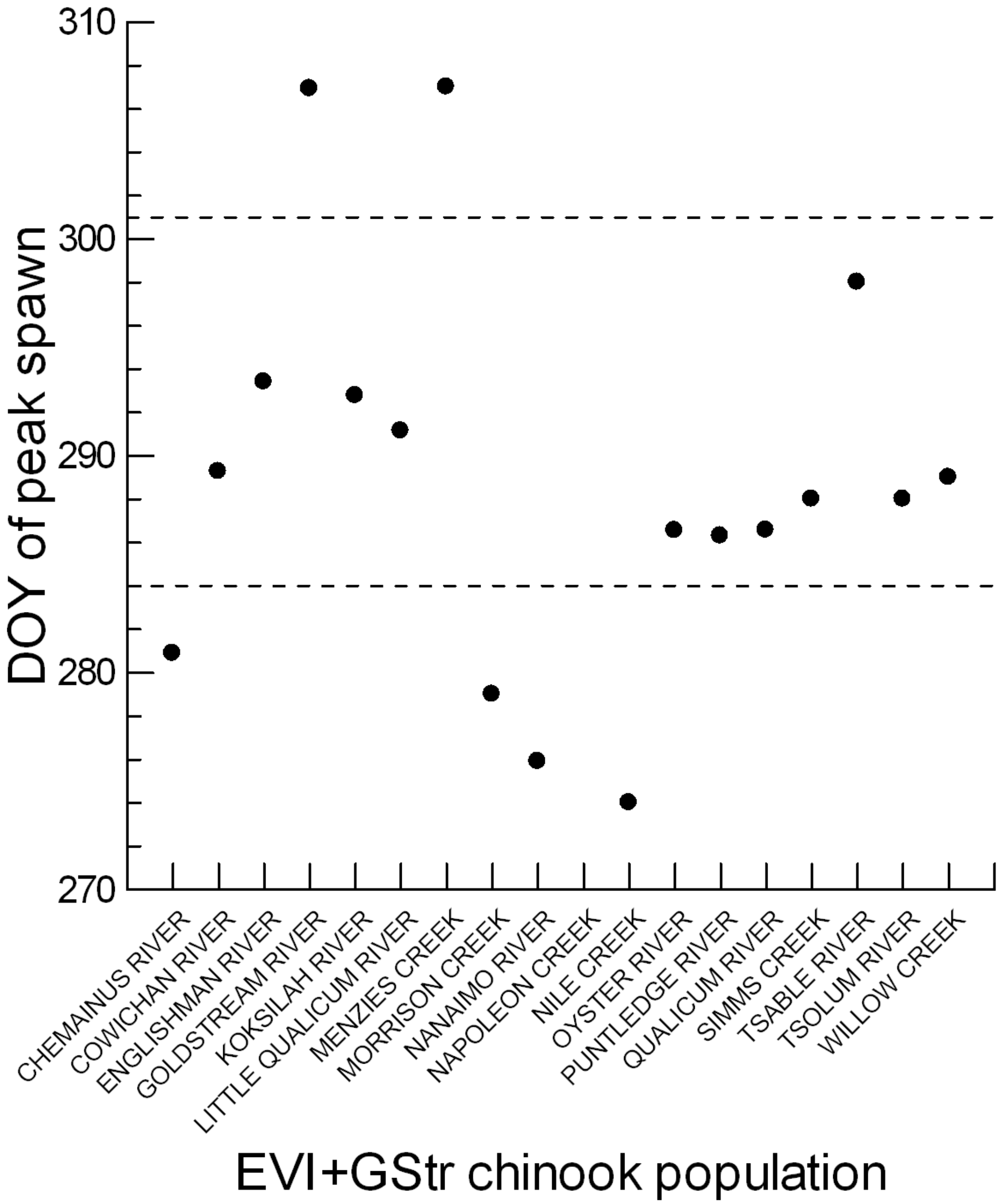


Figure 56. The mean date of spawning (DOY) for chinook populations in the EVI+GStr JAZ ecotypic CU. The horizontal lines at DOY 284 (EFALL) and 301 (MFALL) divide the populations into early, mid and late timing groups.

Table 39. A summary of the 68 Conservation Units for chinook salmon in index order, which is roughly geographical from south to north. The number of sites indicated is the total in our database and is not to be interpreted as the number of sites where chinook salmon are persistently found. The names are suggestions only.

Conservation Unit	Acronym	index	number of sites	classification step	comments
Okanagan	OK	1	1	ecotypic	confirmed by genetics
Boundary Bay	BB	2	2	ecotypic	confirmed by genetics
LFR fall white	LFR-fall	3	1	genetics/life-history/timing	hatchery and feral populations have established elsewhere in the LFR
LFR spring	LFR-spring	4	3	genetics/life-history/timing	includes native populations in Chehalis and Stave
LFR Upper Pitt	LFR-UPITT	5	1	genetics/timing	intermediate timing between true springs and summer runs
LFR summer	LFR-summer	6	10	genetics/life-history/timing	
Maria Slough	Maria	7	1	genetics/life-history	
FR Canyon-Nahatlatch	NAHAT	8	1	ecotypic	
MFR Portage	Portage	9	1	genetics/life-history	
MFR spring	MFR-spring	10	21	timing/habitat	headwater streams
MFR summer	MFR-summer	11	19	timing/habitat	headed by large lake
UFR spring	UFR-spring	12	38	ecotypic	confirmed by genetics
STh summer age 0.3	STh-0.3	13	7	genetics/life-history/timing	does not include 2 sites in upper Shuswap River with similar life history and age
STh summer age 1.3	STh-1.3	14	3	genetics/life-history/timing	
Shuswap River summer age 0.3	STh-SHUR	15	2	genetics/life-history	genetically and geographically distinct from CU#13
STh Bessette Creek	STh-BESS	16	3	genetics/life-history	similar to CU#14 but different age (1.2). Different optimum for adult size?
LTHOM spring age 1.2	LTh	17	9	ecotypic	confirmed by genetics and life history
NTHOM spring age 1.3	NTh-spr	18	6	ecotypic/timing/habitat	confirmed by genetics and life history, headwater streams
NTHOM summer age 1.3	NTh-sum	19	7	ecotypic/timing/habitat	confirmed by genetics and life history, headed by large lakes
South Coast-Georgia Str	SC+GStr	20	35	ecotypic/timing	confirmed by genetics

Conservation Unit	Acronym	index	number of sites	classification step	comments
E Vancouver Island-Goldstream	Goldstr	21	1	genetics/timing	status as wild CU uncertain
E Vancouver Island-Cowichan&Koksilah	CWCH-KOK	22	3	genetics/timing/other	relatively unimpacted by hatchery interventions
E Vancouver Island-Nanaimo Spring	NanR-Spr	23	?	genetics/timing	only spring population in JAZ
E Vancouver Island-Nanaimo Summer	NanR-Sum	24	?	genetics/timing	one of 2 summer populations in JAZ
E Vancouver Island-Nanaimo & Chemainus Fall	midEVI-Fall	25	4	genetics/timing	includes Chemainus R
E Vancouver Island-Puntledge Summer	PuntR-Sum	26	?	genetics/timing	one of 2 summer populations in JAZ
E Vancouver Island-Qualicum Puntledge Fall	QP-Fall	27	13	genetics/timing	heavily impacted by hatchery interventions and habitat loss
S Coast-Southern Fjords	SC+SFj	28	22	timing/habitat	
NE Vancouver Island	NEVI	29	12	timing/habitat	
Port San Juan	PSJ	30	3	timing/habitat	San Juan and Gordon Rivers
SW Vancouver Island	SWVI	31	49	timing/habitat	excludes feral populations associated with Robertson Creek hatchery
Nootka & Kyuquot	NoKy	32	49	timing/habitat	
NW Vancouver Island	NWVI	33	14	ecotypic	confirmed by genetics
Homathko	HOMATH	34	2	genetics	
Klinaklini	KLINA	35	2	genetics	
Docee	DOCEE	36	1	genetics/life-history	
Rivers Inlet	RI	37	13	genetics/life-history/habitat	
Wannock	WANN	38	1	genetics/life-history/habitat	
Bella Coola-Bentinck	BCR-BENT	39	7	life history/habitat	ocean type, coastal climate
Dean River	DEAN	40	3	life history/habitat	stream type, transitional climate
NCC-late timing	NCC-lake	41	10	timing/habitat	
NCC-early timing	NCC-stream	42	31	timing/habitat	
QCI-North	QCIN	43	2	ecotypic	confirmed by genetics
QCI-East	QCIE	44	5	ecotypic	confirmed by genetics; excludes Pallant Creek
Skeena Estuary	SKEst	45	3	ecotypic	
Ecstall	ECST	46	4	genetics	
Gitnadoix	GITN	47	5	genetics	
Lower Skeena	LSK	48	16	genetics/timing	
Kalum-Early	KALUM-E	49	5	genetics/timing	

Conservation Unit	Acronym	index	number of sites	classification step	comments
Kalum-Late	KALUM-L	50	4	genetics/timing	
Lakelse	Lakelse	51	5	timing	
Middle Skeena	MSK	52	8	timing/habitat	late timing small lakes
Middle Skeena-large lakes	MSK-LGLKS	53	17	timing/habitat	late timing; includes some sites in the USK JAZ
Middle Skeena mainstem tributaries	MSK-M/S	54	6	timing	very early timing
Upper Bulkley River	MSK-UprBulk	55	4	timing	middle timing; considerable hatchery intervention-wild status uncertain
Upper Skeena	USK	56	3	genetics/timing	the most interior of sites in the USK JAZ
Portland Sound-Observatory Inlet-Lower Nass	LNR-P	57	13	genetics/timing	in the Nass River, includes sites upstream to but not including the Tseax River
Upper Nass	UNR	58	16	genetics/timing	Tseax and upstream
Unuk	UNUK	59	?	ecotypic/ecology	age 1.4; late timing; inside rearing
Stikine-early timing	LSTK-early	60	6	timing/habitat	age 1.4/;early June timing; outside rearing
Stikine-late timing	LSTK-late	61	3	timing/habitat	early July timing; smaller fish than early run
Whiting	WHITING	62	?	ecotypic	no information beyond presence
Taku-early timing	TAKU-early	63	3	timing/habitat	age 1.3; mid-May timing; outside rearing
Taku-mid timing	TAKU-mid	64	1	timing/habitat	age 1.3; mid-June timing; outside rearing
Taku-late timing	TAKU-late	65	4	timing/habitat	age 1.3; early July timing; outside rearing
Lynn Canal	LYNN	66	?	ecotypic	age 1.4early July timing; late July spawning; inside rearing
Alsek	Alsek	67	2	ecotypic/timing/ecology	some sites in the Yukon Territory
Yukon River-Teslin headwaters	Teslin	68	4	genetics	some sites in the Yukon Territory
hatchery excluded		999	6		hatchery site or transplanted population

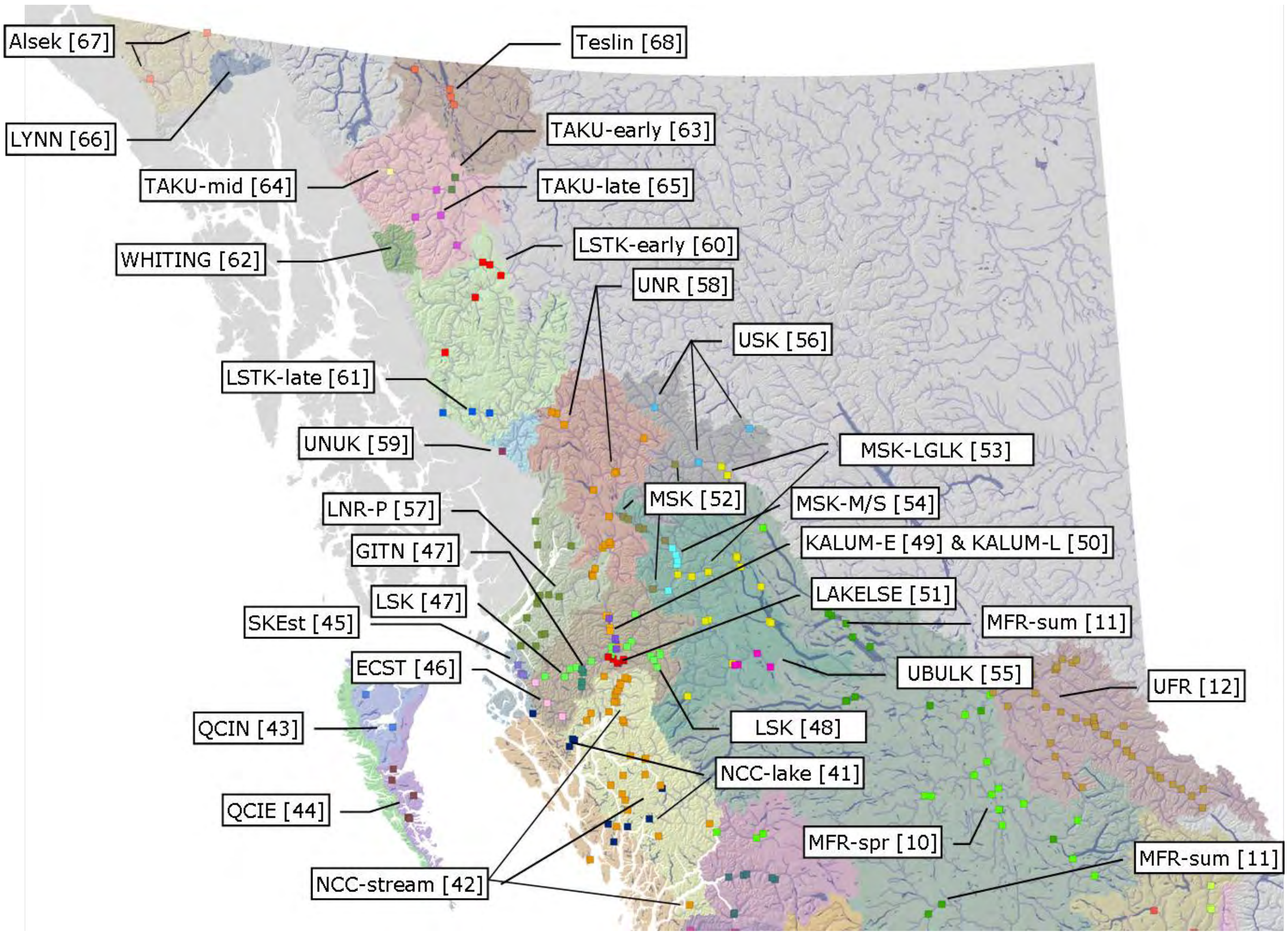


Figure 57. A map showing chinook CUs #41 to #68 in northern British Columbia and the three CUs in the middle and upper Fraser River (#10-#12).. All sites within each CU are shown with color-coded symbols. The labels identify each CU by pointing to a site in the CU. The number in brackets is the CU index number.

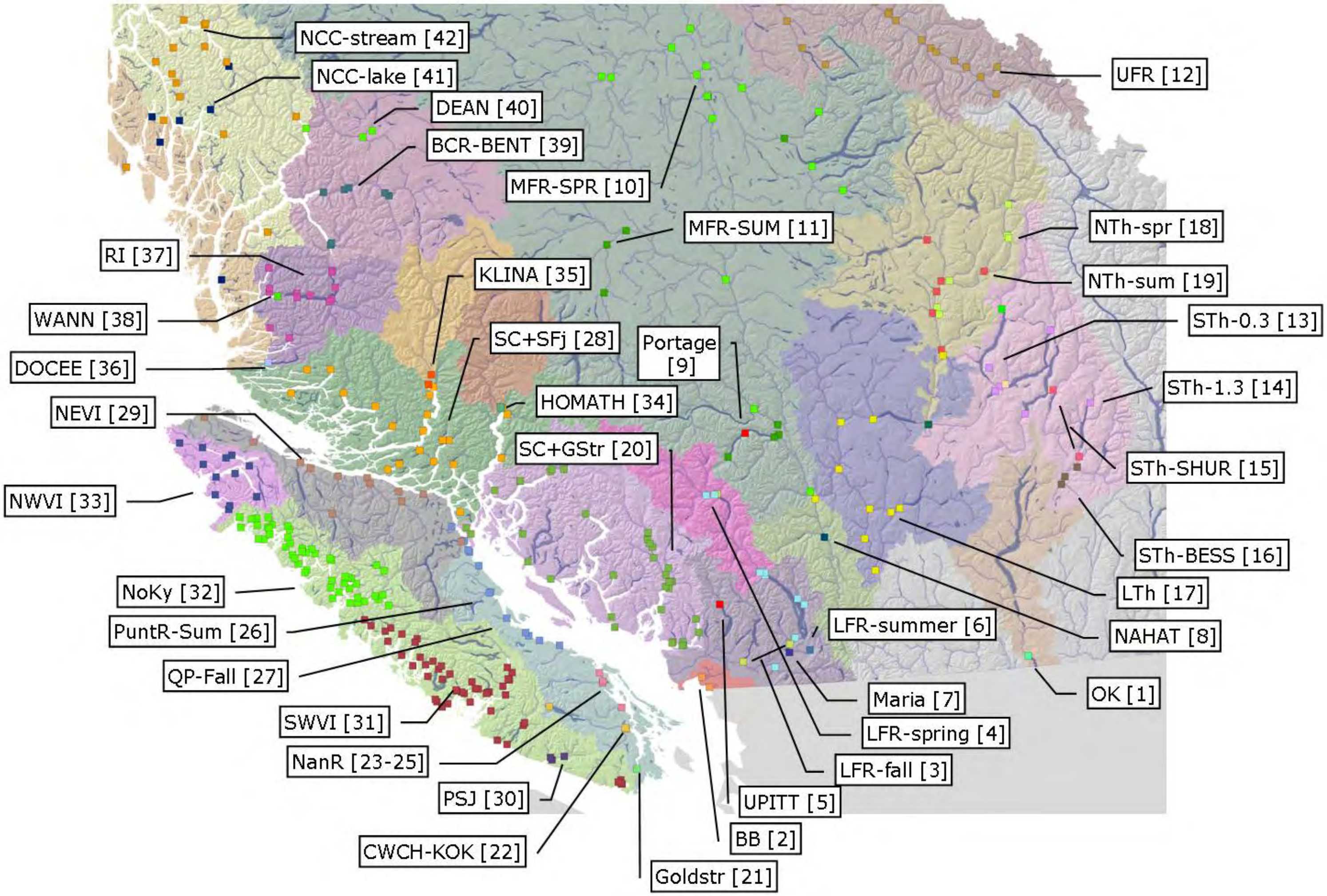


Figure 58. A map showing chinook CUs #1 to #37 in southern and central British Columbia. All sites within each CU are shown with color-coded symbols. The labels identify each CU by pointing to a site in the CU. The number in brackets is the CU index number.

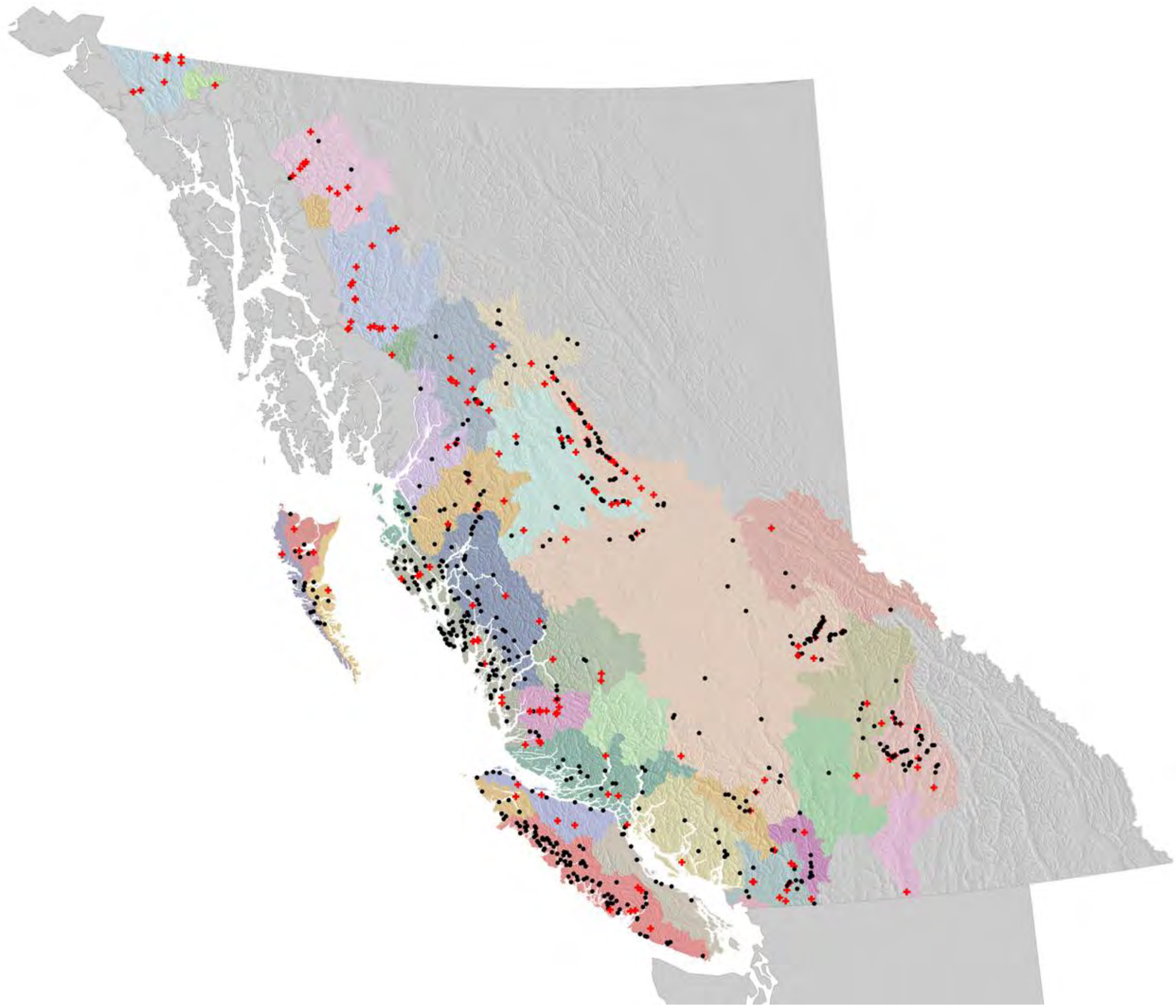


Figure 59. A map of British Columbia showing the sites with sockeye salmon in our database (●) including those with a genetic sample (✚).

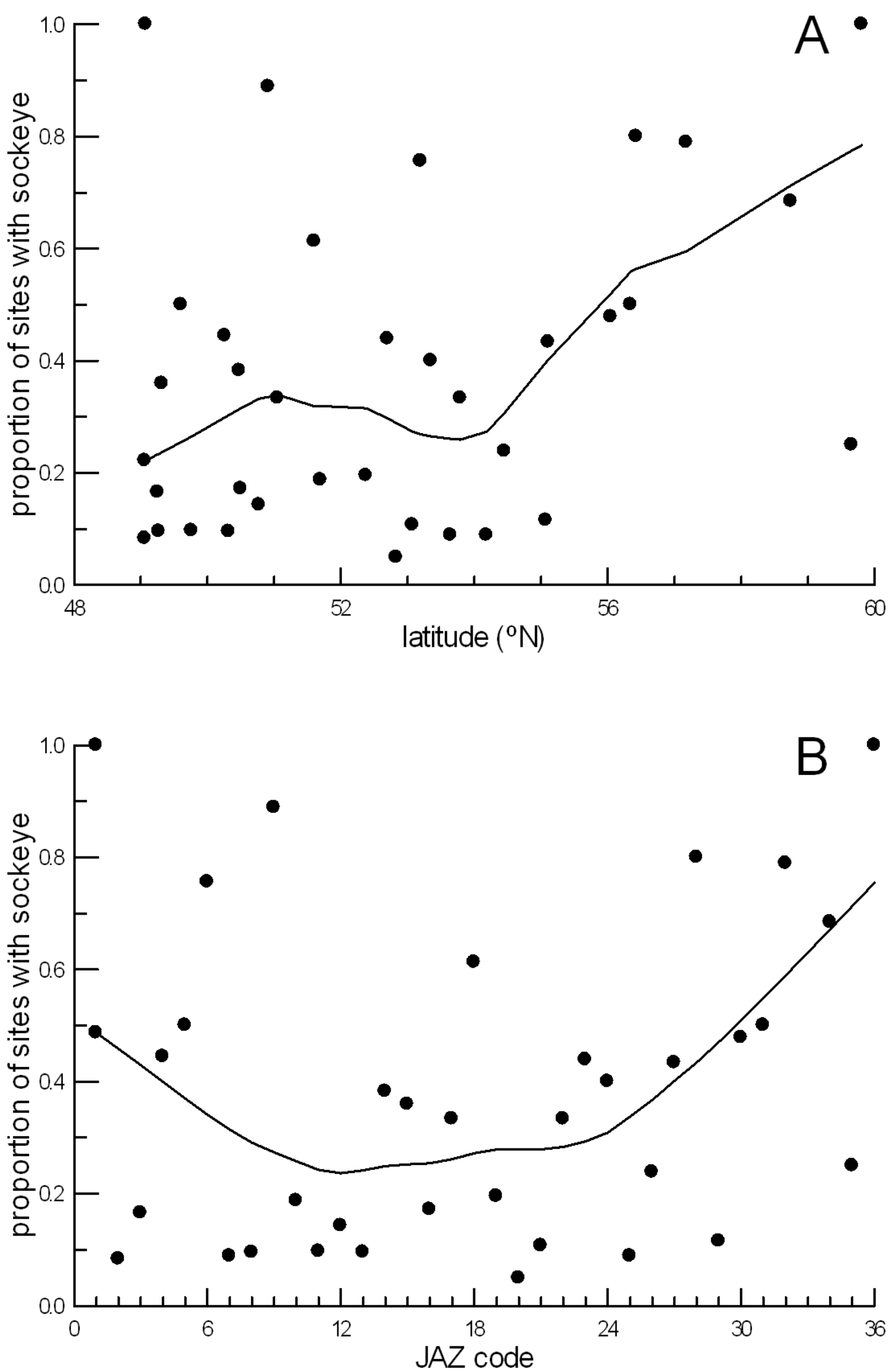


Figure 60. The graphs show how the proportion of sites within the JAZ ecotypes that have sockeye vary with A) mean latitude of sites within the JAZ ecotype and B) JAZ code. The JAZ codes increase from south to north and roughly indicate the mean latitude of ocean entry for each JAZ ecotype. The solid lines are LOWESS smoothing functions.

Table 40. The table summarizes the occurrence of sockeye salmon in British Columbia by life history type and by JAZ ecotype.

JAZ		life history type		number of sites in JAZ		% occurrence of sockeye	
acronym	code	LAKE	RIVER	with sockeye	total	%lake type	% sites with sockeye
OK+ORWA	1	1	0	1	1	100.0%	100.0%
BB+GStr	2	0	1	1	12	0.0%	8.3%
LFR+GStr	3	19	5	24	145	79.2%	16.6%
LILL+GStr	4	8	0	8	18	100.0%	44.4%
FRCany+GStr	5	4	6	10	20	40.0%	50.0%
MFR+GStr	6	146	6	152	201	96.1%	75.6%
UFR+GStr	7	3	1	4	45	75.0%	8.9%
LTh+GStr	8	0	2	2	21	0.0%	9.5%
STh+GStr	9	72	0	72	81	100.0%	88.9%
NTh+GStr	10	9	0	9	48	100.0%	18.8%
SC+GStr	11	2	11	13	134	15.4%	9.7%
SC+SFj	12	8	9	17	119	47.1%	14.3%
EVI+GStr	13	0	9	9	94	0.0%	9.6%
EVI+SFj	14	8	5	13	34	61.5%	38.2%
WVI+WVI	15	32	60	92	256	34.8%	35.9%
WVI+WQCI	16	4	7	11	64	36.4%	17.2%
HK+SFj	17	0	2	2	6	0.0%	33.3%
RSI+HStr	18	15	4	19	31	78.9%	61.3%
BCD+HStr	19	2	6	8	41	25.0%	19.5%
QCI+HStr	20	2	5	7	142	28.6%	4.9%
QCI+WQCI	21	2	7	9	84	22.2%	10.7%
QCI+NQCI	22	5	3	8	24	62.5%	33.3%
HecLow+HStr	23	67	23	90	205	74.4%	43.9%
NC+HStr	24	12	38	50	125	24.0%	40.0%
HecLow+NSKEst	25	3	1	4	45	75.0%	8.9%
LSK+NSKEst	26	22	4	26	109	84.6%	23.9%
MSK+NSKEst	27	48	4	52	120	92.3%	43.3%
USK+NSKEst	28	15	1	16	20	93.8%	80.0%
LNR-P+NSKEst	29	2	7	9	78	22.2%	11.5%
UNR+NSKEst	30	8	3	11	23	72.7%	47.8%
UNUK+TBFj	31	1	0	1	2	100.0%	50.0%
LStk+TBFj	32	2	13	15	19	13.3%	78.9%
Taku+TBFj	34	4	9	13	19	30.8%	68.4%
LYNN+TBFj	35	0	1	1	4	0.0%	25.0%
Alsek+AKCst	36	3	7	10	10	30.0%	100.0%
Totals		529	260	789	2400	67.0%	32.9%

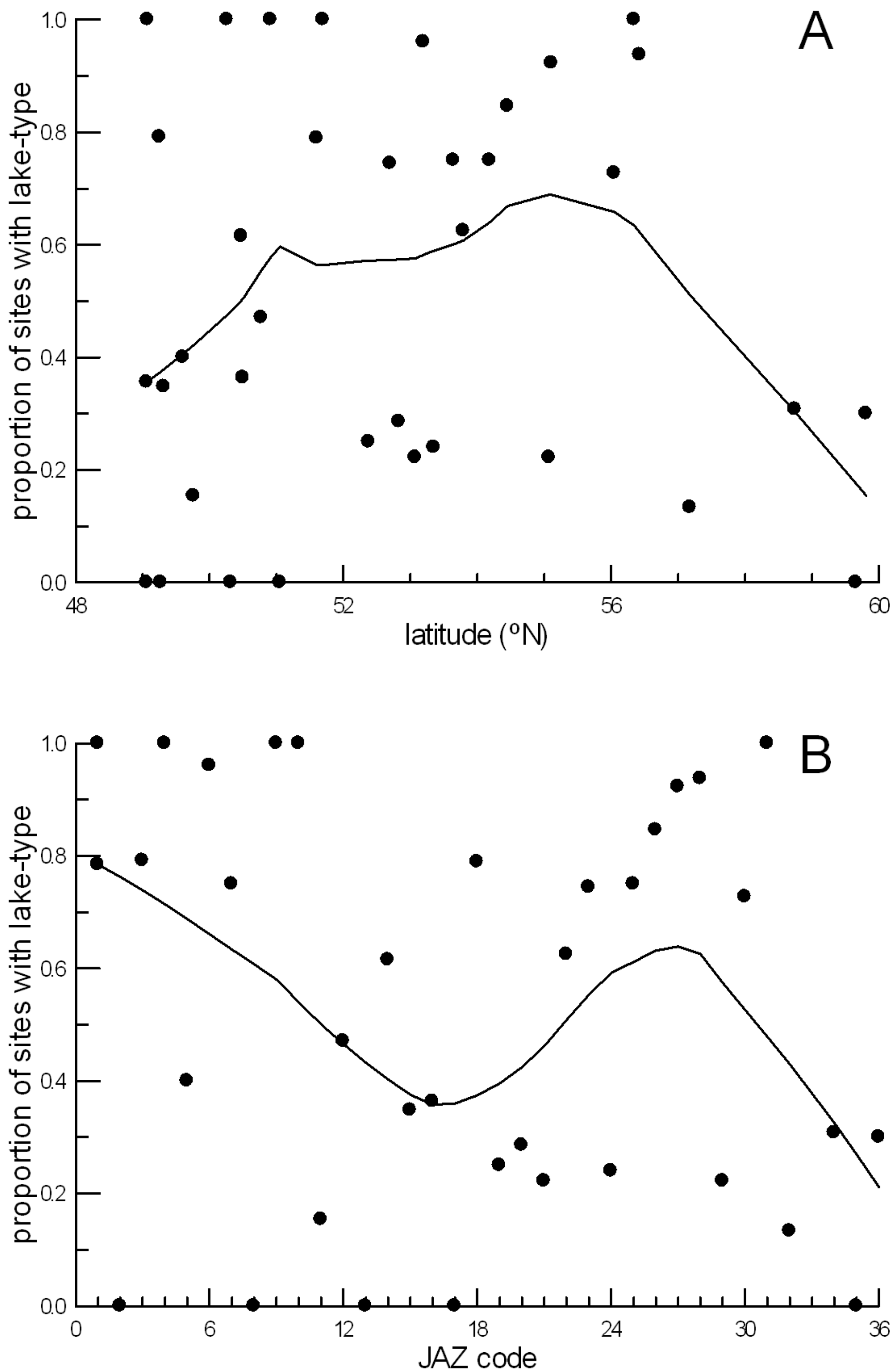


Figure 61. The graphs show how the proportion of sites within the JAZ ecotypes that have lake-type sockeye vary with A) mean latitude of sites within the JAZ ecotype and B) JAZ code. The JAZ codes increase from south to north and roughly indicate the mean latitude of ocean entry for each JAZ ecotype. The solid lines are LOWESS smoothing functions.

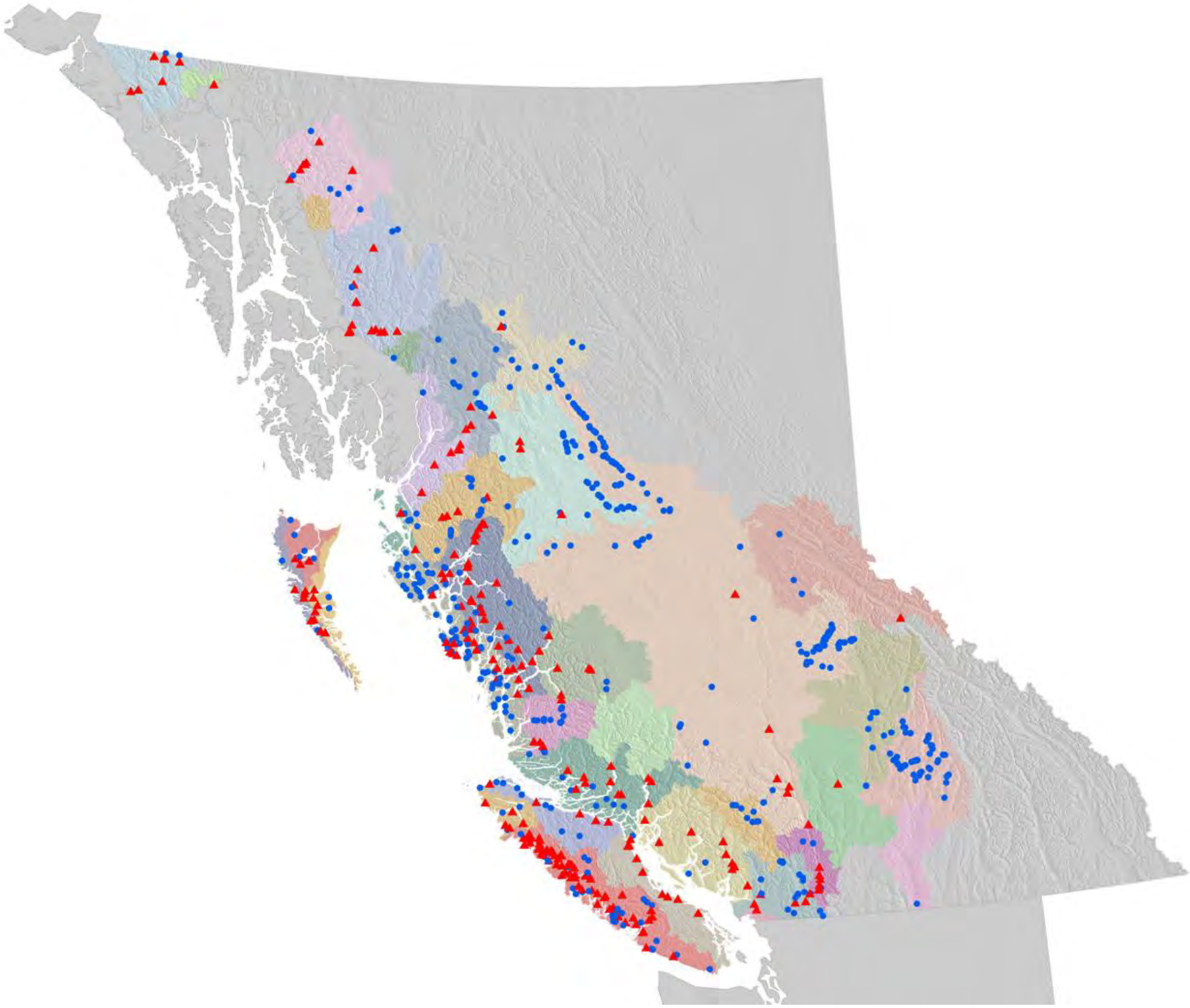


Figure 62. A map of British Columbia showing the distribution of lake-type (●) and river-type (▲) forms of sockeye salmon.

Table 41. A summary of a discriminant analysis of sockeye life-history type using some simple physiographic, climatological and hydrological variables.

Group frequencies

lake	river
504	251

Group means

variable	lake	river
latitude	52.8	52.2
longitude	-125.3	-127.6
mean mainstem gradient (º)	2.11	3.93
mean tributary gradient (º)	13.6	18.2
%watershed area in glaciers	1.14	2.45
%watershed area in tundra	9.2	12.7
%watershed area in lakes	7.5	1.4
lake count	58.0	35.9
mean annual precipitation (mm)	1925.3	3214.4
mean annual air temperature (ºC)	3.95	5.43
total link magnitude	32299.0	7675.7
maximum stream order	4.47	4.04
mean elevation (m)	803.7	626.3
mean valley floor width	1.69	2.46
$\log_{10}$ *K*-factor	3.97	4.19

Stepping summary (df=6,744)

variables in the order added to discriminant fuction	Approx. F-ratio	p-value
MAX_P_MAG	154.0	<<0.001
lake_PERC	135.9	<<0.001
GRAD_T_MN	107.2	<<0.001
ORDER_MAX	85.5	<<0.001
TEMP_ANN_M	74.7	<<0.001
GRAD_MS_MN	65.6	<<0.001
LONG	58.3	<<0.001
LAT	51.9	<<0.001
lake COUNT	46.5	<<0.001

Jackknifed Classification Matrix

	lake	river	%correct
lake	378	126	75
river	40	210	84
Total	418	336	78

Canonical Discriminant Functions : Standardized by Within Variances

variable	component 1
GEOLOC_LAT	0.38
GEOLOC_LON	0.61
GRAD_MS_MN	-0.29
GRAD_T_MN	-0.27
lake_PERC	0.61
lake_COUNT	-0.12
TEMP_ANN_M	-0.24
MAX_P_MAG	0.27
ORDER_MAX	-0.48

Canonical Scores of Group Means

life history type	component 11
lake	0.53
river	-1.06

Figure 60…

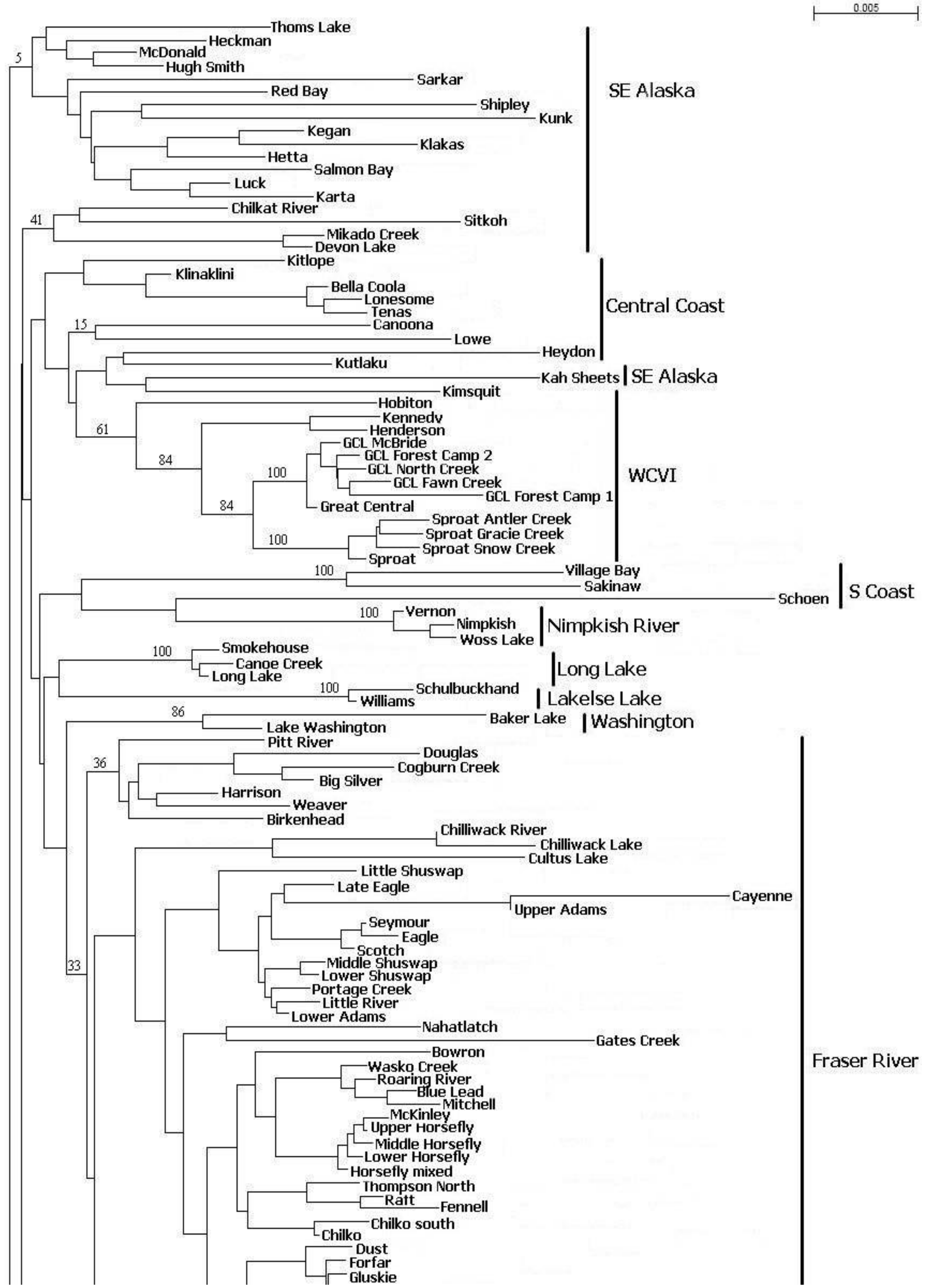
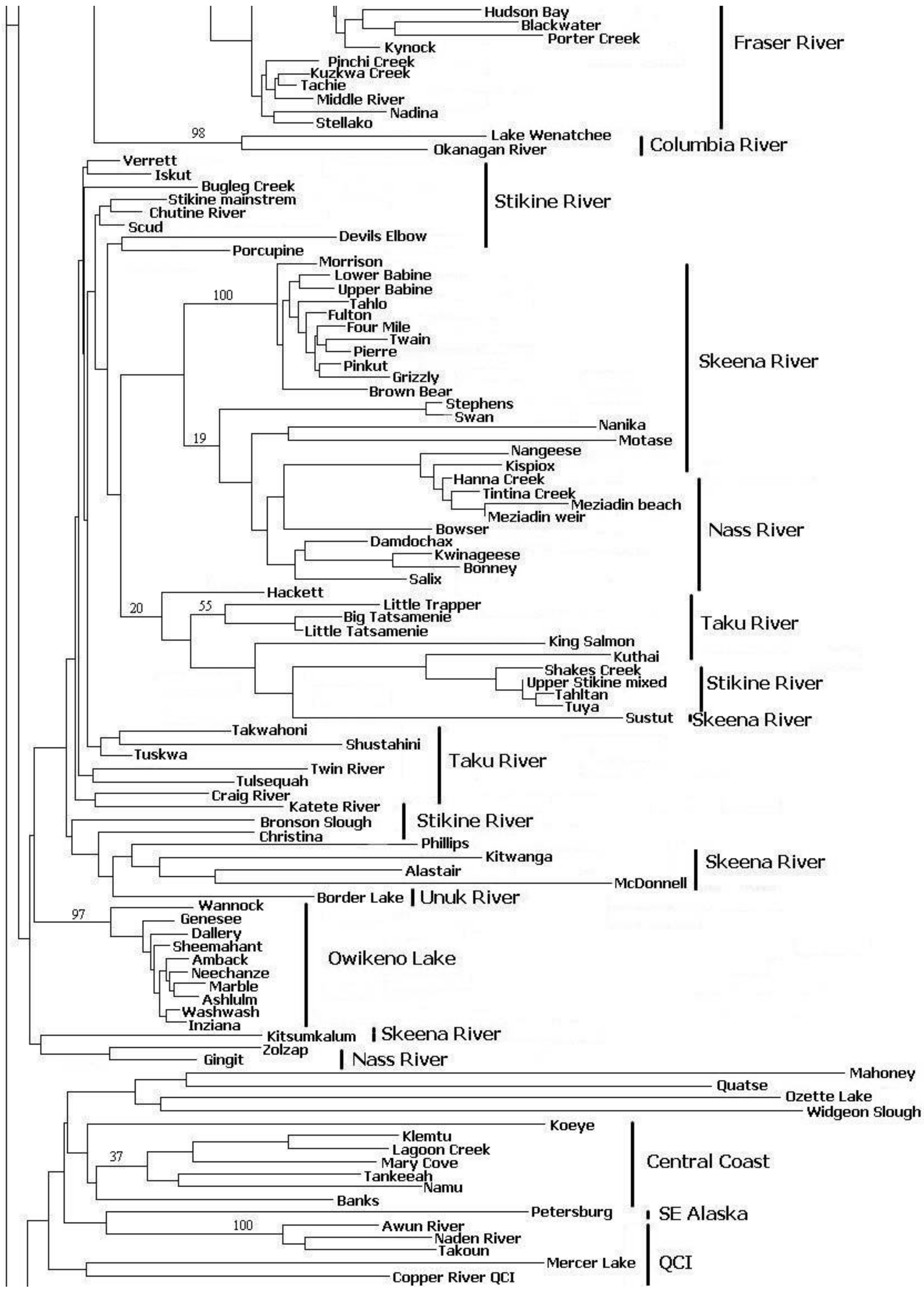

0.005
Thoms Lake
Heckman
McDonald
Hugh Smith
Sarkar
Red Bay
Shipley
Kunk
Kegan
Klakas
Hetta
Salmon Bay
Luck
Karta
Chilkat River
Sitkoh
Mikado Creek
Devon Lake
SE Alaska
Kitlope
Klinaklini
Bella Coola
Lonesome
Tenas
Canoona
Lowe
Heydon
Central Coast
Kutlaku
Kah Sheets
SE Alaska
Kimsquit
Hobiton
Kennedy
Henderson
GCL McBride
GCL Forest Camp 2
GCL North Creek
GCL Fawn Creek
GCL Forest Camp 1
Great Central
Sproat Antler Creek
Sproat Gracie Creek
Sproat Snow Creek
Sproat
WCVI
Village Bay
Sakinaw
Schoen
S Coast
Vernon
Nimpkish
Woss Lake
Nimpkish River
Smokehouse
Canoe Creek
Long Lake
Long Lake
Schulbuckhand
Williams
Lakelse Lake
Baker Lake
Lake Washington
Washington
Pitt River
Douglas
Cogburn Creek
Big Silver
Harrison
Weaver
Birkenhead
Chilliwack River
Chilliwack Lake
Cultus Lake
Little Shuswap
Late Eagle
Cayenne
Upper Adams
Seymour
Eagle
Scotch
Middle Shuswap
Lower Shuswap
Portage Creek
Little River
Lower Adams
Nahatlatch
Gates Creek
Bowron
Wasko Creek
Roaring River
Blue Lead
Mitchell
McKinley
Upper Horsefly
Middle Horsefly
Lower Horsefly
Horsefly mixed
Thompson North
Raft
Fennell
Chilko south
Chilko
Dust
Forfar
Gluskie
Fraser River
5
41
15
61
84
100
84
100
100
100
100
100
86
36
33

Figure 60…



Hudson Bay
Blackwater
Porter Creek
Kynock
Pinchi Creek
Kuzkwa Creek
Tachie
Middle River
Nadina
Stellako
Fraser River
98
Lake Wenatchee
Okanagan River
Columbia River
Verrett
Iskut
Bugleg Creek
Stikine mainstrem
Chutine River
Scud
Devils Elbow
Porcupine
Stikine River
Morrison
Lower Babine
Upper Babine
100
Tahlo
Fulton
Four Mile
Twain
Pierre
Pinkut
Grizzly
Brown Bear
Skeena River
Stephens
Swan
Nanika
19
Motase
Nangeese
Kispiox
Hanna Creek
Tintina Creek
Meziadin beach
Meziadin weir
Bowser
Nass River
Damdochax
Kwinageese
Bonney
Salix
Hackett
Little Trapper
20
55
Big Tatsamenie
Little Tatsamenie
Taku River
King Salmon
Kuthai
Shakes Creek
Upper Stikine mixed
Tahltan
Tuya
Stikine River
Sustut
Skeena River
Takwahoni
Shustahini
Tuskwa
Twin River
Taku River
Tulsequah
Craig River
Katete River
Bronson Slough
Stikine River
Christina
Phillips
Kitwanga
Skeena River
Alastair
McDonnell
Border Lake
Unuk River
Wannock
97
Genesee
Dallery
Sheemahant
Amback
Neechanze
Marble
Ashlulm
Washwash
Inziana
Owikeno Lake
Kitsumkalum
Skeena River
Zolzap
Gingit
Nass River
Mahoney
Quatse
Ozette Lake
Widgeon Slough
Koeye
Klemtu
Lagoon Creek
37
Mary Cove
Tankeeah
Namu
Central Coast
Banks
Petersburg
SE Alaska
Awun River
100
Naden River
Takoun
Mercer Lake
QCI
Copper River QCI

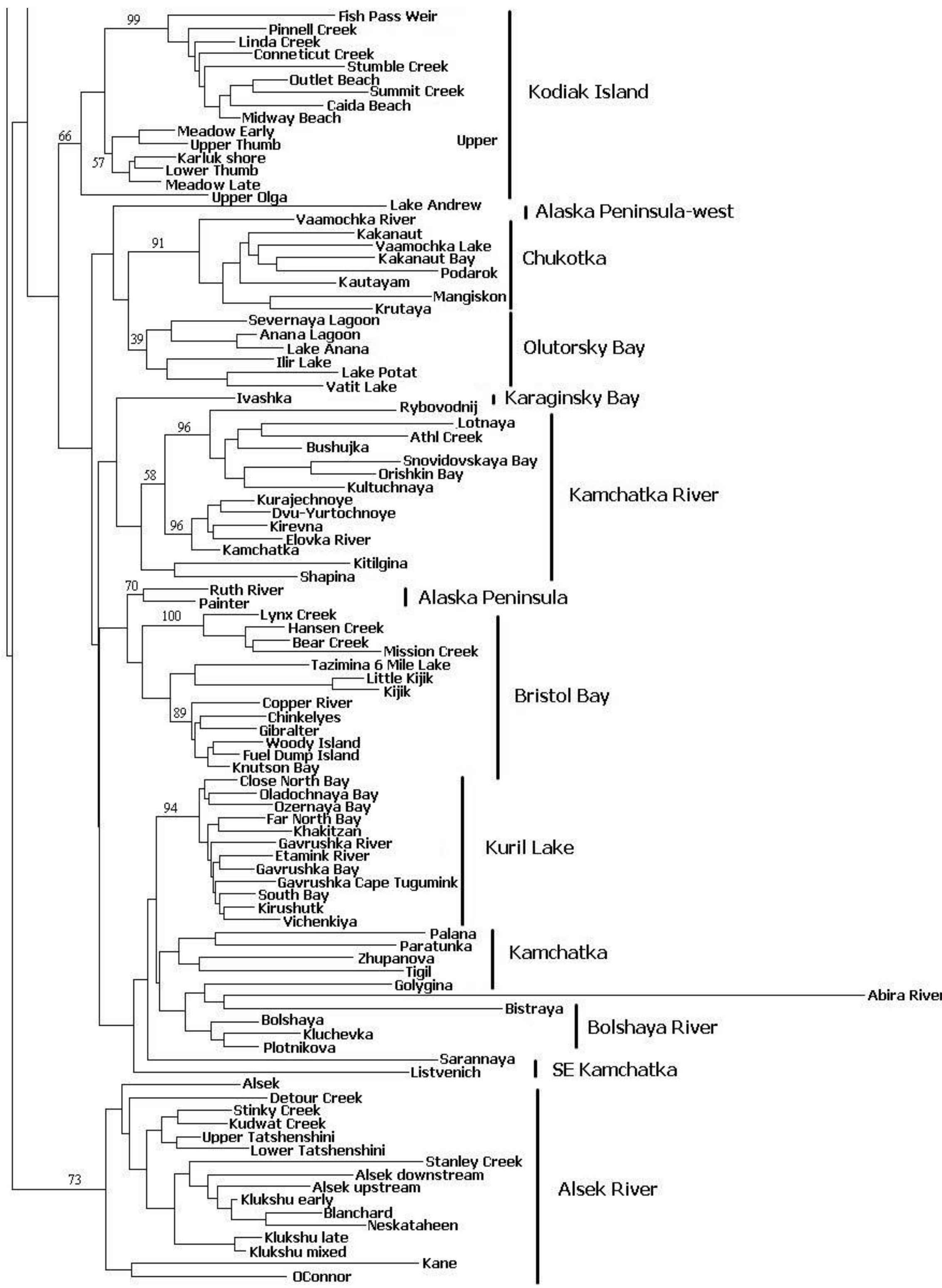


Figure 63. Neighbor-joining dendrogram of Cavalli-Sforza and Edwards chord distance for sockeye salmon surveyed at 14 microsatellite loci (Beacham et. al. 2006a).

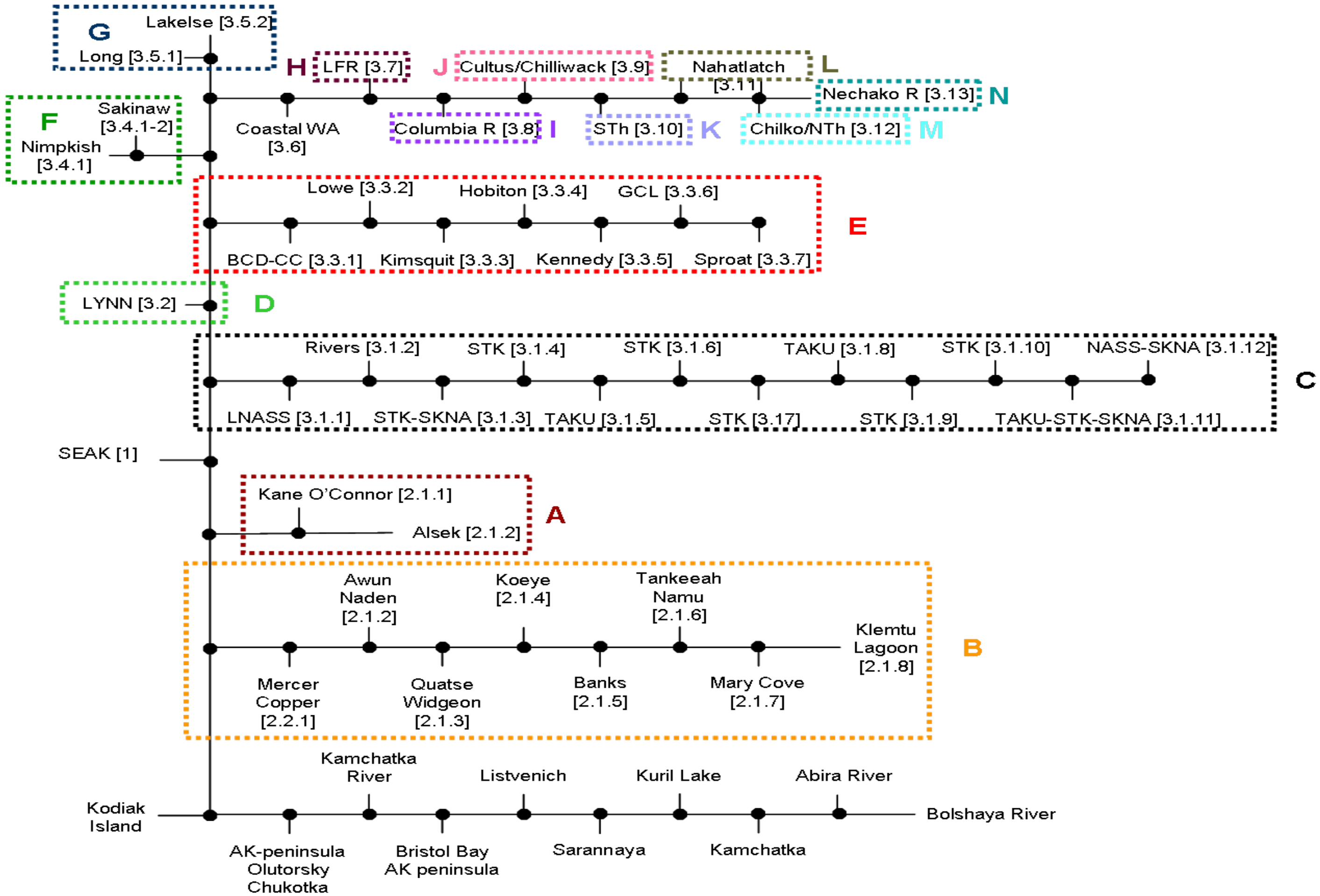


Figure 64. A schematic depiction of the dendrogram of genetic distances between sockeye populations. The first two or three levels of the hierarchical classification are shown in brackets. The genetic clusters are identified by the letters and dotted boxes. For brevity, not all of the sites at a node are listed.

Table 42. The table contains a five-level hierarchical genetic classification of the sockeye populations from Beacham et al. (2006a). The entries are sorted by their genetic class and have been condensed for many foreign areas. For sites within Canada the GFE_ID, life history, rearing lake (if of lake-type), and the ecotypic classification of sites within British Columbia are shown.

		genetic classification				
GFE_ID	Site	class	cluster	life history	lake (if lake-type)	JAZ
SEAK	Hugh Smith	01.01				
SEAK	McDonald	01.01				
SEAK	Heckman	01.01				
SEAK	Thoms Lake	01.01				
SEAK	Sarkar	01.02				
SEAK	Red Bay	01.03				
SEAK	Kunk	01.04				
SEAK	Shipley	01.04				
SEAK	Karta	01.05				
SEAK	Luck	01.05				
SEAK	Salmon Bay	01.05				
SEAK	Hetta	01.06				
SEAK	Klakas	01.06				
SEAK	Kegan	01.06				
202325	Chilkat River	02.01.01-01	A	river		LYNN+TBFj
2324	Alsek River	02.01.02-01	A	river		Alsek+AKCst
202334	Detour Creek	02.01.02-02	A	river		Alsek+AKCst
202335	Kudwat Creek	02.01.02-03.01	A	river		Alsek+AKCst
2012193	Stinky Creek	02.01.02-03.01	A	river		Alsek+AKCst
2325	L Tatshenshini	02.01.02-03.02	A	river		Alsek+AKCst
2325	U Tatshenshini	02.01.02-03.02	A	river		Alsek+AKCst
2332	Klukshu-mixed	02.01.02-04	A	lake	Klukshu	Alsek+AKCst
2332	Klukshu-late	02.01.02-04	A	lake	Klukshu	Alsek+AKCst
202326	O'Connor River	02.01.02-05.01	A	river		Alsek+AKCst
2002334	Stanley Creek	02.01.02-05.01	A	river		Alsek+AKCst
2324	Alsek-DS	02.01.02-05.02	A	river		Alsek+AKCst
2324	Alsek-US	02.01.02-05.03	A	river		Alsek+AKCst
2332	Klukshu-early	02.01.02-05.04	A	lake	Klukshu	Alsek+AKCst
2334	Blanchard River	02.01.02-05.05	A	lake	Blanchard	Alsek+AKCst
2339	Neskatahin Lake	02.01.02-05.06	A	lake	Neskatahin	Alsek+AKCst
1548	Mercer Creek	02.02.01-01	B	lake	Mercer	QCI+WQCI
1579	Copper Creek	02.02.01-02	B	lake	Skidegate	QCI+HStr
SEAK	Petersburg	02.02.02-01	B			
1567	Awun River	02.02.02-02	B	lake	Awun	QCI+NQCI
1559	Naden River	02.02.02-03	B	lake	Marian	QCI+NQCI
1571	Yakoun River	02.02.02-04	B	lake	Yakoun	QCI+NQCI
WA	Ozette Lake	02.02.03-01.01	B			
21	Widgeon Creek	02.02.03-01.02	B	river		LFR+GStr
1106	Quatse River	02.02.03-02	B	lake	Quatse	EVI+SFj
SEAK	Mahoney	02.02.03-03	B			
957	Koeye River	02.02.04	B	lake	Koeye	HecLow+HStr

GFE_ID	Site	genetic classification: class	cluster	life history	lake (if lake-type)	JAZ
1942	Banks Lakes Creek	02.02.05	B	lake	Banks	HecLow+HStr
1001	Tankeeah River	02.02.06-01	B	lake	Tankeeah River	HecLow+HStr
959	Namu River	02.02.06-02	B	lake	Namu	HecLow+HStr
1830	Mary Cove Creek	02.02.07	B	lake	Mary Cove Creek	HecLow+HStr
1829	Lagoon Creek	02.02.08-01	B	lake	Roderick	HecLow+HStr
2030	Klemtu Creek	02.02.08-02	B	river		HecLow+HStr
Kodiak Island	Upper Olga	02.03				
Kodiak Island	Meadow Late	02.03				
Kodiak Island	Lower Thumb	02.03				
Kodiak Island	Karluk shore	02.03				
Kodiak Island	Upper Thumb	02.03				
Kodiak Island	Meadow early	02.03				
Kodiak Island	Midway Beach	02.03				
Kodiak Island	Caida Beach	02.03				
Kodiak Island	Summit Creek	02.03				
Kodiak Island	Outlet Beach	02.03				
Kodiak Island	Stumble Creek	02.03				
Kodiak Island	Conneticut Creek	02.03				
Kodiak Island	Linda Creek	02.03				
Kodiak Island	Pinnell Creek	02.03				
Kodiak Island	Fish Pass Weir	02.03				
AK Pen W	Lake Andrew	02.04				
Chukotka	Krutaya	02.04				
Chukotka	Mangiskon	02.04				
Chukotka	Kautayam	02.04				
Chukotka	Podarok	02.04				
Chukotka	Kakanaut Bay	02.04				
Chukotka	Vaamochka River	02.04				
Olutorsky Bay	Vatit Lake	02.04				
Olutorsky Bay	Lake Potat	02.04				
Olutorsky Bay	Ilir Lake	02.04				
Olutorsky Bay	Lake Anana	02.04				
Olutorsky Bay	Anana Lagoon	02.04				
Olutorsky Bay	Severnaya Lagoon	02.04				
Kamchatka River	Shapina	02.05				
Kamchatka River	Kitilgina	02.05				
Kamchatka River	Kamchatka	02.05				
Kamchatka River	Elovka River	02.05				
Kamchatka River	Kireyna	02.05				
Kamchatka River	Dvu-Yurtochnoye	02.05				
Kamchatka River	Kurajechnoye	02.05				
Kamchatka River	Kultuchanaya	02.05				
Kamchatka River	Drishkin Bay	02.05				
Kamchatka River	Snovidovskaya Bay	02.05				
Kamchatka River	Bushujka	02.05				
Kamchatka River	Athl Creek	02.05				
Kamchatka River	Lotnaya	02.05				

GFE_ID	Site	genetic classification class	cluster	life history	lake (if lake-type)	JAZ
Kamchatka River	Rybovodnij	02.05				
Karaginsky Bay	Ivashka	02.05				
AK Pen	Painter	02.06				
AK Pen	Ruth River	02.06				
Bristol Bay	Knutson Bay	02.06				
Bristol Bay	Fuel Dump Island	02.06				
Bristol Bay	Woody Island	02.06				
Bristol Bay	Gibralter	02.06				
Bristol Bay	Chinkelyes	02.06				
Bristol Bay	Copper River	02.06				
Bristol Bay	Kjiik	02.06				
Bristol Bay	Little Kijiik	02.06				
Bristol Bay	Tazimina 6 Mile Lake	02.06				
Bristol Bay	Mission Creek	02.06				
Bristol Bay	Bear Creek	02.06				
Bristol Bay	Hansen Creek	02.06				
Bristol Bay	Lynx Creek	02.06				
SE Kamchatka	Listvenich	02.07				
SE Kamchatka	Sarannaya	02.08				
Kuril Lake	Vichenkiya	02.09				
Kuril Lake	Kirushutk	02.09				
Kuril Lake	South Bay	02.09				
Kuril Lake	Gavrushka Cape Tugumink	02.09				
Kuril Lake	Gavruska Bay	02.09				
Kuril Lake	Etamink River	02.09				
Kuril Lake	Gavrushka	02.09				
Kuril Lake	Khaktzan	02.09				
Kuril Lake	Far North Bay	02.09				
Kuril Lake	Ozernaya Bay	02.09				
Kuril Lake	Oladochnay Bay	02.09				
Kuril Lake	Close North Bay	02.09				
Kamchatka	Tigil	02.10				
Kamchatka	Zhupanova	02.10				
Kamchatka	Paratunka	02.10				
Kamchatka	Palana	02.10				
Abira	Abira River	02.11				
Bolshaya	Bistraya	02.11				
Kamchatka	Golygina	02.11				
Bolshaya	Plotnikova	02.12				
Bolshaya	Kluchevka	02.12				
Bolshaya	Bolshaya	02.12				
519	Kitsumkalum Lake	03.01.01-01	C	lake	Kitsumkalum	LSK+NSKEst
653	Gingit Creek	03.01.01-02	C	river		LNR-P+NSKEst
647	Ksi Ts'Oohl Ts'Ap	03.01.01-03	C	river		LNR-P+NSKEst
935	Wannock River	03.01.02-01	C	lake	Owikeno	RSI+HStr
942	Genesee Creek	03.01.02-02	C	lake	Owikeno	RSI+HStr

GFE_ID	Site	genetic classification: class	cluster	life history	lake (if lake-type)	JAZ
937	Amback Creek	03.01.02-03	C	lake	Owikeno	RSI+HStr
938	Dallery Creek	03.01.02-03	C	lake	Owikeno	RSI+HStr
939	Ashlulm Creek	03.01.02-03	C	lake	Owikeno	RSI+HStr
941	Neechanze River	03.01.02-03	C	lake	Owikeno	RSI+HStr
943	Sheemahant River	03.01.02-03	C	lake	Owikeno	RSI+HStr
944	Inziana River	03.01.02-03	C	lake	Owikeno	RSI+HStr
945	Washwash River	03.01.02-03	C	lake	Owikeno	RSI+HStr
1455	Marble River	03.01.02-03	C	lake	Alice	WVI+WQCI
2192	Bronson Creek	03.01.03-01	C	river		LStk+TBFj
2145	Christina Creek	03.01.03-02	C	lake	Christina	LStk+TBFj
7990651	Border Lake	03.01.03-03	C	lake	Border	Unuk+TBFj
824	Phillips River	03.01.03-04	C	lake	Phillips	SC+SFj
488	Kitwanga River	03.01.03-05	C	lake	Kitwancool	MSK+NSKEst
461	Alastair Lake	03.01.03-06	C	lake	Alastair	LSK+NSKEst
200534	Zymoetz River-Upper Below McDonell	03.01.03-07	C	lake	McDonell	LSK+NSKEst
2119	Katete River	03.01.04-01	C	river		LStk+TBFj
2186	Craig River	03.01.04-02	C	river		LStk+TBFj
212203	Tulsequah River	03.01.05-01	C	river		Taku+TBFj
202186	Twin River	03.01.05-02	C	river		LStk+TBFj
2178	Iskut River	03.01.06-01	C	river		LStk+TBFj
2193	Verrett River	03.01.07	C	river		LStk+TBFj
2180	Tuskwa Creek	03.01.08-01	C	river		Taku+TBFj
220302	Shustanini Creek	03.01.08-02	C	river		Taku+TBFj
220301	Takwahoni Creek	03.01.08-03	C	river		Taku+TBFj
2148	Scud River	03.01.09-01	C	river		LStk+TBFj
2196	Chutine River	03.01.09-02	C	river		LStk+TBFj
2118	Stikine River	03.01.09-03	C	river		LStk+TBFj
2138	Porcupine River	03.01.10-01	C	river		LStk+TBFj
202184	Devil's Elbow	03.01.10-02	C	river		LStk+TBFj
2233	Hackett River	03.01.11-01	C	river		Taku+TBFj
2211	Tatsatua Creek-Upper	03.01.11-02	C	lake	Tatsamenie	Taku+TBFj
2212	Tatsatua Creek	03.01.11-02	C	lake	Tatsatua	Taku+TBFj
2222	Little Trapper Lake	03.01.11-02	C	lake	Little Trapper	Taku+TBFj
200007	King Salmon Creek	03.01.11-03	C	river		Taku+TBFj
620	Sustut River	03.01.11-04	C	lake	Sustut	USK+NSKEst
2490	Kuthai Lake	03.01.11-05	C	lake	Kuthai	Taku+TBFj
200010	Shakes Creek	03.01.11-06.01	C	river		LStk+TBFj
2118	Stikine River	03.01.11-06.02	C	river		LStk+TBFj
2155	Tuya River	03.01.11-06.02	C	lake	Tuya	LStk+TBFj
2199	Tahltan River	03.01.11-06.02	C	lake	Tahltan	LStk+TBFj
592	Upper Babine	03.01.12-01	C	lake	Babine	MSK+NSKEst
592	Lower Babine	03.01.12-01	C	lake	Babine	MSK+NSKEst
601	Morrison Creek	03.01.12-01	C	lake	Babine	MSK+NSKEst
602	Tahlo Creek-Lower	03.01.12-01	C	lake	Tahlo/ Morrison	MSK+NSKEst

GFE_ID	Site	genetic classification: class	cluster	life history	lake (if lake-type)	JAZ
610	Pierre Creek	03.01.12-01	C	lake	Babine	MSK+NSKEst
611	Twain Creek	03.01.12-01	C	lake	Babine	MSK+NSKEst
616	Four Mile Creek	03.01.12-01	C	lake	Babine	MSK+NSKEst
619	Shass Creek	03.01.12-01	C	lake	Babine	MSK+NSKEst
657	Brown Bear Creek	03.01.12-01	C	river		UNR+NSKEst
501254	Fulton River	03.01.12-01	C	lake	Babine	MSK+NSKEst
501255	Pinkut Creek	03.01.12-01	C	lake	Babine	MSK+NSKEst
586	Club Creek-lower	03.01.12-02	C	lake	Stephens	MSK+NSKEst
2106	Swan Lake	03.01.12-02	C	lake	Swan	MSK+NSKEst
561	Nanika River	03.01.12-03.01	C	lake	Morice	MSK+NSKEst
7990593	Motase Lake	03.01.12-03.02	C	lake	Motase	USK+NSKEst
7990600	Bowser River	03.01.12-04	C	lake	Bowser	UNR+NSKEst
581	Nangeese River	03.01.12-04.01	C	river		MSK+NSKEst
566	Kispiox River	03.01.12-04.02	C	river		MSK+NSKEst
200598	Hanna Creek	03.01.12-04.03	C	lake	Meziadin	UNR+NSKEst
210598	Tintina Creek	03.01.12-04.04	C	lake	Meziadin	UNR+NSKEst
7990598	Meziadin weir	03.01.12-04.05	C	lake	Meziadin	UNR+NSKEst
7990598	Meziadin beach	03.01.12-04.05	C	lake	Meziadin	UNR+NSKEst
623	Salix Creek	03.01.12-05.01	C	lake	Bear	USK+NSKEst
7990604	Damdochax Creek	03.01.12-05.01	C	lake	Damdochax	UNR+NSKEst
2300125	Bonney Creek	03.01.12-05.03	C	lake	Fred Wright	UNR+NSKEst
200659	Kwinageese River-Upper	03.01.12-05.04	C	lake	Kwinageese	UNR+NSKEst
1923	Mikado Lake Creek	03.02.01	D	lake	Mikado	HecLow+HStr
1924	Devon Lake Creek	03.02.01	D	lake	Devon	HecLow+HStr
202325	Chilkat River	03.02.02	D	river		LYNN+TBFj
SEAK	Stikoh	03.02.03	D			
7990614	Kitlope River	03.03.01-01	E	lake	Kitlope	NC+HStr
850	Klinaklini River	03.03.01-02	E	river		HK+SFj
968	Bella Coola River	03.03.01-03.01	E	river		BCD+HStr
212270	Tenas Lake	03.03.01-03.02	E	lake	South Atnarko Lakes	BCD+HStr
212271	Lonesome Lake	03.03.01-03.02	E	lake	South Atnarko Lakes	BCD+HStr
1838	Canoona River	03.03.02-01	E	lake	Canoona	NC+HStr
1092	Lowe Inlet System	03.03.02-02	E	lake	Lowe/Simpson /Weir	HecLow+HStr
SEAK	Kutlaku Lake	03.03.03-01.01	E			
831	Heydon Creek	03.03.03-01.02	E	lake	Heydon	SC+SFj
977	Kimsquit River	03.03.03-02.01	E	lake	Kimsquit	NC+HStr
SEAK	Kah Sheets	03.03.03-02.02	E			
1245	Hobiton Creek	03.03.04	E	lake	Hobiton	WVI+WVI
1273	Henderson Lake	03.03.05	E	lake	Henderson	WVI+WVI
1304	Kennedy Lake Feeder Streams #2	03.03.05	E	lake	Kennedy	WVI+WVI
3416	GCL Lake	03.03.06-01	E	lake	GCL/Sproat	WVI+WVI
3416	GCL Forest Camp 1	03.03.06-02.01	E	lake	GCL/Sproat	WVI+WVI
3416	GCL-North Creek	03.03.06-02.02	E	lake	GCL/Sproat	WVI+WVI

GFE_ID	Site	genetic classification class	cluster	life history	lake (if lake-type)	JAZ
3416	GCL-Fawn Creek	03.03.06-02.03	E	lake	GCL/Sproat	WVI+WVI
3416	GCL-Forest Camp	03.03.06-02.03	E	lake	GCL/Sproat	WVI+WVI
3416	GCL McBride	03.03.06-02.03	E	lake	GCL/Sproat	WVI+WVI
3444	Sproat	03.03.07-01	E	lake	GCL/Sproat	WVI+WVI
3444	Sproat-Snow Creek	03.03.07-02.01	E	lake	GCL/Sproat	WVI+WVI
3444	Sproat-Gracie Creek	03.03.07-02.02	E	lake	GCL/Sproat	WVI+WVI
3444	Sproat-Antler Creek	03.03.07-02.02	E	lake	GCL/Sproat	WVI+WVI
1132	Village Bay	03.04.01-01	F	lake	Village Bay	SC+SFj
764	Ruby Creek	03.04.01-02	F	lake	Sakinaw	SC+GStr
2300009	Schoen Creek	03.04.02	F	lake	Schoen	EVI+SFj
1277	Vernon Bay Creek	03.04.03-01	F	river		WVI+WVI
1112	Nimpkish River	03.04.03-02	F	lake	Nimpkish	EVI+SFj
300041	Woss River	03.04.03-02	F	lake	Woss	EVI+SFj
914	Docee River	03.05.01	G	lake	Long	RSI+HStr
915	Canoe Creek	03.05.01	G	lake	Long	RSI+HStr
916	Smokehouse Creek	03.05.01	G	lake	Long	RSI+HStr
517	Williams Creek	03.05.02-01	G	lake	Lakelse	LSK+NSKEst
511	Schulbuckhand Creek	03.05.02-02	G	lake	Lakelse	LSK+NSKEst
WA	Baker Lake	03.06.01-01				
WA	Lake Washington	03.06.01-02				
2443	Pitt Lake	03.07.01	H	lake	Pitt	LFR+GStr
198	Birkenhead River	03.07.02	H	lake	Lillooet	LILL+GStr
179	Harrison River	03.07.03-01	H	river		LFR+GStr
183	Weaver Creek	03.07.03-02	H	lake	Harrison (U/S)	LFR+GStr
195	Douglas Creek	03.07.04	H	lake	Harrison (D/S)	LFR+GStr
192	Big Silver Creek	03.07.05-01	H	lake	Harrison (D/S)	LFR+GStr
190	Cogburn Creek	03.07.05-02	H	lake	Harrison (D/S)	LFR+GStr
442	Okanagan River	03.08.01	I	lake	Osoyoos	OK+ORWA
Columbia River	Lake Wenatchee	03.08.02	I			
2441	Cultus Lake	03.09.01	J	lake	Cultus	LFR+GStr
62	Chilliwack R	03.09.02-01	J	lake	Chilliwack	LFR+GStr
62	Chilliwack Lk	03.09.02-02	J	lake	Chilliwack	LFR+GStr
240	L Shuswap	03.10.01	K	lake	Mara	STh+GStr
240	L Shuswap	03.10.02-01	K	lake	Mara	STh+GStr
241	M Shuswap	03.10.02-01	K	lake	Mabel	STh+GStr
129	Portage Creek	03.10.02-02	K	lake	Seton	MFR+GStr
219	Little River	03.10.02-03	K	lake	Little Shuswap	STh+GStr
220	Adams River	03.10.02-03	K	lake	Shuswap	STh+GStr
225	Scotch Creek	03.10.03	K	lake	Shuswap	STh+GStr
229	Seymour River	03.10.03	K	lake	Shuswap	STh+GStr
232	Eagle River	03.10.03	K	lake	Shuswap	STh+GStr
232	Late Eagle	03.10.04-01	K	lake	Shuswap	STh+GStr
221	Adams River-Upper	03.10.04-02	K	lake	Adams	STh+GStr
224	Cayenne Creek	03.10.04-03	K	lake	Adams	STh+GStr

GFE_ID	Site	genetic classification class	cluster	life history	lake (if lake-type)	JAZ
125	Nahatlatch River	03.11.01	L	lake	Nahatlatch	FRCany+GStr
132	Gates Creek	03.11.02	L	lake	Anderson/ Seton	MFR+GStr
286	Chilko River	03.12.01-01	M	lake	Chilko	MFR+GStr
2431	Chilko-South	03.12.01-01	M	lake	Chilko	MFR+GStr
256	North Thompson River	03.12.01-02.01	M	lake	Kamloops	NTh+GStr
269	Raft River	03.12.01-02.02	M	lake	Kamloops	NTh+GStr
2746	Fennell Creek/Saskum Creek	03.12.01-02.02	M	lake	North Barriere	NTh+GStr
157	Bowron River	03.12.02	M	lake	Bowron	UFR+GStr
291	Horsefly mixed	03.12.03-01	M	lake	Quesnel	MFR+GStr
291	L Horsefly	03.12.03-01	M	lake	Quesnel	MFR+GStr
291	M Horsefly	03.12.03-01	M	lake	Quesnel	MFR+GStr
2401	McKinley Creek	03.12.03-01	M	lake	Quesnel	MFR+GStr
2445	Horsefly River-Upper	03.12.03-01	M	lake	Quesnel	MFR+GStr
2414	Wasko Creek-Lower	03.12.03-02.01	M	lake	Quesnel	MFR+GStr
2412	Roaring River	03.12.03-02.02	M	lake	Quesnel	MFR+GStr
293	Mitchell River	03.12.03-02.03	M	lake	Quesnel	MFR+GStr
2422	Blue Lead Creek	03.12.03-02.03	M	lake	Quesnel	MFR+GStr
308	Pinchi Creek	03.13.01-01.01	N	lake	Stuart	MFR+GStr
309	Tachie River	03.13.01-01.02	N	lake	Stuart	MFR+GStr
310	Middle River-Rossette Bar	03.13.01-01.02	N	lake	Trembleur	MFR+GStr
312	Kuzkwa River	03.13.01-01.02	N	lake	Stuart	MFR+GStr
297	Stellako River	03.13.01-02.01	N	lake	Fraser	MFR+GStr
303	Nadina River	03.13.01-02.02	N	lake	Francois	MFR+GStr
328	Dust Creek	03.13.02-01	N	lake	Takla	MFR+GStr
319	Forfar Creek	03.13.02-02	N	lake	Trembleur	MFR+GStr
320	Gluske Creek	03.13.02-03	N	lake	Takla	MFR+GStr
318	O'Ne-Ell Creek	03.13.02-04.01	N	lake	Trembleur	MFR+GStr
338	Hudson Bay Creek	03.13.02-04.02	N	lake	Takla	MFR+GStr
345	Blackwater Creek	03.13.02-04.03	N	lake	Takla	MFR+GStr
347	Porter Creek	03.13.02-04.03	N	lake	Takla	MFR+GStr

† A transplant of Tahltan Lake sockeye above an impassable barrier on the Tuya River. Outplanted fry are hatchery incubated.

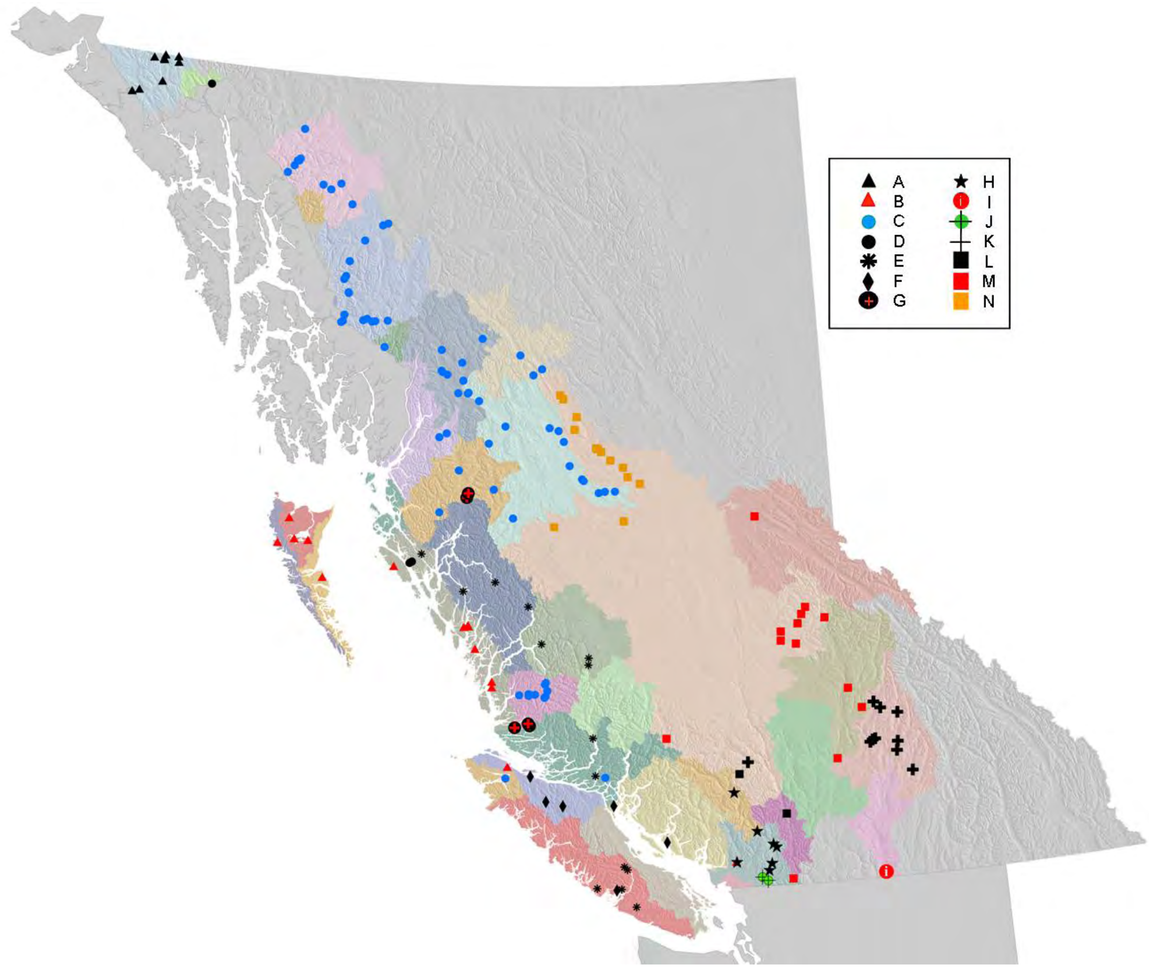


Figure 65. A map of British Columbia showing the geographical distribution of the 14 genetic clusters of sockeye salmon. The colored polygons are the JAZ ecotypes.

Table 43. Ecotypic CUs for river-type sockeye in British Columbia.

JAZ Acronym	JAZ code	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic clusters
OK+ORWA	1	0	1	0%	possible	-	-
BB+GStr	2	1	12	8%	documented	-	-
LFR+GStr	3	5	145	3%	documented	02.02.03-01.02; 03.07.03-01	B; H
LILL+GStr	4	0	18	0%	possible	-	-
FRCany+GStr	5	6	20	30%	documented	-	-
MFR+GStr	6	6	201	3%	documented	-	-
UFR+GStr	7	1	45	2%	documented	-	-
LTh+GStr	8	2	21	10%	documented	-	-
STh+GStr	9	0	81	0%	possible	-	-
NTh+GStr	10	0	48	0%	possible	-	-
SC+GStr	11	11	134	8%	documented	-	-
SC+SFj	12	9	119	8%	documented	-	-
EVI+GStr	13	9	94	10%	documented	-	-
EVI+SFj	14	5	34	15%	documented	-	-
WVI+WVI	15	60	256	23%	documented	03.04.03-01	F
WVI+WQCI	16	7	64	11%	documented	-	-
HK+SFj	17	2	6	33%	documented	03.03.01-02	E
RSI+HStr	18	4	31	13%	documented	-	-
BCD+HStr	19	6	41	15%	documented	03.03.01-03.01	E
QCI+HStr	20	5	142	4%	documented	-	-
QCI+WQCI	21	7	84	8%	documented	-	-
QCI+NQCI	22	3	24	13%	documented	-	-
HecLow+HStr	23	23	205	11%	documented	02.02.08-02	B
NC+HStr	24	38	125	30%	documented	-	-
HecLow+NSKEst	25	1	45	2%	documented	-	-
LSK+NSKEst	26	4	109	4%	documented	-	-
MSK+NSKEst	27	4	120	3%	documented	03.01.12-04.01; 03.01.12-04.02	C
USK+NSKEst	28	1	20	5%	documented	-	-

JAZ Acronym	JAZ code	sites present	total sites	% sites present	1. presence	2. genetic classes present in JAZ	2. genetic clusters
LNR-P+NSKEst	29	7	78	9%	documented	03.01.01-02; 03.01.01-03	C
UNR+NSKEst	30	3	23	13%	documented	03.01.12-01	C
UNUK+TBFj	31	0	2	0%	probable	-	-
LStk+TBFj	32	13	19	68%	documented	03.01.03-01; 03.01.04-01; 03.01.04-02; 03.01.05-02; 03.01.06-01; 03.01.07; 03.01.09-01; 03.01.09-02; 03.01.10-01; 03.01.10-02; 03.01.11-06.01; 03.01.11-06.02	C
Whtng+TBFj	33	-	1	-	probable	-	-
Taku+TBFj	34	9	19	47%	documented	03.01.05-01; 03.01.08-01; 03.01.08-02; 03.01.08-03; 03.01.11-01; 03.01.11-03	C
LYNN+TBFj	35	1	4	25%	documented	03.02.02	D
Alsek+AKCst	36	7	9	78%	documented	02.01.01-01; 02.01.01-02; 02.01.02-02; 02.01.02-03.01; 02.01.02-03.02; 02.01.02-05.01	A
TesHW+Ber	37	-	4	-	documented	-	-
Liard+AO	38	-	1	-	unlikely	-	-
Yuk+Ber	37	-	?	-	possible	-	-
MacR+AO	39	-	1	-	possible	-	-
		260	2406	11%			

Table 44. Distribution of sites by life-history type and level three of the genetic classification. Sites in clusters A and B have a genetic class of 2.n while those in clusters C to N have a genetic class of 3.n.

	number of sites by life history type			
genetic cluster	lake	river	total	%lake-type
A	3	7	10	30.0%
B	12	2	14	85.7%
C	45	24	69	65.2%
D	2	1	3	66.7%
E	12	2	14	85.7%
F	5	1	6	83.3%
G	5		5	100.0%
H	6	1	7	85.7%
I	1		1	100.0%
J	2		2	100.0%
K	18		18	100.0%
L	2		2	100.0%
M	13		13	100.0%
N	15		15	100.0%
total number of sites	140	39	179	78.2%
total sites	537	252	789	68.1%

Table 45. The crosswalk between the genetic classification at the third level (cluster) and the JAZ ecotypic CUs for river-type sockeye only.

		genetic cluster								
JAZ	JAZ index	A	B	C	D	E	F	H	row total	clusters in JAZ
BB+GStr	2								0	0
LFR+GStr	3		1					1	2	2
FRCany+GStr	5								0	0
MFR+GStr	6								0	0
UFR+GStr	7								0	0
LTh+GStr	8								0	0
SC+GStr	11								0	0
SC+SFj	12								0	0
EVI+GStr	13								0	0
EVI+SFj	14								0	0
WVI+WVI	15						1		1	1
WVI+WQCI	16								0	0
HK+SFj	17					1			1	1
RSI+HStr	18								0	0
BCD+HStr	19					1			1	1
QCI+HStr	20								0	0
QCI+WQCI	21								0	0
QCI+NQCI	22								0	0
HecLow+HStr	23		1						1	1
NC+HStr	24								0	0
HecLow+NSKEst	25								0	0
LSK+NSKEst	26								0	0
MSK+NSKEst	27			2					2	1
USK+NSKEst	28								0	0
LNR-P+NSKEst	29			2					2	1
UNR+NSKEst	30			1					1	1
LStk+TBFj	32			13					13	1
Taku+TBFj	34			6					4	1
LYNN+TBFj	35				1				1	1
Alsek+AKCst	36	7							7	1
column totals		7	2	24	1	2	1	1	38	
JAZ in clusters		1	2	5	1	2	1	1		

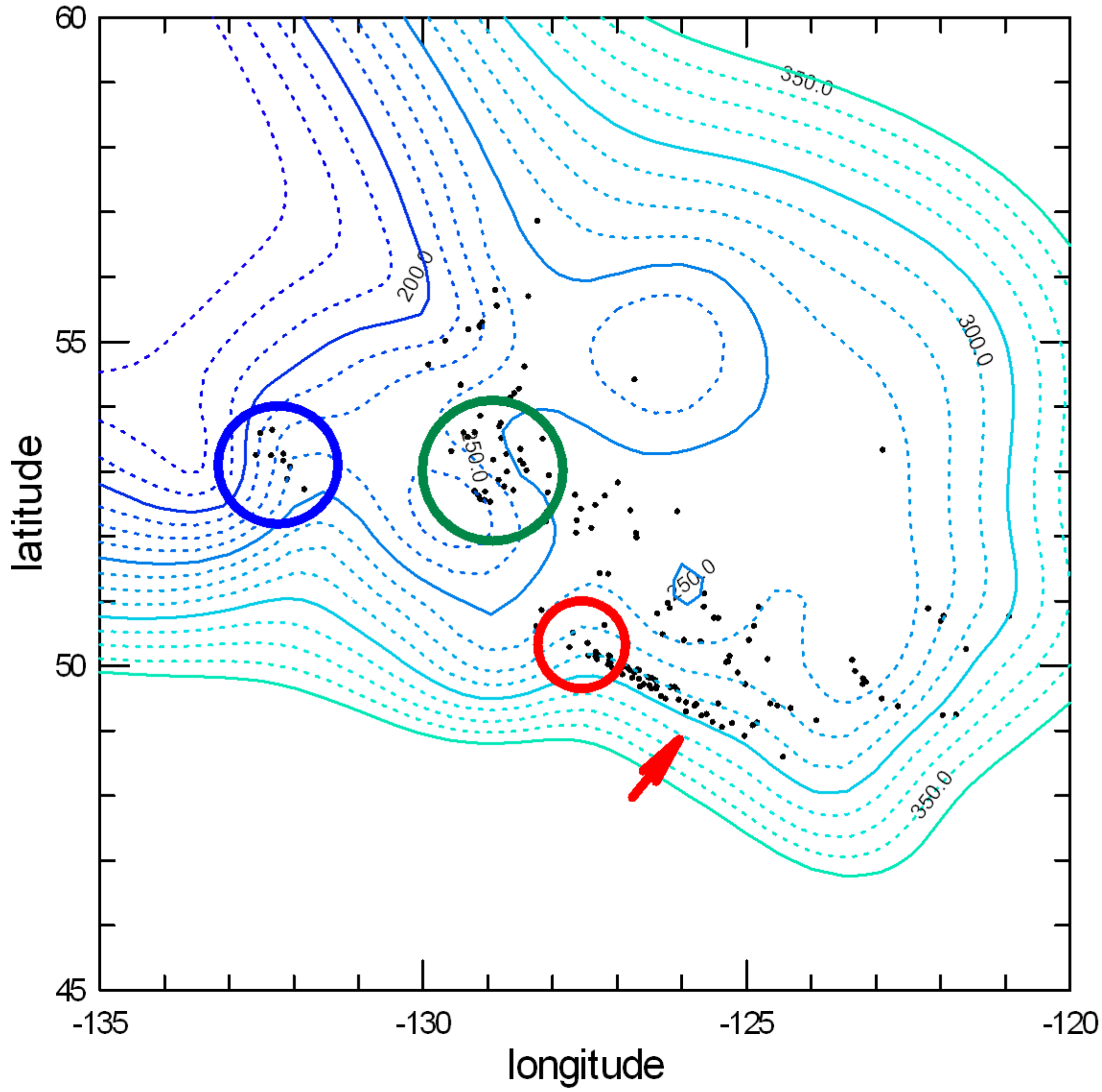


Figure 66. A contour plot of the DOY of peak spawning for river-type sockeye populations in British Columbia. The blue circle highlights the strong gradient in spawning timing on the Queen Charlotte Islands. The green circle and red circle identify similarly strong gradients in the HecLow+HStr and NC+HStr JAZ ecotypes and the WVI+WQCI JAZ ecotype respectively. The red arrow identify the very consistent spawning times for populations over the WVI+WVI JAZ ecotypes.

Table 46. Multiple regression model predicting DOY peak spawn for river-type sockeye.

Dep Var: DOY_PK_SPAWN N: 178 Multiple R: 0.753 Squared multiple R: 0.567
Adjusted squared multiple R: 0.549 Standard error of estimate: 21.2

Effect	Coefficient	Std Error	t	P(2 Tail)
CONSTANT	1019.8	118.632	8.60	<0.001
GEOLOC_LAT	-14.7	2.228	-6.59	<0.001
GRAD_MS_MN	1.340	0.439	3.05	0.003
PPT_AUG_M	-0.262	0.121	-2.16	0.032
PPT_SEP_M	0.115	0.077	1.49	0.139
PPT_DEC_M	0.047	0.025	1.88	0.062
TEMP_DEC_M	-8.835	1.501	-5.89	<0.001
ELEV_MEAN	-0.054	0.013	-4.29	<0.001

Analysis of Variance

Source	Sum-of-Squares	df	Mean-Square	F-ratio	P
Regression	99940	7	14277.2	31.8	<0.001
Residual	76347	170	449.1		

Table 47. Multiple regression model predicting DOY peak spawn for lake-type sockeye.

Dep Var: DOY_PK N: 321 Multiple R: 0.596 Squared multiple R: 0.355
Adjusted squared multiple R: 0.336 Standard error of estimate: 21.6

Effect	Coefficient	Std Error	t	P(2 Tail)
CONSTANT	411.380	63.169	6.512	<0.001
GEOLOC_LAT	-4.840	0.885	-5.469	<0.001
GRAD_MS_MN	-1.421	0.550	-2.582	0.010
PERCTUNDRA	0.375	0.133	2.828	0.005
TEMP_SEP_M	21.705	4.002	5.424	<0.001
TEMP_OCT_M	-27.678	5.636	-4.911	<0.001
TEMP_NOV_M	14.908	5.055	2.949	0.003
TEMP_DEC_M	-6.567	3.177	-2.067	0.040
ORDER_MAX	2.380	1.258	1.892	0.059
VFW_MEAN	-2.074	0.474	-4.372	<0.001

Analysis of Variance

Source	Sum-of-Squares	df	Mean-Square	F-ratio	P
Regression	80047	9	8894.2	19.0	<0.001
Residual	145505	311	467.9		

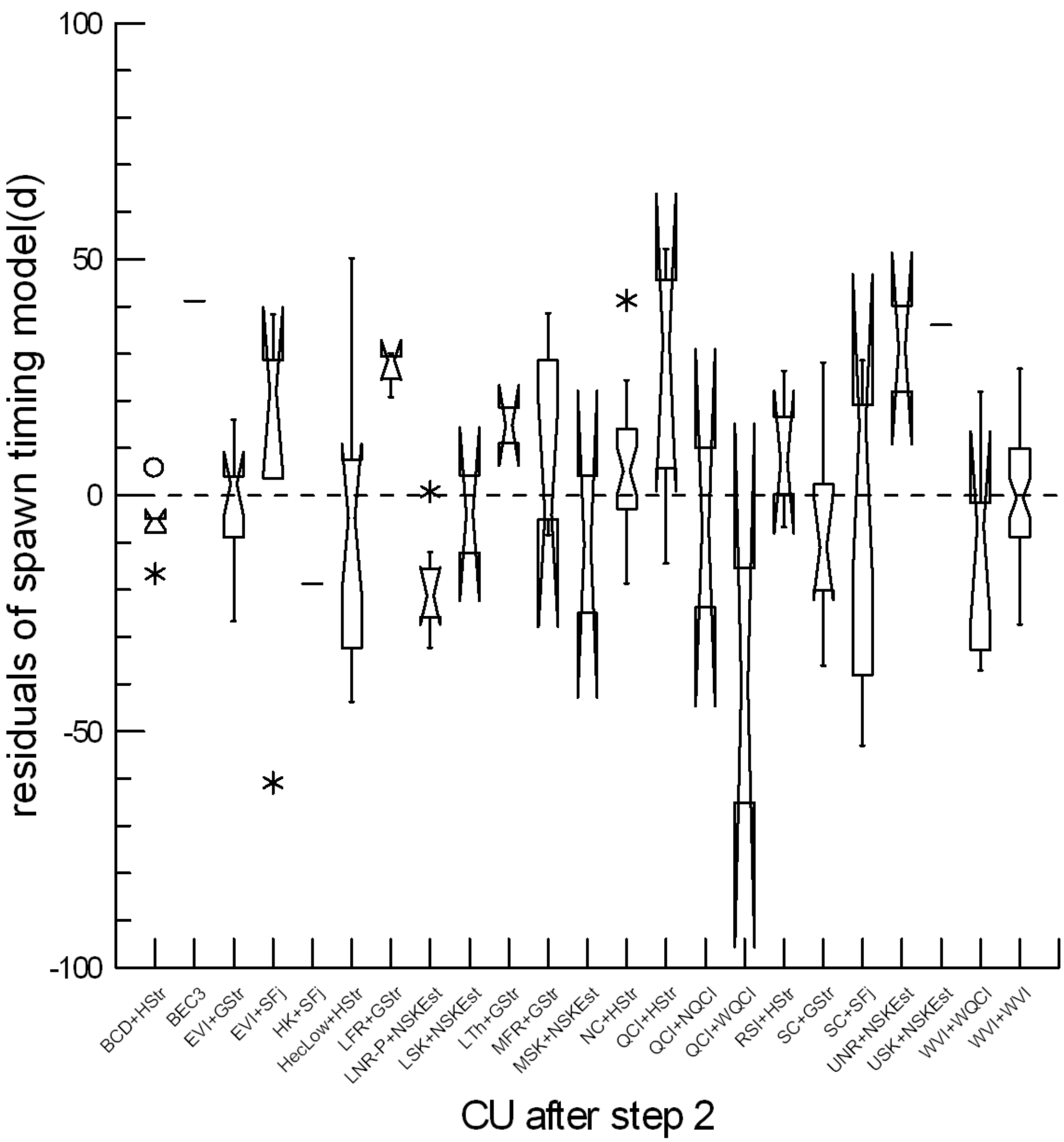


Figure 67. Box plots for the residuals of the spawn timing model for river-type sockeye in British Columbia. Note the differences between JAZ ecotypes with a common FAZ, e.g. EVI+GStr vs. EVI+SFj and the three JAZ on the Queen Charlotte Islands.

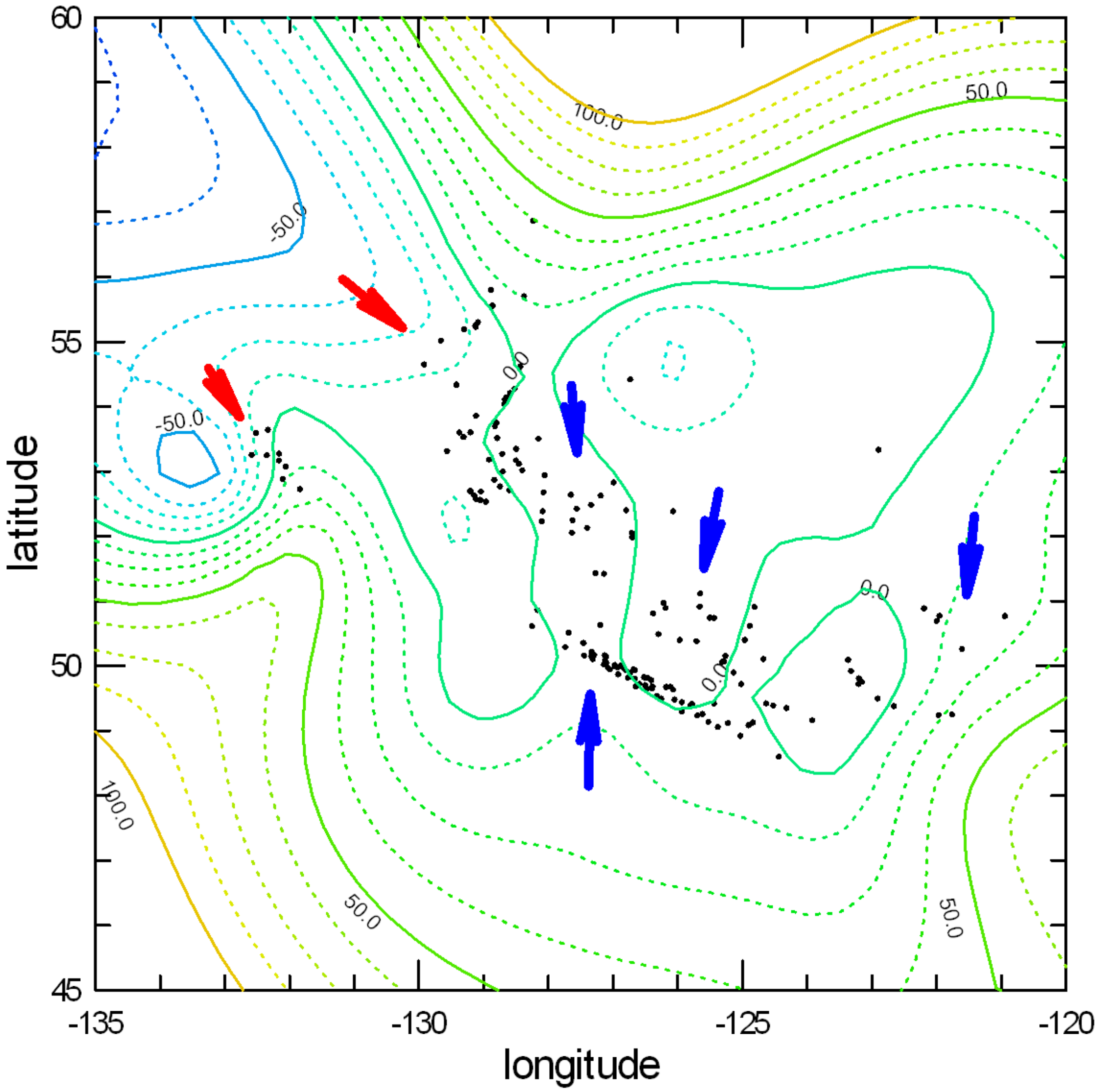


Figure 68. A contour plot of the residuals for the spawn time model for river-type sockeye of British Columbia. The red arrow sites where spawning was consistently earlier than predicted while blue arrow indicates areas where spawning was consistently later than predicted by the model.

Table 48. Summary statistics for the mean DOY of peak spawning for lake- and ocean-type sockeye categorized by JAZ ecotypic CU. The P values are for t-tests of the equality of type means within the JAZ ecotype.

	lake-type		river-type		
JAZ	mean DOY		mean DOY		*P*
OK+ORWA	1	294			
BB+GStr			1		
LFR+GStr	8	265.4	3	307.7	
LILL+GStr	5	261.2			
FRCany+GStr	4	272.7			
MFR+GStr	79	234.8	5	270.5	
UFR+GStr	2	237.3			
LTh+GStr			2	298.1	
STh+GStr	47	283.0			
NTh+GStr	7	253.9			
SC+GStr	2	247.5	11	257.2	
SC+SFj	8	235.0	8	255.3	
EVI+GStr			9	268.9	
EVI+SFj	8	263.3	5	265.5	
WVI+WVI	32	265.2	58	292.4	
WVI+WQCI	4	205.5	6	266.0	
HK+SFj			2	249.0	
RSI+HStr	15	273.8	4	261.6	
BCD+HStr	2		6	256.2	
QCI+HStr	2	214.8	5	260.1	
QCI+WQCI	2	210.6	6	185.5	
QCI+NQCI	5	228.2	3	209.7	
HecLow+HStr	64	237.2	23	225.1	
NC+HStr	12	255.0	38	257.3	
HecLow+NSKEst	3	263.3	1		
LSK+NSKEst	21	253.5	2	243.4	
MSK+NSKEst	48	248.9	4	230.9	
USK+NSKEst	13	252.1	1	254.5	
LNR-P+NSKEst	2	220.7	7	213.1	
UNR+NSKEst	8	251.6	3	258.8	
UNUK+TBFj	1				
LStk+TBFj	2		13		
Taku+TBFj	4		9		
LYNN+TBFj			1		
Alsek+AKCst	3		5		
Overall	414	250.0	241	263.9	

Table 49. The 24 Conservation Units of river-type sockeye within British Columbia. The existence of two of the CUs (UFR and SKNA-HI) is uncertain since both consist of one population of unknown status. The number of sites indicated is the total in our database and is not to be interpreted as the number of sites where river-type sockeye salmon are persistently found.

Name	Acronym	index	number of sites	classification step	comments
Boundary Bay	BB	R01	1	ecotypic	Data limited
Widgeon	Widgeon	R02	1	genetics	Very distinctive genetically
Lower Fraser	LFR	R03	4	genetics	
Fraser Canyon	FRCany	R04	6	ecotypic	
Middle Fraser	MFR	R05	6	timing	Supported by genetics
Upper Fraser	UFR	R06	1	ecotypic	Status of the single site is uncertain
Thompson River	THOM	R07	2	ecotypic/timing	Genetically similar to sites in MFR but timing different
E Vancouver Island & Georgia Strait	EVI-GStr	R08	25	timing	Combines 2 ecotypic CUs in which timing and timing residuals are uniform & there is only 1 genetic sample. We assumed the genetic patterning of the lake-type populations in the region
Southern Fjords	SFj	R09	11	genetics/other	
W Vancouver Island	WVI+WQCI	R10	60	timing	
NW Vancouver Island	NWVI	R11	7	timing	
Rivers-Smith Inlets	RSI	R12	4	ecotypic/other	Data limited. We assumed the same genetic patterning as lake-type, where Rivers Inlet populations are distinctive.
E Queen Charlotte Islands	EQCI	R13	5	ecotypic	weakly supported by timing
W Queen Charlotte Islands	WQCI	R14	7	ecotypic	
N Queen Charlotte Islands	NQCI	R15	3	ecotypic	
Northern Coastal Fjords	NCFj	R16	48	timing/other	Includes BCD and NC+HStr JAZ. Timing is distinctive as are the genetics of the lake-type populations.
Northern Coastal	NC	R17	20	timing/other	The HecLow+HStr JAZ. Timing is distinctive. Lake-type populations are genetically distinctive. Includes 1 site from the HecLow+NSKEst, for which there is no information.
Skeena River	SKNA	R18	9	genetics/timing	Includes the LSK and MSK JAZ. No differences in timing or genetics
Skeena River-high interior	SKNA-HI	R19	1	ecotypic	Only 1 site with no information and unknown status.
Lower Nass - Portland	LNR-P	R20	7	ecotypic/timing	Distinctive timing
Upper Nass River	UNR	R21	3	ecotypic/timing	Distinctive timing

Name	Acronym	index	number of sites	classification step	comments
Northern Transboundary Fjords	TBFj	R22	22	genetics	Includes Taku and LSTK JAZ as well as Unuk and Whiting Rivers if river-type populations are found there. No timing information. Within watershed genetic differentiation at the class-3 and class-4 levels is apparent in both major watersheds and can be explained by a simple habitat model in the Taku. Beacham et al. (2004) found no genetic differentiation in the river-type sockeye of these two systems so we have combined them all into one CU
Chilkat River	CHILKAT	R23	1	ecotypic	supported by genetics
Alsek River	ALSEK	R24	7	ecotypic	No timing information. No habitat explanation of the genetic structure at level-4 of the hierarchy. Some sites in this CU are located in the Yukon Territory.

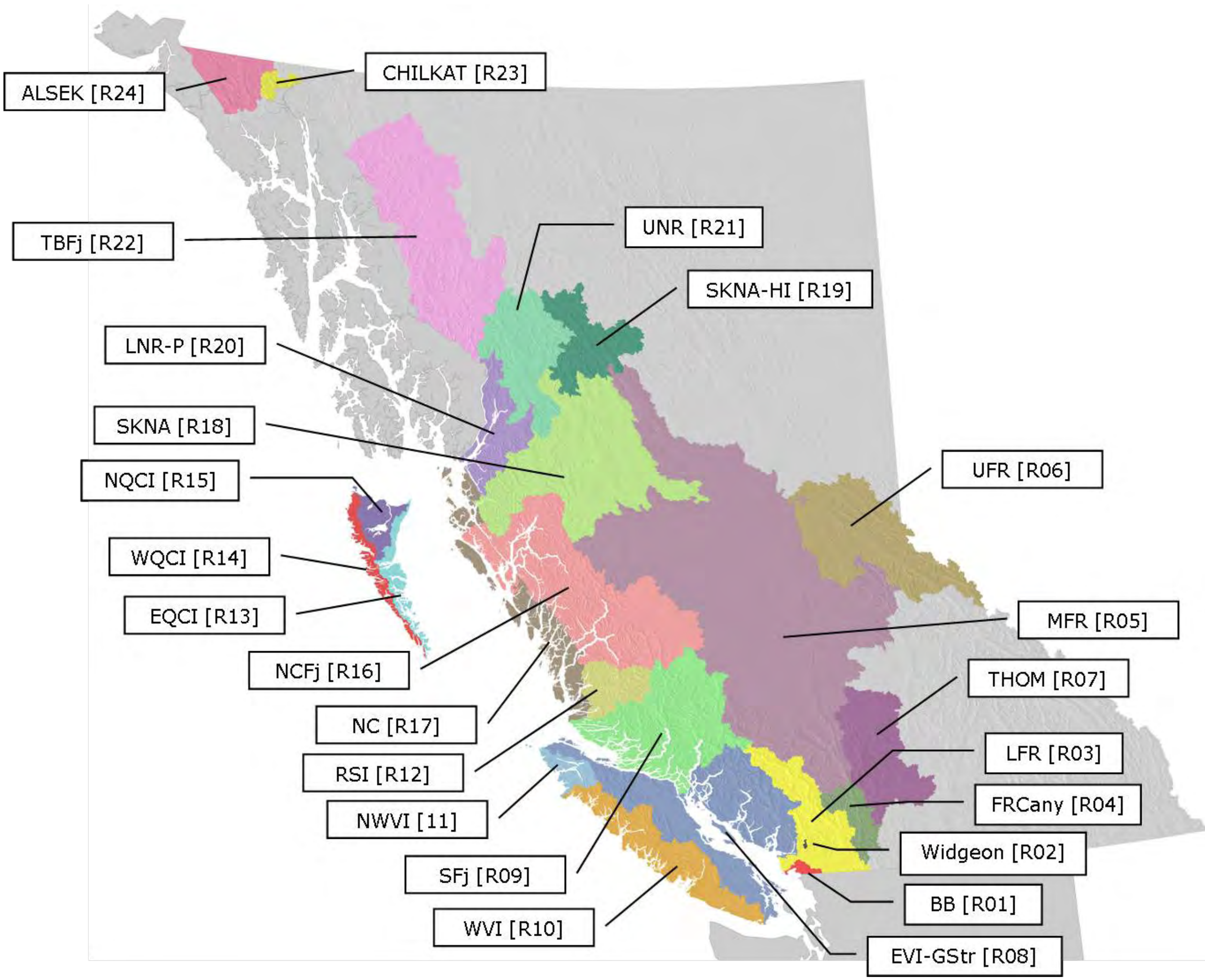


Figure 69. The 24 Conservation Units of river-type sockeye in British Columbia.

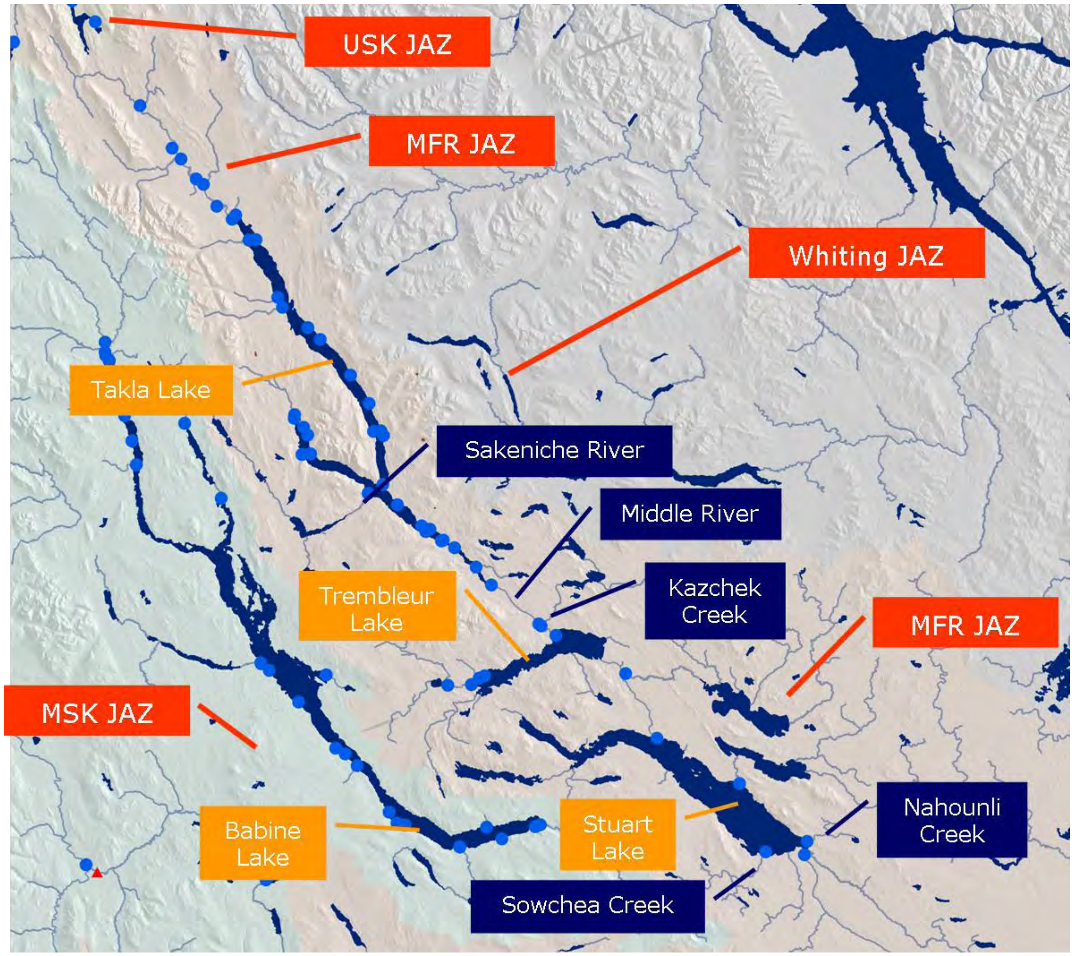


Figure 70. A detailed map of the Stuart, Trembleur, and Takla Lakes area in the MFR JAZ. The blue dots are spawning tributaries of the lake-type sockeye populations. Sowchea and Nahounli Creeks are the only spawning sites for the ESTU run-timing group in Stuart Lake. Sakeniche River and Kazchek Creek are the principal spawning locations for the Summer run-timing component in the Takla and Trembleur Lakes, respectively.

Table 50. This table contains summary information for all of the lake-type sockeye CUs in British Columbia. CUs were named after the primary nursery lake(s). In cases where the lake was unnamed, the CU is named after the stream or other geographical locator. The CU index identifies the type ("L"), the FAZ ecotypic zone of the streams (not the lake), and a unique number within that zone. In the Fraser River, a run-timing designation is used to describe CUs and to distinguish CUs where there are two in the same nursery lake. Two table entries (L-6-11 & L-6-16) were not recognized as CUs for reasons described in the text. The number of sites indicated is the number of sites in our database where sockeye of the associated CU are known to spawn and is not to be interpreted as the total number of sites in the CU where sockeye are persistently present.

CU index	Conservation Unit	FAZ	number of sites	number of lakes	total surface area (ha)	average elevation (m)	map number
L-1-1	Osoyoos	Okanagan	1	1	1512	276	1
L-3-1	Chehalis-L	Lower Fraser	1	1	629	221	2
L-3-2	Chilliwack-ES	Lower Fraser	2	1	1182	621	3
L-3-3	Cultus-L	Lower Fraser	2	1	631	46	4
L-3-4	Harrison (D/S)-L	Lower Fraser	1	1	22192	11	5
L-3-5	Harrison (U/S)-L	Lower Fraser	7	-	-	-	6
L-3-6	Pitt-ES	Lower Fraser	4	1	5348	4	7
L-4-1	Lillooet-L	Lillooet	2	1	3220	194	8
L-5-1	Kawkawa-L	Fraser Canyon	8	1	76	60	9
L-5-2	Nahatlatch-ES	Fraser Canyon	2	1	303	300	10
L-6-1	Anderson/Seton-ES	Middle Fraser	2	1	2872	263	11
L-6-2	Chilko-ES	Middle Fraser	2	1	18447	1175	12
L-6-3	Chilko-S	Middle Fraser	1	-	-	-	13
L-6-4	Francois-ES	Middle Fraser	3	1	25164	717	14
L-6-5	Francois-S	Middle Fraser	3	-	-	-	15
L-6-6	Fraser-ES	Middle Fraser	3	1	5385	676	16
L-6-7	Fraser-S	Middle Fraser	2	-	-	-	17
L-6-8	McKinley-S	Middle Fraser	1	1	513	865	18
L-6-9	Nadina-ES	Middle Fraser	1	1	930	928	19
L-6-10	Quesnel-S	Middle Fraser	1	4	32863	768.75	20
L-6-11	Seton-L	Middle Fraser	67	1	2475	243	21
L-6-12	Stuart-ESTU	Middle Fraser	1	1	35919	681	23
L-6-13	Stuart-S	Middle Fraser	2	-	-	-	24
L-6-14	Takla/Trembleur-ESTU	Middle Fraser	6	1	36253	690	25
L-6-15	Taseko-ES	Middle Fraser	45	1	2124	1327	27
L-6-16	Takla/Trembleur-S	Middle Fraser	2	1	36253	690	26
L-7-1	Bowron-ES	Upper Fraser	6	1	1021	914	30
L-7-2	Indianpoint/Indian-ES	Upper Fraser	2	2	625	951.5	31
L-9-1	Adams/Shuswap-ES	South Thompson	1	6	40364	3855	32
L-9-2	Adams/Shuswap-L	South Thompson	25	-	-	-	33
L-9-3	Kamloops-L	South Thompson	45	2	6014	486.5	34
L-10-1	Kamloops-ES	North Thompson	1	1	5517	335	41
L-11-1	Sakinaw	S Coastal Streams	9	1	681	7	43
L-11-2	Tzoonie	S Coastal Streams	1	1	19	1346	44
L-11-3	Fulmore	S Coastal Streams	1	1	867	36	45

CU index	Conservation Unit	FAZ	number of sites	number of lakes	total surface area (ha)	average elevation (m)	map number
L-11-4	Heydon	S Coastal Streams	1	1	799	36	46
L-11-5	Kakweiken	S Coastal Streams	1	1	32	61	47
L-11-6	Loose	S Coastal Streams	1	1	275	44	48
L-11-7	Mackenzie	S Coastal Streams	1	1	153	31	49
L-11-8	Phillips	S Coastal Streams	1	1	309	13	50
L-11-9	Tom Browne	S Coastal Streams	1	1	488	14	51
L-11-10	Village Bay	S Coastal Streams	1	1	101	14	52
L-12-1	Georgie/Songhees	E Vancouver Island	1	2	508	225.5	53
L-12-2	Ida/Bonanza	E Vancouver Island	1	2	991	265	54
L-12-3	Nahwitti	E Vancouver Island	1	1	245	199	55
L-12-4	Nimpkish	E Vancouver Island	1	1	3679	25	56
L-12-5	Quatse	E Vancouver Island	1	1	152	84	57
L-12-6	Schoen	E Vancouver Island	1	1	246	402	58
L-12-7	Shushartie	E Vancouver Island	1	1	25	134	59
L-12-8	Woss	E Vancouver Island	1	1	1379	147	60
L-13-1	Alice	W Vancouver Island	1	1	1074	61	61
L-13-2	Canoe Creek	W Vancouver Island	1	1	29	15	62
L-13-3	O'Connell	W Vancouver Island	1	1	121	58	63
L-13-4	William/Brink	W Vancouver Island	1	2	208	75	64
L-13-5	Cecilia	W Vancouver Island	1	2	46	17	65
L-13-6	Cheewat	W Vancouver Island	1	1	138	5	66
L-13-7	Clayoquot	W Vancouver Island	1	1	49	17	67
L-13-8	Deserted	W Vancouver Island	1	1	40	5	68
L-13-9	Fairy	W Vancouver Island	1	1	32	3	69
L-13-10	Great Central/Sproat	W Vancouver Island	2	2	9561	58.5	70
L-13-11	Henderson	W Vancouver Island	3	1	1552	5	71
L-13-12	Hesquiat	W Vancouver Island	1	1	471	7	72
L-13-13	Hobiton	W Vancouver Island	1	1	363	14	73
L-13-14	Jansen	W Vancouver Island	1	1	54	14	74
L-13-15	Kanim	W Vancouver Island	1	1	120	9	75
L-13-16	Kennedy	W Vancouver Island	1	1	6542	7	76
L-13-17	Maggie	W Vancouver Island	7	1	238	33	77
L-13-18	Megin	W Vancouver Island	1	1	167	27	78
L-13-19	Muchalat	W Vancouver Island	1	1	531	202	79
L-13-20	Muriel	W Vancouver Island	3	1	162	12	80
L-13-21	Nitinat	W Vancouver Island	1	1	2733	2	81
L-13-22	Owossitsa	W Vancouver Island	1	1	69	16	82
L-13-23	Park River	W Vancouver Island	1	2	24	6	83
L-13-24	Power	W Vancouver Island	1	1	65	8	84
L-13-25	Sooke	W Vancouver Island	1	1	589	183	85
L-15-1	Long	Rivers-Smith Inlets	1	1	2133	6	86
L-15-2	Owikeno	Rivers-Smith Inlets	3	1	9302	10	87
L-16-1	South Atnarko Lakes	Bella Coola - Dean Rivers	12	4	770	537.75	88
L-17-1	Mathers	Queen Charlottes	2	1	170	37	89
L-17-2	Skidegate	Queen Charlottes	1	1	712	41	90
L-17-3	Ain/Skundale/Ian	Queen Charlottes	1	3	2084	39	91
L-17-4	Awun	Queen Charlottes	1	1	480	17	92

CU index	Conservation Unit	FAZ	number of sites	number of lakes	total surface area (ha)	average elevation (m)	map number
L-17-5	Jalun	Queen Charlottes	1	1	105	114	93
L-17-6	Marian	Queen Charlottes	1	1	167	19	94
L-17-7	Yakoun	Queen Charlottes	1	1	820	103	95
L-17-8	Fairfax	Queen Charlottes	1	1	35	21	96
L-17-9	Mercer	Queen Charlottes	1	1	107	16	97
L-18-1	Backland	N Coastal Streams	1	1	101	68	98
L-18-2	Canoona	N Coastal Streams	1	1	348	37	99
L-18-3	Dome	N Coastal Streams	1	1	44	64	100
L-18-4	Evelyn	N Coastal Streams	1	1	57	39	101
L-18-5	James Bay	N Coastal Streams	1	1	37	85	102
L-18-6	Kainet Creek	N Coastal Streams	1	1	62	22	103
L-18-7	Kimsquit	N Coastal Streams	1	1	165	358	104
L-18-8	Kitkiata	N Coastal Streams	1	1	264	31	105
L-18-9	Kitlope	N Coastal Streams	1	1	1171	13	106
L-18-10	Quartcha Creek	N Coastal Streams	1	1	33	175	107
L-18-11	Soda Creek	N Coastal Streams	1	2	222	108.5	108
L-18-12	Whalen	N Coastal Streams	1	1	2140	120	109
L-19-1	Banks	Hecate Lowlands	1	1	164	18	110
L-19-2	Bloomfield	Hecate Lowlands	1	1	147	8	111
L-19-3	Bolton Creek	Hecate Lowlands	1	6	39	91.16667	112
L-19-4	Borrowman Creek	Hecate Lowlands	1	2	26	74	113
L-19-5	Busey Creek	Hecate Lowlands	1	2	76	99	114
L-19-6	Cartwright Creek	Hecate Lowlands	1	2	46	59	115
L-19-7	Citeyats	Hecate Lowlands	1	2	355	9.5	116
L-19-8	Curtis Inlet	Hecate Lowlands	1	1	275	5	117
L-19-9	Dallain Creek	Hecate Lowlands	1	2	20	17.5	118
L-19-10	Deer	Hecate Lowlands	1	4	326	35	119
L-19-11	Devon	Hecate Lowlands	1	1	173	7	120
L-19-12	Douglas Creek	Hecate Lowlands	1	2	11	97	121
L-19-13	Elizabeth	Hecate Lowlands	1	1	641	14	122
L-19-14	Elsie/Hoy	Hecate Lowlands	1	2	146	30.5	123
L-19-15	End Hill Creek	Hecate Lowlands	1	1	119	15	124
L-19-16	Evinrude Inlet	Hecate Lowlands	1	3	224	46.33333	125
L-19-17	Freeda	Hecate Lowlands	1	2	205	6.5	126
L-19-18	Hartley Bay	Hecate Lowlands	1	2	283	33.5	127
L-19-19	Hevenor Inlet	Hecate Lowlands	1	2	114	31.5	128
L-19-20	Higgins Lagoon	Hecate Lowlands	1	1	13	43	129
L-19-21	Kakushdish Creek	Hecate Lowlands	1	1	52	17	130
L-19-22	Kdelmashan Creek	Hecate Lowlands	1	3	43	25	131
L-19-23	Keecha	Hecate Lowlands	1	1	326	13	132
L-19-24	Kent Inlet Lagoon Creek	Hecate Lowlands	1	1	99	18	133
L-19-25	Kenzuwash Creeks	Hecate Lowlands	1	1	68	12	134
L-19-26	Keswar Creek	Hecate Lowlands	1	1	99	30	135
L-19-27	Kildidt Creek	Hecate Lowlands	1	1	96	28	136
L-19-28	Kildidt Lagoon Creek	Hecate Lowlands	1	1	50	23	137
L-19-29	Bonilla	Hecate Lowlands	1	1	221	5	138
L-19-30	Kisameet	Hecate Lowlands	1	1	134	26	139
L-19-31	Koeye	Hecate Lowlands	1	1	449	53	140

CU index	Conservation Unit	FAZ	number of sites	number of lakes	total surface area (ha)	average elevation (m)	map number
L-19-32	Kooryet	Hecate Lowlands	1	1	498	21	141
L-19-33	Kunsoot River	Hecate Lowlands	1	1	15	41	142
L-19-34	Kwakwa Creek	Hecate Lowlands	1	1	78	5	143
L-19-35	Roderick	Hecate Lowlands	1	1	595	69	144
L-19-36	Lewis Creek	Hecate Lowlands	1	3	63	42.66667	145
L-19-37	Limestone Creek	Hecate Lowlands	1	2	35	49.5	146
L-19-38	Lowe/Simpson/Weir	Hecate Lowlands	1	3	1686	20.66667	147
L-19-39	Mary Cove Creek	Hecate Lowlands	1	1	31	16	148
L-19-40	McDonald Creek	Hecate Lowlands	1	4	23	12.75	149
L-19-41	Mcloughlin	Hecate Lowlands	1	1	23	19	150
L-19-42	Mikado	Hecate Lowlands	1	1	148	19	151
L-19-43	Monckton Inlet Creek	Hecate Lowlands	1	2	21	5	152
L-19-44	Namu	Hecate Lowlands	1	1	319	9	153
L-19-45	Port John	Hecate Lowlands	1	1	92	44	154
L-19-46	Powles Creek	Hecate Lowlands	1	2	49	51.5	155
L-19-47	Price Creek	Hecate Lowlands	1	1	93	23	156
L-19-48	Ryan Creek	Hecate Lowlands	1	2	46	13.5	157
L-19-49	Salter	Hecate Lowlands	1	1	65	12	158
L-19-50	Scoular/Kilpatrick	Hecate Lowlands	1	2	94	20	159
L-19-51	Sheneeza Inlet	Hecate Lowlands	1	1	42	23	160
L-19-52	Ship Point Creek	Hecate Lowlands	1	1	39	17	161
L-19-53	Spencer Creek	Hecate Lowlands	1	1	50	19	162
L-19-54	Stannard Creek	Hecate Lowlands	1	5	39	28.6	163
L-19-55	Talamoosa Creek	Hecate Lowlands	1	2	53	23	164
L-19-56	Tankeeah River	Hecate Lowlands	1	1	150	7	165
L-19-57	Treneman Creek	Hecate Lowlands	1	4	36	504.5	167
L-19-58	Tsimtack/Moore/Roger	Hecate Lowlands	1	3	560	5.666667	168
L-19-59	Tuno Creek East	Hecate Lowlands	1	2	87	13	169
L-19-60	Tuno Creek West	Hecate Lowlands	1	2	44	9	170
L-19-61	Tyler Creek	Hecate Lowlands	1	2	60	79.5	171
L-19-62	Wale Creek	Hecate Lowlands	1	3	314	46.33333	172
L-19-63	Watt Bay	Hecate Lowlands	1	1	53	6	173
L-19-64	West Creek	Hecate Lowlands	1	1	22	23	174
L-19-65	Yaaklele Lagoon	Hecate Lowlands	1	2	32	11.5	175
L-19-66	Yeo	Hecate Lowlands	1	1	83	35	176
L-19-67	Prudhomme	Hecate Lowlands	1	1	182	33	177
L-19-68	Shawatlan	Hecate Lowlands	2	1	163	15	178
L-20-1	Alastair	Lower Skeena	1	1	684	45	179
L-20-2	Aldrich	Lower Skeena	3	1	76	861	180
L-20-3	Dennis	Lower Skeena	1	1	89	848	181
L-20-4	Ecstall/Lower	Lower Skeena	1	2	125	32	182
L-20-5	Johnston	Lower Skeena	1	1	188	24	183
L-20-6	Kitsumkalum	Lower Skeena	1	1	1905	148	184
L-20-7	Lakelse	Lower Skeena	6	1	1368	76	185
L-20-8	McDonell	Lower Skeena	7	1	226	827	186
L-21-1	Atna	Middle Skeena	2	1	513	779	187
L-21-2	Babine	Middle Skeena	1	1	46499	711	188
L-21-3	Bulkley	Middle Skeena	30	1	240	712	189

CU index	Conservation Unit	FAZ	number of sites	number of lakes	total surface area (ha)	average elevation (m)	map number
L-21-4	Club	Middle Skeena	1	1	38	525	190
L-21-5	Kitwancool	Middle Skeena	1	1	777	390	191
L-21-6	Maxan	Middle Skeena	1	1	643	789	192
L-21-7	Morice	Middle Skeena	1	1	9708	763	193
L-21-8	Nilkitkwa	Middle Skeena	3	1	483	709	194
L-21-9	Stephens	Middle Skeena	1	1	189	518	195
L-21-10	Swan	Middle Skeena	2	1	1738	525	196
L-21-11	Tahlo/Morrison	Middle Skeena	5	2	1460	755.5	197
L-22-1	Asitika	Upper Skeena	2	1	37	1298	198
L-22-2	Azuklotz	Upper Skeena	1	1	165	787	199
L-22-3	Bear	Upper Skeena	1	1	1894	788	200
L-22-4	Damshilgwit	Upper Skeena	3	1	32	623	201
L-22-5	Johanson	Upper Skeena	1	2	195	1459	202
L-22-6	Kluatantan	Upper Skeena	1	1	27	1009	203
L-22-7	Kluayaz	Upper Skeena	1	1	138	1012	204
L-22-8	Motase	Upper Skeena	1	1	394	987	205
L-22-9	Sicintine	Upper Skeena	1	1	69	977	206
L-22-10	Slamgeesh	Upper Skeena	1	1	45	616	207
L-22-11	Spawning	Upper Skeena	2	1	20	1445	208
L-22-12	Sustut	Upper Skeena	1	2	292	1304	209
L-23-1	Clements	Lower Nass - Portland	1	1	17	96	210
L-23-2	Leverson	Lower Nass - Portland	1	1	116	81	211
L-24-1	Bowser	Upper Nass	1	1	3455	368	212
L-24-2	Damdochax	Upper Nass	1	1	204	588	213
L-24-3	Fred Wright	Upper Nass	1	1	388	578	214
L-24-4	Kwinageese	Upper Nass	1	1	258	631	215
L-24-5	Meziadin	Upper Nass	1	1	3603	246	216
L-24-6	Owegee	Upper Nass	3	1	49	515	217
L-25-1	Border	Unuk River	1	1	41	95	218
L-26-1	Christina	Lower Stikine	1	1	147	100	219
L-26-2	Tahltan	Lower Stikine	1	1	486	809	220
L-28-1	Kuthai	Taku	1	1	154	728	221
L-28-2	Little Trapper/Trapper	Taku	1	1	201	730	222
L-28-3	Tatsamenie	Taku	1	2	2166	781.5	223
L-28-4	Tatsatua	Taku	1	1	77	725	224
L-30-1	Blanchard	Alsek	1	1	118	1062	225
L-30-2	Klukshu	Alsek	1	-	-	-	226
L-30-3	Neskatahin	Alsek	1	-	-	-	227

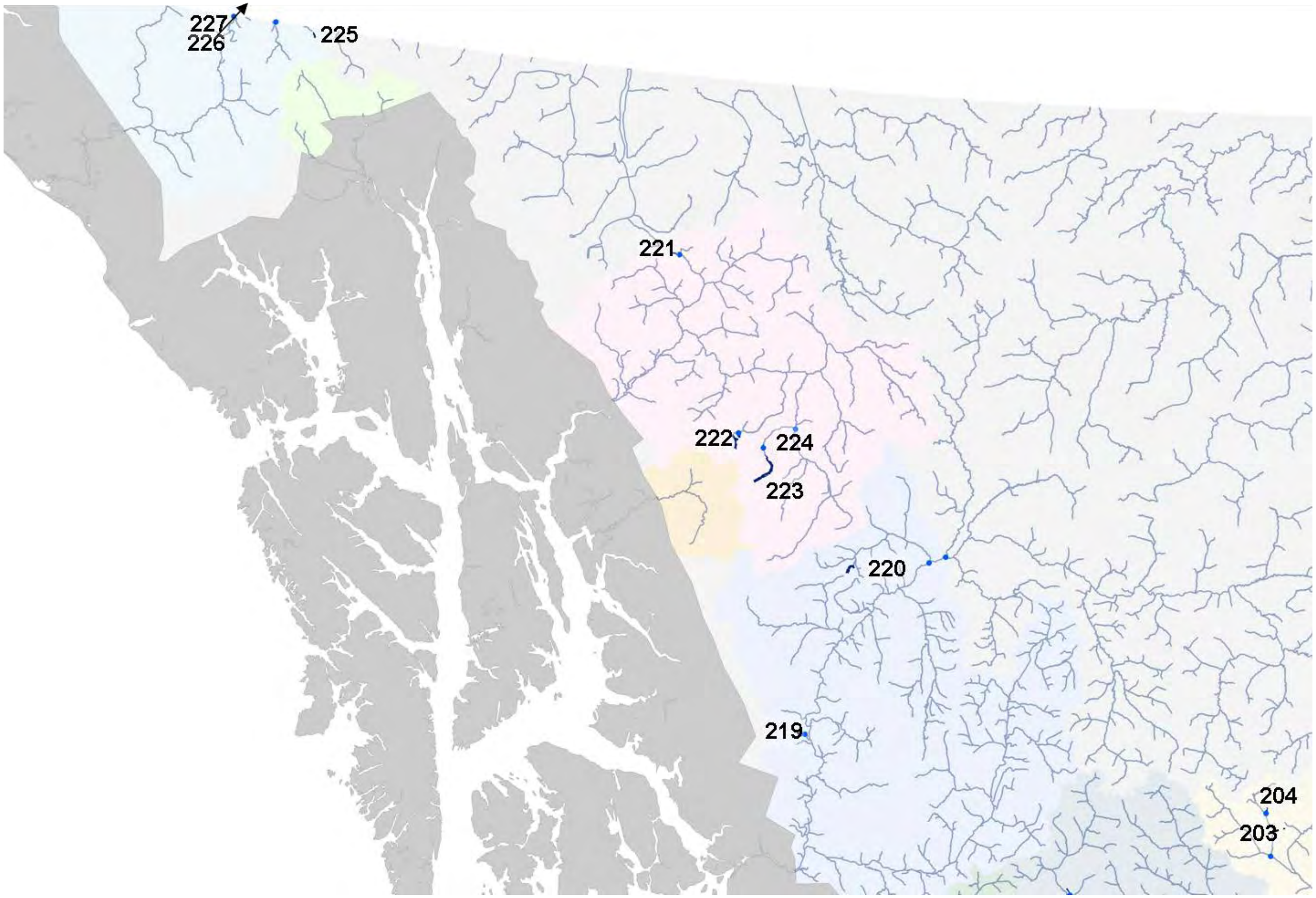


Figure 71. Lake-type sockeye CUs in northern British Columbia. The nursery lakes of the two CUs in the Alsek River drainage are in the Yukon Territory and not shown on the map. The numbers are keyed to their respective CUs in Table 50.

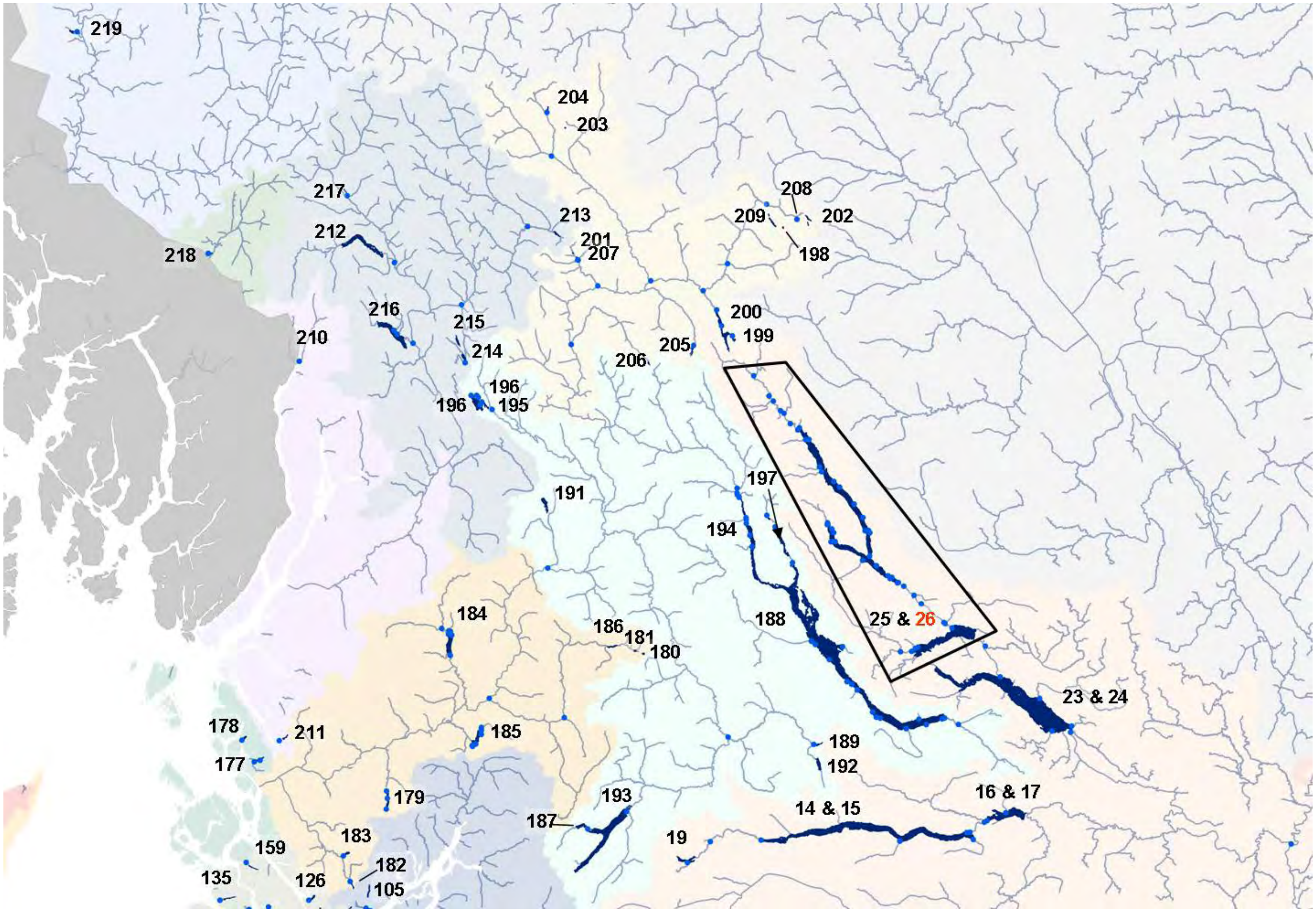


Figure 72. Lake-type sockeye CUs in the Skeena and Nass Rivers of northern coastal British Columbia and in the Stuart/ Trembleur/ Takla Lakes complex of the mid-Fraser River. The numbers are keyed to their respective CUs in Table 50.

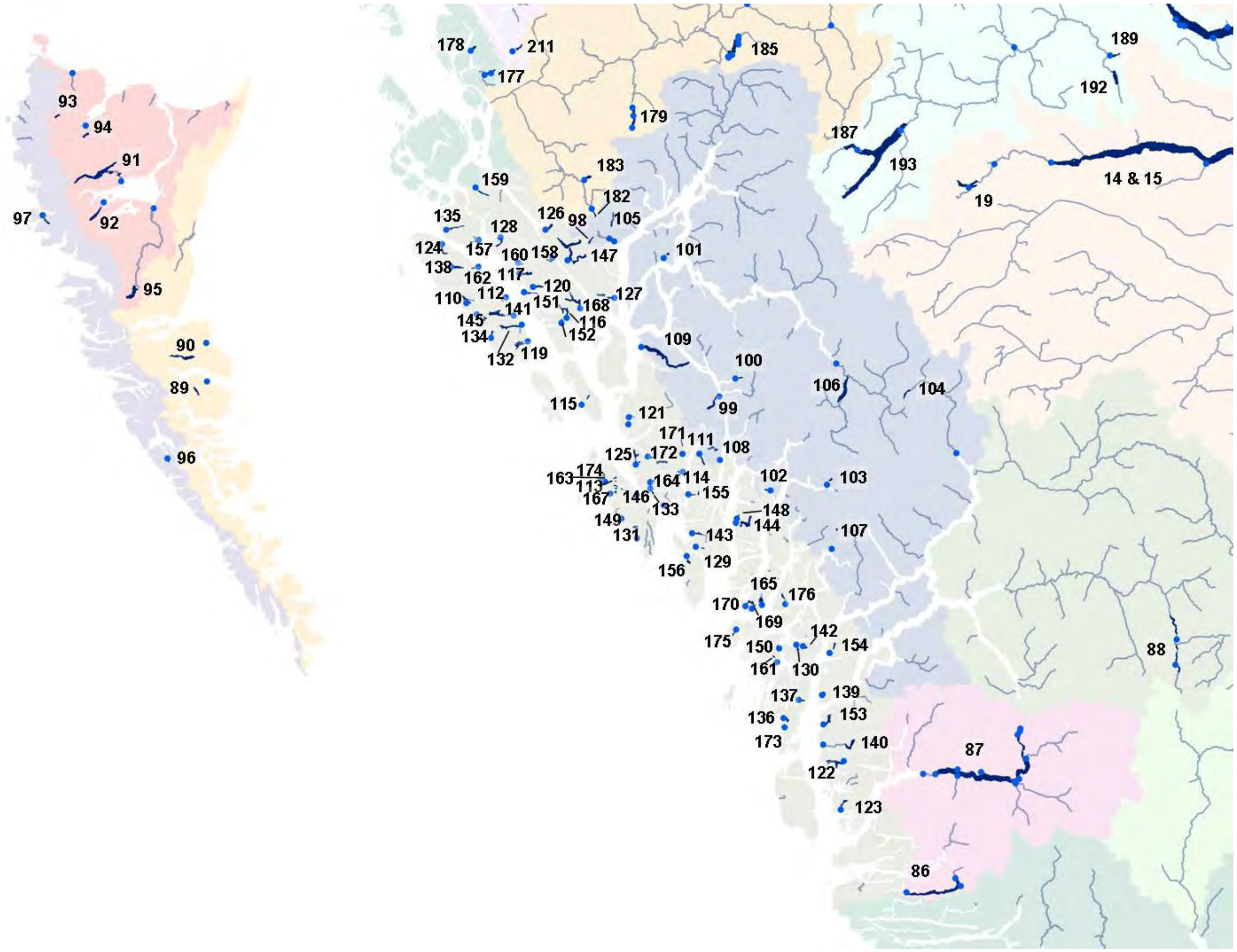


Figure 73. Lake-type sockeye CUs in central coastal British Columbia including the Queen Charlotte Islands. The numbers are keyed to their respective CUs in Table 50.

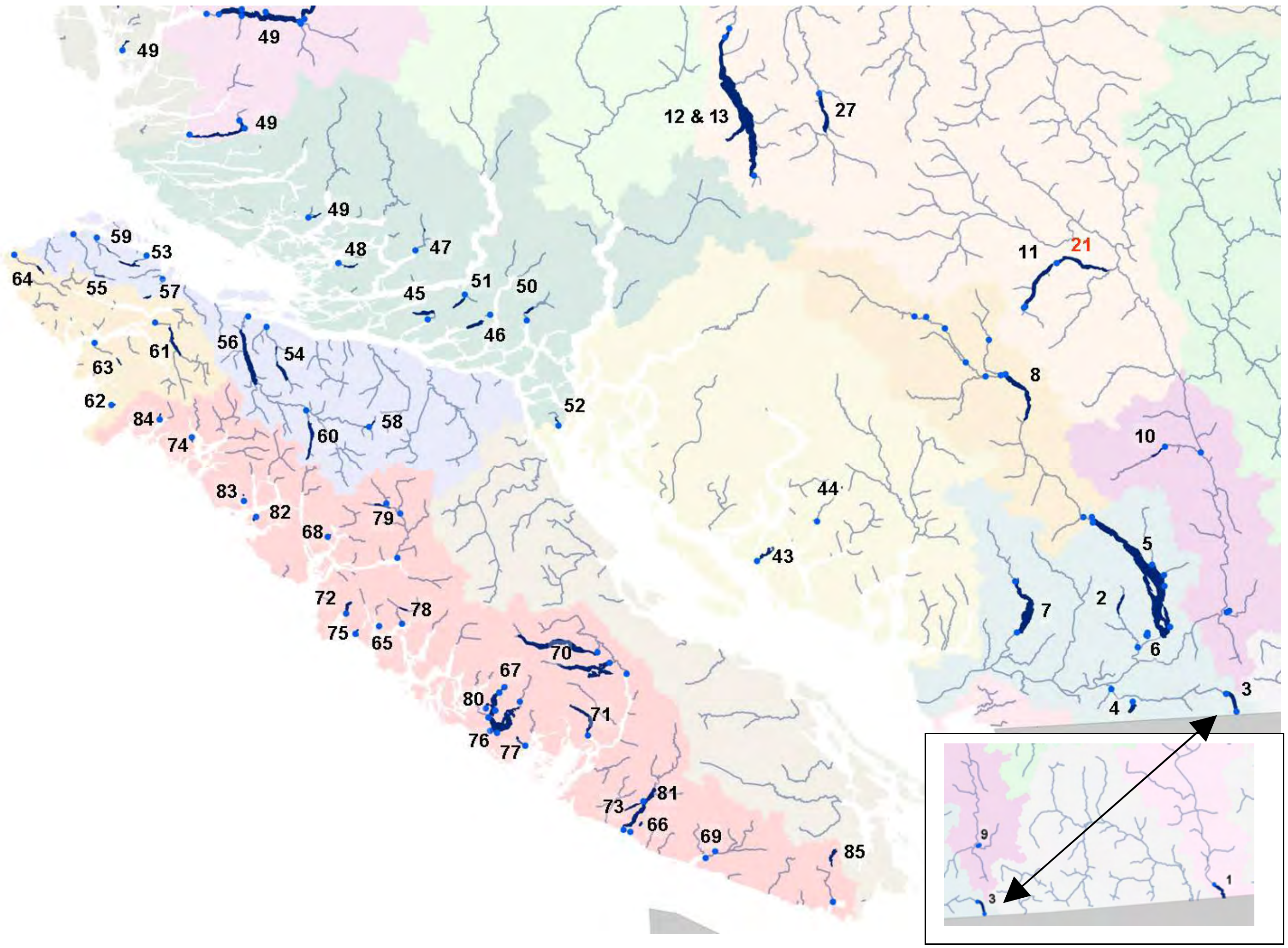


Figure 74. Lake-type sockeye CUs in southwestern British Columbia. The inset map shows the location of the Okanagan CU (#1). The arrow links CU #3 (Chilliwack Lake) to indicate the position of the inset map relative to the larger map. The numbers are keyed to their respective CUs in Table 50.

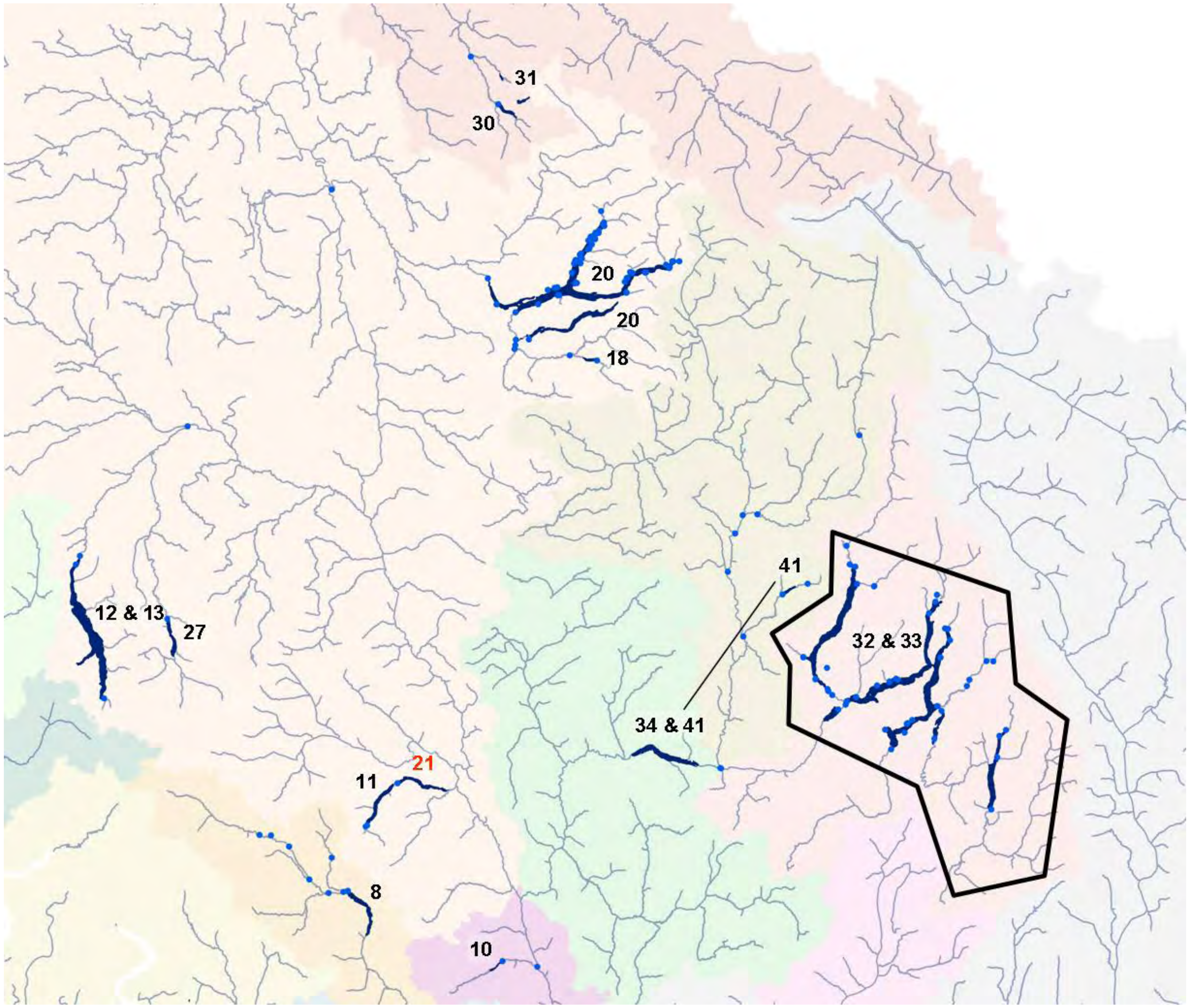


Figure 75. Lake-type sockeye CUs in central British Columbia. The numbers are keyed to their respective CUs in Table 50.

Appendix 1. Freshwater Adaptive Zones of British Columbia

Table 51. The number, descriptive name and acronym for each of the 32 Freshwater Adaptive Zones (FAZ) in British Columbia. The FAZ index increases with latitude. The mean coordinates are of the SEDS sites within each FAZ.

FAZ	FAZ acronym	FAZ code	number of sites	mean latitude	mean longitude
Okanagan	OK	1	1	49.08	-119.51
Boundary Bay	BB	2	12	49.06	-122.67
Lower Fraser	LFR	3	145	49.26	-122.18
Lillooet	LILL	4	18	50.26	-122.70
Fraser Canyon	FRCany	5	20	49.61	-121.47
Middle Fraser	MFR	6	203	53.18	-122.97
Upper Fraser	UFR	7	45	53.65	-120.89
Lower Thompson	LTh	8	21	50.32	-120.99
South Thompson	STh	9	81	50.91	-119.18
North Thompson	NTh	10	48	51.70	-119.70
S Coastal Streams	SC	11	253	50.24	-124.93
E Vancouver Island	EVI	12	128	49.59	-125.03
W Vancouver Island	WVI	13	321	49.56	-126.14
Homathko - Klinaklini Rivers	HK	14	6	51.06	-125.25
Rivers-Smith Inlets	RSI	15	31	51.61	-127.10
Bella Coola - Dean Rivers	BCD	16	41	52.38	-126.51
Queen Charlottes	QCI	17	250	53.01	-131.98
N Coastal Streams	NC	18	125	53.35	-128.42
Hecate Lowlands	HecLow	19	250	52.97	-129.11
Lower Skeena	LSK	20	114	54.46	-128.79
Middle Skeena	MSK	21	121	55.10	-127.25
Upper Skeena	USK	22	22	56.43	-127.45
Lower Nass - Portland	LNR-P	23	78	55.08	-129.81
Upper Nass	UNR	24	24	56.05	-129.01
Unuk River	UNUK	25	2	56.35	-130.74
Lower Stikine	LStk	26	19	57.21	-131.43
Whiting River	Whtng	27	1	58.18	-133.20
Taku	Taku	28	19	58.75	-132.76
Lynn Canal	Lynn	29	4	59.66	-136.04
Alsek	Alsek	30	9	59.81	-137.31
Teslin Headwaters	TesHW	31	4	59.72	-132.32
Lower Liard	Liard	32	1	59.52	-124.07

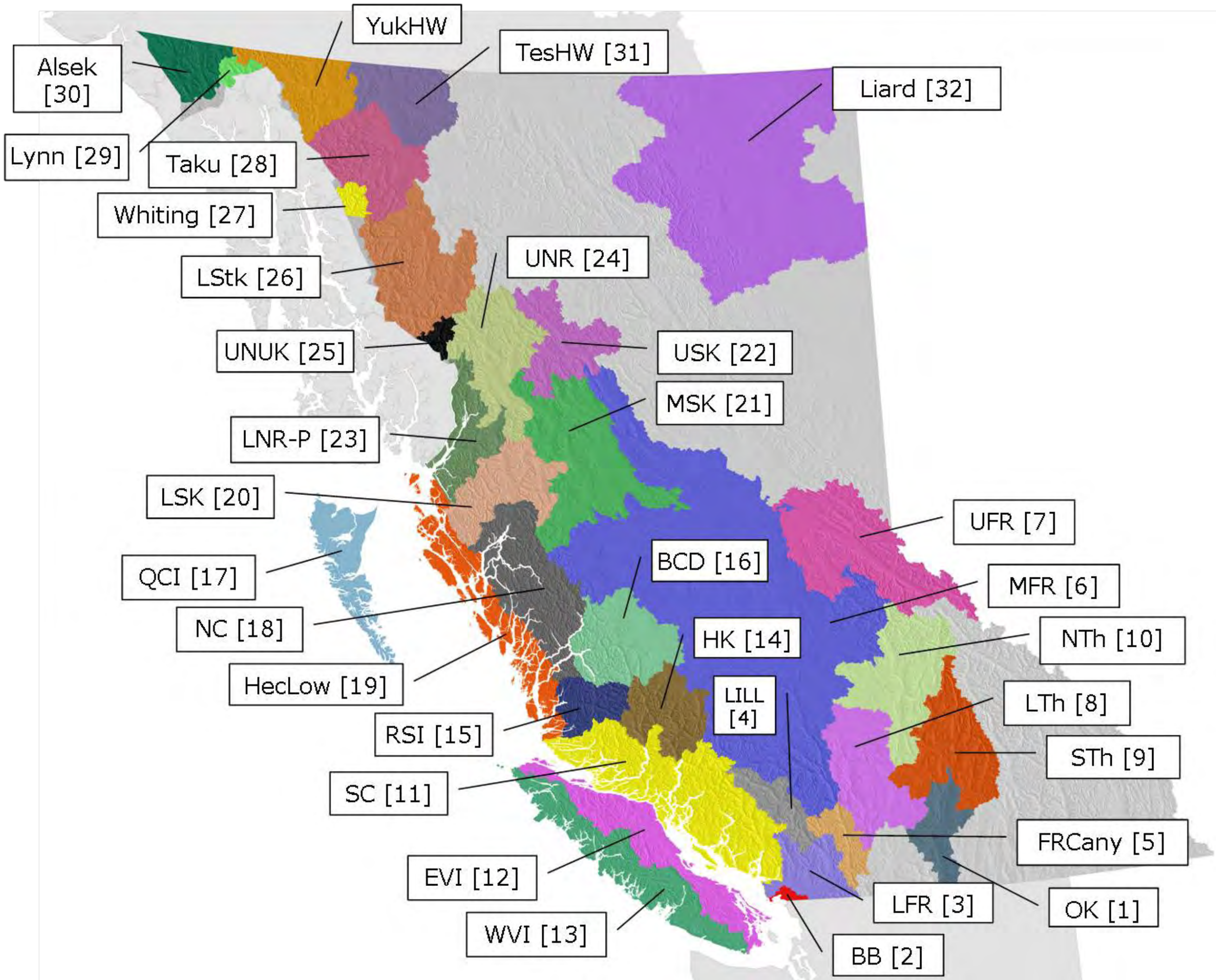


Figure 76. Map of British Columbia showing the Freshwater Adaptive Zones (FAZ) from Table 50.

Table 52. A summary of the zoogeography of the Freshwater Adaptive Zones in British Columbia.

Freshwater Adaptive Zone	Pacific Salmon Species	Refugium(a)	Zoogeography
Alsek	Chinook, Coho, Sockeye	Pacific and Beringian	Except for salmon, this FAZ is poorly known but probably contains the same suite of euryhaline species that occur along the entire coast: anadromous lampreys, smelts, salmon, trout, Dolly Varden (*Salvelinus malma*), threespine sticklebacks, and sculpins (*Cottus aleuticus* and *Cottus asper*). In addition, the round whitefish (*Prosopium cylindraceum*) occurs in the upper river and probably also in the lower river. These species, suggest a Beringian component in the fauna that is absent from the Central and South Coastal systems. The absence of bull trout (*Salvelinus confluentus*) differentiates the FAZ from the Taku and Iskut-Stikine FAZs.
Chilkat	Chinook, Coho, Sockeye	Pacific and Beringian	Except for salmon, the fish fauna for this FAZ is poorly known. It likely contains the same suite of euryhaline species that occur along the entire coast: anadromous lampreys, smelts, salmon, trout, Dolly Varden (*Salvelinus malma*), threespine sticklebacks, and sculpins (*Cottus aleuticus* and *Cottus asper*). In addition, the round whitefish (*Prosopium cylindraceum*) occurs in the upper river and probably also in the lower river. These species, suggest a Beringian component in the fauna.
Taku	Chinook, Coho, Sockeye	Pacific, Beringian and Great Plains	This FAZ drains into the North Pacific Ocean but one of its tributaries the Nanika River has postglacially captured tributaries that once flowed into the Upper Yukon or Teslin FAZ. Thus, the upper river contains the Beringian forms of northern pike, round whitefish, and lake trout. Some of the Pacific salmon in this region may have dispersed postglacially from Beringia. In addition, the round whitefish (*Prosopium cylindraceum*) occurs in the upper river and probably also in the lower river. Bull trout may be present in this drainage system and may occur in the lower river. A minnow, the lake chub (*Cousius plumbeus*) of Great Plains or Nahanni origin occurs at least as far downstream as Tulsequah, and the slimy sculpin (*Cottus cognatus*) extends as far downstream as the Alaskan border.
North Coastal	Chinook, Coho, Sockeye	Pacific and Beringian	This FAZ forms a transition between FAZs with some Bering influences and those that were colonized mainly from the Pacific Refugium.
Lower Iskut-Stikine	Chinook, Coho, Sockeye	Pacific and Beringian	Like the previous two FAZs except for salmon, the fish fauna of the Lower Iskut-Stikine FAZ are not well documented. However, judging from the upstream fauna this FAZ forms a transition between FAZs with some Bering influences and those that were colonized mainly from the Pacific Refugium. There are some Beringian species in the upper river (e.g., lake trout, *Salvelinus namaycush,* and Arctic grayling, *Thymallus arcticus*). The round whitefish is absent from the system but a Pacific species the mountain whitefish, *Prosopium williamsoni,* and bull trout are present and may reach the lower river.
Unuk	Chinook, Coho, Sockeye	Pacific	The fish fauna of the Unuk River is not well known, except for Pacific salmon and the eulachon (*Thaleichthys pacificus*).

Freshwater Adaptive Zone	Pacific Salmon Species	Refugium(a)	Zoogeography
Nass	Chinook, Chum, Coho, Pink, Sockeye	Pacific	Like the three previous FAZs, the fish fauna of the lower Nass river is not well known, except for Pacific salmon and the eulachon (*Thaleichthys pacificus*). The upper river, however, contains primary freshwater fishes of Columbia origin (e.g., peamouth, northern pikeminnow, longnose dace reside shiner, largescale suckers (*Catostomus macrocheilus*) and longnose suckers. The reside shiner and the longnose suckers (*Catostomus catostomus*) reach the lower river.
Lower Nass - Portland	Chinook, Chum, Coho, Sockeye	Pacific	The fish fauna of the Unuk River is not well known, except for Pacific salmon and the eulachon (*Thaleichthys pacificus*).
Lower Skeena	Chinook, Chum, Coho, Sockeye	Pacific	This is the most distinct FAZ on the northern and central coasts. Three minnows (peamouth, pikeminnow, and redside shiner) and one sucker (the largescale sucker) extend downstream at least to Lakelse Lake. The rest of fauna is euryhaline and similar to that in other coastal FAZs.
Hecate Lowlands	Chinook, Chum, Coho, Pink, Sockeye	Pacific	The fish fauna of the Hecate Lowlands FAZ is not well known, except for Pacific salmon and eulachon.
Queen Charlotte – Haida Gwaii	Chinook, Chum, Coho, Pink, Sockeye	Pacific	The Queen Charlotte – Haida Gwaii FAZ contains the islands of the Queen Charlotte Archipelago (Haida Gwaii). There are no true freshwater fish on the islands; however, its fish assemblage includes Pacific lamprey, western brook lamprey, *Lampetra richardsoni,* coastal cutthroat trout, *Oncorhynchus clarkia clarkia;* rainbow trout, *Oncorhynchus mykiss,* and prickly sculpin. Although these probably are recent (postglacial) immigrants, this FAZ is home to a remarkable diversity of threespine sticklebacks, some of which are shared with the E Vancouver Island FAZ.
Bella Coola - Dean	Chinook, Chum, Coho, Pink, Sockeye	Pacific and Great Plains	The Dean and Bella Coola Rivers flow from the Interior Plateau down through the Coast Mountains. The usual suite of euryhaline species - lampreys, Pacific salmon, trout, sticklebacks and sculpins, occur in the lower rivers. There are differences in the fish faunas of the upper reaches of these rivers but no recorded differences in the lower reaches. The upper Bella Coola and Dean Rivers were briefly connected to the Fraser system during glacial recession. They contain peamouth, longnose dace, reside shiner, northern pikeminnow, longnose suckers, largescale suckers as well as bull trout and mountain whitefish. The upper Dean River also contains lake chub.
Rivers-Smith	Chinook, Chum, Coho, Pink, Sockeye	Pacific	The Rivers-Smith FAZ contains predominately Pacific euryhaline species – lampreys, Pacific trout, sticklebacks, sculpins and productive runs of Pacific salmon.

Freshwater Adaptive Zone	Pacific Salmon Species	Refugium(a)	Zoogeography
Homathko - Klinaklini	Chinook, Chum, Coho, Pink, Sockeye	Pacific and Great Plains	The Homathko - Klinaklini Rivers flow from the Interior Plateau down through the Coast Mountains. The usual suite of euryhaline species - lampreys, Pacific salmon, trout, sticklebacks and sculpins, as well as bull trout occur in the lower rivers. There are differences in the fish faunas of the upper reaches of these rivers but no recorded differences in the lower reaches. The upper Homathko and Klinaklini Rivers were briefly connected to the Fraser system during glacial recession. The upper Homathko contains a sparse freshwater fish fauna: bull trout, redside shiners, and longnose suckers. The freshwater fish fauna of the upper Klinaklini is richer than that of the upper Homathko river. It contains peamouth, redside shiner, longnose dace, northern pikeminnows, longnose suckers, and largescale suckers.
E Vancouver Island	Chinook, Chum, Coho, Pink, Sockeye	Pacific	E Vancouver Island FAZ includes E Vancouver Island and associated islands in the Georgia Strait. The native freshwater fish fauna of this FAZ consists almost entirely of euryhaline species. There is, however, one primary freshwater fish (the peamouth) on Vancouver Island. This moderately euryhaline minnow occurs on both the east and west coasts of the island. There is also an endemic lamprey (Vancouver lamprey, *Lampetra macrostoma*) and the Enos Lake pair of sympatric threespine stickleback on the Island. These endemics have evolved *in situ* within the last 12,000 years but together with the peamouth, they define this FAZ.
W Vancouver Island	Chinook, Chum, Coho, Pink, Sockeye	Pacific	W Vancouver Island FAZ includes W Vancouver Island and associated Pacific islands. The native freshwater fish fauna of this FAZ consists almost entirely of euryhaline species. There is, however, one primary freshwater fish (the peamouth) on the Island.
South Coastal	Chinook, Chum, Coho, Pink, Sockeye	Pacific and Great Plains	The South Coastal FAZ consists of a series of small independent rivers that drain the Coast Mountains. All of these rivers drain directly into the Georgia, Johnston and Queen Charlotte straits. Again, the freshwater fish fauna of this FAZ is made-up mainly of euryhaline species. There are peamouth on the Sechelt Peninsula and Nelson Island, and pairs of sympatric sticklebacks on Texada and Lasqueti Islands. The occurrence of Bull trout in some South Coastal rivers such as the Squamish River separates this FAZ from either of the Vancouver Island FAZs.
Boundary Bay	Chinook, Chum, Coho, Pink, Sockeye	Pacific and Great Plains	The Boundary Bay FAZ connects a series of small independent rivers that drain the Cascade Mountains. The freshwater fish of this FAZ consist mostly of euryhaline species.

Freshwater Adaptive Zone	Pacific Salmon Species	Refugium(a)	Zoogeography
Lower Fraser	Chinook, Chum, Coho, Pink, Sockeye	Pacific and Great Plains	The Fraser Canyon separates the Lower Fraser FAZ from the Middle and Upper Fraser FAZs. The lower river extends from the river's delta upstream to Boston Bar. Although the Lower Fraser FAZ contains the usual suite of euryhaline species (e.g., lampreys, sturgeon, smelts, salmon and trout, sticklebacks, and sculpins), it differs from other coastal FAZs in the presence of a substantial primary freshwater fish fauna. Five minnows (brassy minnow, *Hybognathus hanksoni,* peamouth, northern pikeminnow, longnose dace, leopard dace, and an undescribed dace (the Nooksack dace)), four suckers (bridgelip sucker, largescale sucker, mountain sucker, and an genetically distinctive form (the Salish sucker) of the longnose sucker) characterize this FAZ. Most of the freshwater species in this FAZ survived glaciation in the unglaciated portion of the Columbia River system; however, the Nooksack dace and Salish sucker survived in the smaller Chehalis Refugium.
Lillooet	Chinook, Chum, Coho, Pink, Sockeye	Pacific and Great Plains	Lillooet River drains into the Lower Fraser FAZ. It contains the usual suite of euryhaline species – lampreys, sturgeons, smelts, sculpins, salmon and trout.
Middle Fraser	Chinook, Chum, Coho, Pink, Sockeye	Pacific and Great Plains	This FAZ extends from Boston Bar in the Fraser Canyon upstream to the confluence of the Bowron and Fraser rivers. The presence of chiselmouth, lake chub, and white sucker, as well as the absence of euryhaline species like river lamprey, longfin smelt, eulachon, and threespine sticklebacks differentiate this FAZ from the Lower Fraser FAZ.
Upper Fraser	Chinook, Chum, Coho, Pink, Sockeye	Pacific and Great Plains	The Upper Fraser FAZ is defined by the absence of species that are present in the Middle Fraser FAZ. For example, the upstream distributions of six species (Pacific lamprey, brassy minnow, leopard dace, bridgelip sucker, white sucker, and prickly sculpin) all end somewhere between Prince George and the confluence of the Fraser and Bowron rivers. It is not clear why this happens but relative to the Nechako River at Prince George, summer water temperatures decrease and gradients increase in the Upper Fraser FAZ. This change in the physical environment probably influences the distribution of some species.
Middle Skeena	Chinook, Chum, Coho, Pink, Sockeye	Pacific and Great Plains	Postglacial connections between the Upper Skeena and the Middle Fraser FAZs are reflected in the freshwater fish fauna of the Middle Skeena FAZ. This FAZ contains most of the species that occur in the Middle Fraser FAZ. There are five minnows (lake chub, peamouth, northern pikeminnows, longnose dace, and reside shiners), three suckers (longnose suckers, largescale suckers and white suckers), lake trout, bull trout, and three species of whitefish (lake, Mountain, and pygmy whitefish, *Prosopium coulterii*).

Freshwater Adaptive Zone	Pacific Salmon Species	Refugium(a)	Zoogeography
Upper Skeena	Chinook, Coho, Sockeye	Pacific and Great Plains	Postglacial connections between the Upper Skeena FAZ and the Middle Fraser FAZ are reflected in the freshwater fish fauna of the Upper Skeena FAZ. This FAZ contains most of the species that occur in the Middle Fraser FAZ. There are five minnows (lake chub, peamouth, northern pikeminnows, longnose dace, and reside shiners), three suckers (longnose suckers, largescale suckers and white suckers), lake trout, bull trout, and three species of whitefish (lake, Mountain, and pygmy whitefish, *Prosopium coulterii*).
South Thompson	Chinook, Chum, Coho, Pink, Sockeye	Pacific	South Thompson FAZ is the only drainage unit outside the Columbia drainage that contains native populations of the westslope cutthroat trout (*Oncorhynchus clarkia lewisi*).
North Thompson	Chinook, Chum, Coho, Pink, Sockeye	Pacific	North Thompson FAZ differs from the South Thompson FAZ in the presence of two Columbia drainage species: the mountain sucker and the torrent sculpin.
Lower Thompson	Chinook, Chum, Coho, Pink, Sockeye	Pacific	Lower Thompson FAZ is a transitional zone between the Thompson River drainage and the Middle Fraser FAZ. It supports both South and North Thompson river species as well as Middle Fraser river species.
Okanagan	Chinook, Chum, Coho, Pink, Sockeye	Pacific	This FAZ is one of the warmest river systems in BC. It lacks bull trout. The Okanagan FAZ contains a number of large, deep lakes. Thus, there are pygmy whitefish and burbot (*Lota lota*) in Okanagan and Skaha Lakes. The rest of the fishes are typical mid-Columbia species, and there is still a remnant run of sockeye salmon within the FAZ and at one time lampreys reached Vaseaux Lake.
Lower Liard	Chum	Great Plains and Beringian	The fauna of the Lower Liard FAZ is dominated by Great Plains species (e.g., goldeye, flathead chub, northern pearl dace, northern redbelly dace, and finescale dace). In addition to Great Plains species, the Lower Liard also contains two migratory Bering species (Arctic cisco, *Coregonus autumnalis,* and inconnu, *Stenodus leucicthys*) that are absent from the upper Liard river. A third species, chum salmon (*Oncorhynchus keta*) occasionally appears in the B.C. portion of the Liard system but it is not known if chum salmon are sporadic visitors or a self-sustaining population.
Upper Yukon	Chinook, Chum	Beringian and Great Plains	This FAZ consists of Atlin and Tagish lake and their tributaries. It is isolated from the rest of the Yukon system by velocity barriers on the Lewes River. This FAZ contains a typical Beringian fauna: least cisco, and the Bering forms of lake trout, (*Salvelinus namaycush*), round whitefish, lake whitefish, and slimy sculpins, and one minnow (lake chub) that may be of Great Plains or Nahanni origin.

Freshwater Adaptive Zone	Pacific Salmon Species	Refugium(a)	Zoogeography
Teslin	Chinook, Chum	Beringian	This FAZ consists of Teslin Lake and its tributaries. Its fauna is more diverse than that of the Upper Yukon FAZ. There is a run of chum salmon (*Oncorhynchus keta*) into the system, and the lake contains a lacustrine population of inconnu. It is also the only FAZ in BC where the broad whitefish (*Coregonus nasus*) occurs. Additionally, these are some lakes in the system that appear to hold two, morphological forms of least ciscoes.

Table 53. A summary of the geological, hydrological, thermal and physiographic characteristics of the Freshwater Adaptive Zones in British Columbia.

Freshwater Adaptive Zone	Pacific Salmon Species	Geology	Coast vs. Interior	Mean Annual Peak Flow	Wetland Influence	Lake Influence	Alpine Tundra Cold Water Influence	Glacial Influence	Water Temperature	Degree Days	Stream Gradient
Alsek	Chinook, Coho, Sockeye	Predominately sedimentary and intrusives with some volcanic	interior	high	low	low	high	high	cold	low	moderate - steep
Chilkat	Chinook, Coho, Sockeye	Predominately intrusives	interior	high	low	low	high	high	cold	low	moderate
Taku	Chinook, Coho, Sockeye	Predominately sedimentary and volcanic with some intrusives	interior	moderate	moderate	low	high	high	cold	low to moderate	moderate - steep
North Coastal	Chinook, Coho, Sockeye	Predominately intrusives with some volcanic and sedimentary	coast	high	low	low	high	high	cold	low	moderate-steep
Lower Iskut-Stikine	Chinook, Coho, Sockeye	Predominately volcanic and sedimentary with some intrusives	interior	very high	moderate	low - moderate	high	high	cold	low to moderate	steep
Unuk	Chinook, Coho, Sockeye	Predominately volcanic with some intrusives and sedimentary	interior	very high	low	low	high	high	cold	low to moderate	steep
Nass	Chinook, Chum, Coho, Pink, Sockeye	Predominately sedimentary	coast - interior	very high	moderate	low - moderate	high	high	cold	low to moderate	steep

Freshwater Adaptive Zone	Pacific Salmon Species	Geology	Coast vs. Interior	Mean Annual Peak Flow	Wetland Influence	Lake Influence	Alpine Tundra Cold Water Influence	Glacial Influence	Water Temperature	Degree Days	Stream Gradient
Lower Nass - Portland	Chinook, Chum, Coho, Sockeye	Mix of volcanic and intrusives with some sedimentary	coast	very high	low	low	high	high	cold	moderate	steep
Lower Skeena	Chinook, Chum, Coho, Sockeye	Mix of volcanic, intrusives and sedimentary	coast	very high	moderate	low	high	high	cold	moderate	steep
Hecate Lowlands	Chinook, Chum, Coho, Pink, Sockeye	Predominately intrusives with some volcanic	coast	very high	low	moderate	high	high	cold-cool	drainage pattern of moderate to high	steep
Queen Charlotte – Haida Gwaii	Chinook, Chum, Coho, Pink, Sockeye	Predominately volcanic with some sedimentary	coast	west coast - high; transition and east coast - very high	high	moderate	moderate	none	west coast cold; moderate interior; east coast warm	high	shallow
Bella Coola - Dean	Chinook, Chum, Coho, Pink, Sockeye	Mix of volcanic, intrusives and alluvium	coast - interior	moderate	high	high	drainage pattern none to high	high	cold	low to moderate	shallow to steep
Rivers-Smith	Chinook, Chum, Coho, Pink, Sockeye	Predominately intrusives	coast	very high	low	high	high	high	cold	moderate to high	steep
Homathko - Klinaklini	Chinook, Chum, Coho, Pink, Sockeye	Predominately intrusives with some alluvium, volcanic and sedimentary	coast - interior	high	low	low	high	high	cold	low to moderate	steep
E Vancouver Island	Chinook, Chum, Coho, Pink, Sockeye	Predominately volcanic with some intrusives and sedimentary	coast	very high	low	high	low	very low	warm	high	moderate

Freshwater Adaptive Zone	Pacific Salmon Species	Geology	Coast vs. Interior	Mean Annual Peak Flow	Wetland Influence	Lake Influence	Alpine Tundra Cold Water Influence	Glacial Influence	Water Temperature	Degree Days	Stream Gradient
W Vancouver Island	Chinook, Chum, Coho, Pink, Sockeye	Predominately volcanic and intrusives	coast	very high	low	high	low	very low	warm	high	moderate
South Coastal	Chinook, Chum, Coho, Pink, Sockeye	Predominately intrusives	coast	very high	low	high	high	high	drainage pattern cold to warm	drainage pattern of moderate to high	steep
Boundary Bay	Chinook, Chum, Coho, Pink, Sockeye	Predominately sedimentary with some volcanic	coast	high	low	low	none	none	warm	high	shallow
Lower Fraser	Chinook, Chum, Coho, Pink, Sockeye	Predominately intrusives with some sedimentary and volcanic	coast	high	moderate	high	moderate	moderate	warm to moderate	high	moderate
Lillooet	Chinook, Chum, Coho, Pink, Sockeye	Predominately intrusives with some sedimentary and volcanic	coast	very high	low	low	high	high	cold	moderate	moderate - steep
Middle Fraser	Chinook, Chum, Coho, Pink, Sockeye	Predominately volcanic with some sedimentary, alluvium and intrusives	interior	low	high	high	moderate	moderate	moderate (mixed)	low to moderate	shallow
Upper Fraser	Chinook, Chum, Coho, Pink, Sockeye	Predominately sedimentary with some volcanic	interior	high	moderate	moderate	high	high	drainage pattern cold to moderate	low to moderate	moderate

Freshwater Adaptive Zone	Pacific Salmon Species	Geology	Coast vs. Interior	Mean Annual Peak Flow	Wetland Influence	Lake Influence	Alpine Tundra Cold Water Influence	Glacial Influence	Water Temperature	Degree Days	Stream Gradient
Middle Skeena	Chinook, Chum, Coho, Pink, Sockeye	Predominately sedimentary with some volcanic	interior	low to high	moderate	high	high	moderate	cold (Babine is moderate)	low to moderate	moderate
Upper Skeena	Chinook, Coho, Sockeye	Predominately sedimentary	interior	high	low	low	high	moderate	cold	low	moderate
South Thompson	Chinook, Chum, Coho, Pink, Sockeye	Predominately intrusives with some volcanic and sedimentary	interior	high	low	high	low	moderate	moderate (mixed)	moderate	moderate
North Thompson	Chinook, Chum, Coho, Pink, Sockeye	Mix of intrusives, alluvium and sedimentary	interior	high	low	high	moderate	high	drainage pattern cold to moderate	low to moderate	moderate
Lower Thompson	Chinook, Chum, Coho, Pink, Sockeye	Predominately volcanic with intrusives, sedimentary and alluvium	interior	low	high	moderate	low	moderate	warm	high	shallow
Okanagan	Chinook, Chum, Coho, Pink, Sockeye	Predominately intrusives and volcanic with some metamorphic	interior	low	low	high	none	none	warm	high	moderate
Lower Liard	Chum	Predominately sedimentary	interior	low	high	moderate	drainage pattern high to low	moderate	drainage pattern cold to warm	low	shallow
Upper Yukon	Chinook, Chum	Predominately intrusives with some sedimentary	interior	moderate to high	moderate	high	high	high	cold	low	shallow

Freshwater Adaptive Zone	Pacific Salmon Species	Geology	Coast vs. Interior	Mean Annual Peak Flow	Wetland Influence	Lake Influence	Alpine Tundra Cold Water Influence	Glacial Influence	Water Temperature	Degree Days	Stream Gradient
Teslin	Chinook, Chum	Predominately sedimentary and intrusives with some volcanic	interior	moderate	moderate	high	high	none	cold	low	moderate

Appendix 2. Marine Adaptive Zones of the Pacific/Yukon Region

Table 54. The number, descriptive name and acronym for each of the 12 Marine Adaptive Zones (MAZ) in British Columbia. The MAZ number increases with latitude. The mean coordinates are of the SEDS sites within each MAZ.

MAZ	MAZ acronym	MAZ code	number of sites	mean latitude.	mean longitude.
OR-WA Coastal	ORWA	1	1	49.08	-119.51
Georgia Strait	GStr	2	821	50.91	-122.35
Vancouver Island Coastal Current	WVI	3	257	49.32	-125.73
QCStr-JStr-SFjords	SFj	4	159	50.72	-126.31
Hecate Strait - Q.C. Sound	HStr	5	544	52.80	-129.22
Outer Graham Island	WQCI	6	148	51.96	-130.35
North Graham Island	NQCI	7	24	53.79	-132.35
Nass - Skeena Estuary	NSKEst	8	404	54.94	-128.65
Transboundary Fjords	TBFj	9	45	58.06	-132.41
Alaska Coastal Downwelling	AKCst	10	9	59.81	-137.31
Bering Sea	Ber	11	4	59.72	-132.32
Arctic Ocean	AO	12	1	59.52	-124.07

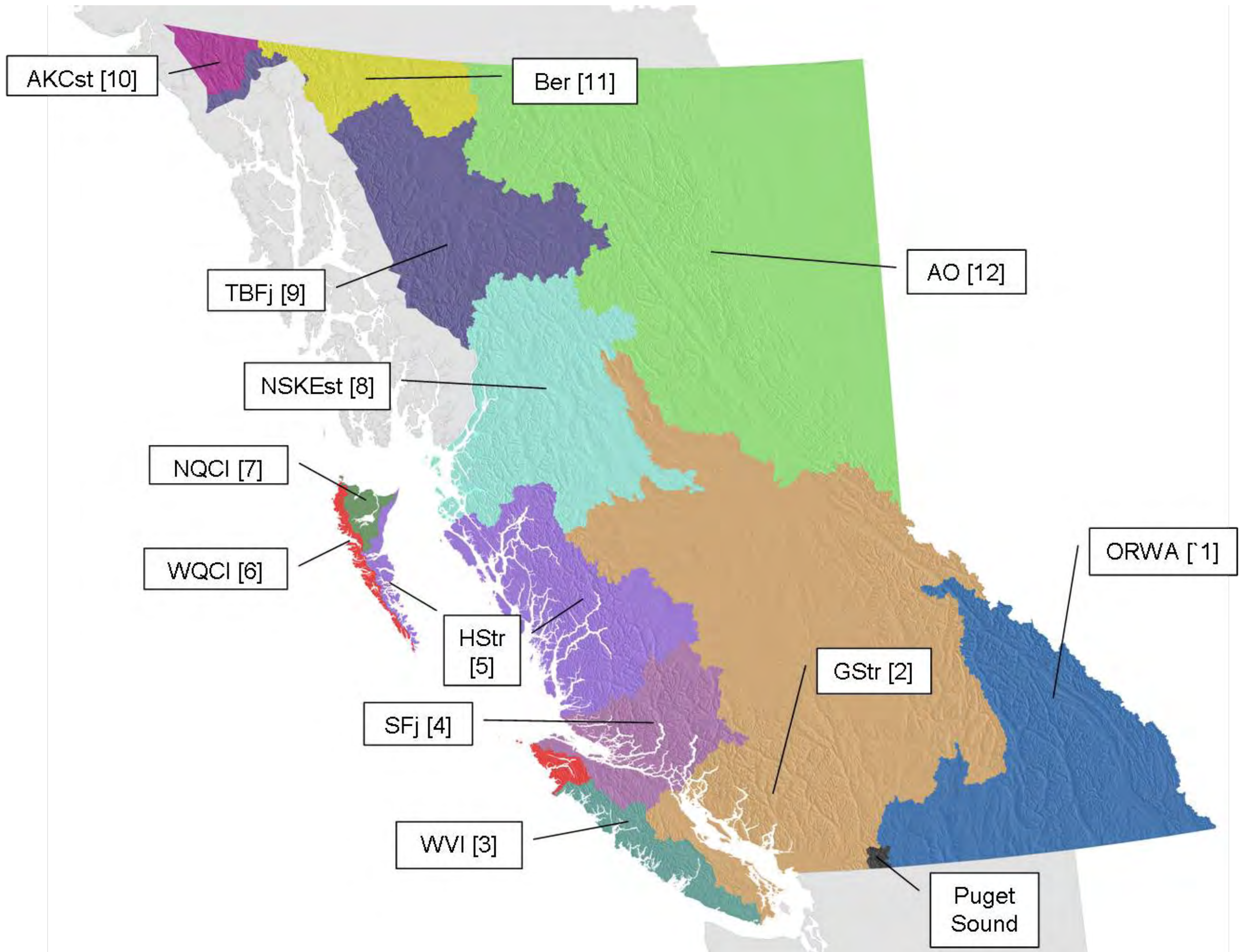


Figure 77. A map of the 12 Marine Adaptive Zones in British Columbia. What is actually shown are the watersheds that discharge into the MAZs.

Appendix 3. Joint Adaptive Zones of British Columbia.

Table 55. The number, descriptive name and acronym for each of the 36 Joint Adaptive Zones in British Columbia. The JAZ number increases with latitude. The mean latitude is of the SEDS sites within each JAZ. Note that the two JAZ in the Yukon River drainage have been given the same code pending final resolution of the adaptive zones in that drainage.

JAZ	JAZ Acronym	JAZ code	n sites	mean latitude	mean longitude
Okanagan | OR-WA Coastal	OK+ORWA	1	1	49.08	-119.51
Boundary Bay | Georgia Strait	BB+GStr	2	12	49.06	-122.67
Lower Fraser | Georgia Strait	LFR+GStr	3	145	49.26	-122.18
Lillooet | Georgia Strait	LILL+GStr	4	18	50.26	-122.70
Fraser Canyon | Georgia Strait	FRCany+GStr	5	20	49.61	-121.47
Middle Fraser | Georgia Strait	MFR+GStr	6	203	53.18	-122.97
Upper Fraser | Georgia Strait	UFR+GStr	7	45	53.65	-120.89
Lower Thompson | Georgia Strait	LTh+GStr	8	21	50.32	-120.99
South Thompson | Georgia Strait	STh+GStr	9	81	50.91	-119.18
North Thompson | Georgia Strait	NTh+GStr	10	48	51.70	-119.70
S Coastal Streams | Georgia Strait	SC+GStr	11	134	49.77	-123.77
S Coastal Streams | QCStr-JStr-SFjords	SC+SFj	12	119	50.78	-126.22
E Vancouver Island | Georgia Strait	EVI+GStr	13	94	49.27	-124.38
E Vancouver Island | QCStr-JStr-SFjords	EVI+SFj	14	34	50.48	-126.82
W Vancouver Island | Vancouver Island Coastal Current	WVI+WVI	15	257	49.32	-125.73
W Vancouver Island | Outer Graham Island	WVI+WQCI	16	64	50.50	-127.79
Homathko - Klinaklini Rivers | QCStr-JStr-SFjords	HK+SFj	17	6	51.06	-125.25
Rivers-Smith Inlets | Hecate Strait - Q.C. Sound	RSI+HStr	18	31	51.61	-127.10
Bella Coola - Dean Rivers | Hecate Strait - Q.C. Sound	BCD+HStr	19	41	52.38	-126.51
Queen Charlottes | Hecate Strait - Q.C. Sound	QCI+HStr	20	142	52.83	-131.73
Queen Charlottes | Outer Graham Island	QCI+WQCI	21	84	53.08	-132.30
Queen Charlottes | North Graham Island	QCI+NQCI	22	24	53.79	-132.35
Hecate Lowlands | Hecate Strait - Q.C. Sound	HecLow+HStr	23	205	52.70	-128.83
N Coastal Streams | Hecate Strait - Q.C. Sound	NC+HStr	24	125	53.35	-128.42
Hecate Lowlands | Nass - Skeena Estuary	HecLow+NSKEst	25	45	54.19	-130.41
Lower Skeena | Nass - Skeena Estuary	LSK+NSKEst	26	114	54.46	-128.79

JAZ	JAZ Acronym	JAZ code	n sites	mean latitude	mean longitude
Middle Skeena | Nass - Skeena Estuary	MSK+NSKEst	27	121	55.10	-127.25
Upper Skeena | Nass - Skeena Estuary	USK+NSKEst	28	22	56.43	-127.45
Lower Nass - Portland | Nass - Skeena Estuary	LNR-P+NSKEst	29	78	55.08	-129.81
Upper Nass | Nass - Skeena Estuary	UNR+NSKEst	30	24	56.05	-129.01
Unuk River | Transboundary Fjords	Unuk+TBFj	31	2	56.35	-130.74
Lower Stikine | Transboundary Fjords	LStk+TBFj	32	19	57.21	-131.43
Whiting River | Transboundary Fjords	Whtng+TBFj	33	1	58.18	-133.20
Taku | Transboundary Fjords	Taku+TBFj	34	19	58.75	-132.76
Lynn Canal | Transboundary Fjords	LYNN+TBFj	35	4	59.66	-136.04
Alsek | Alaska Coastal Downwelling	Alsek+AKCst	36	9	59.81	-137.31
Teslin Headwaters | Bering Sea	TesHW+Ber	37	4	59.72	-132.32
Lower Liard | Arctic Ocean	Liard+AO	38	1	59.52	-124.07
Yukon River | Bering Sea	Yuk+Ber	37	?	?	?
Mackenzie River | Arctic Ocean	MacR+AO	39	1	?	?

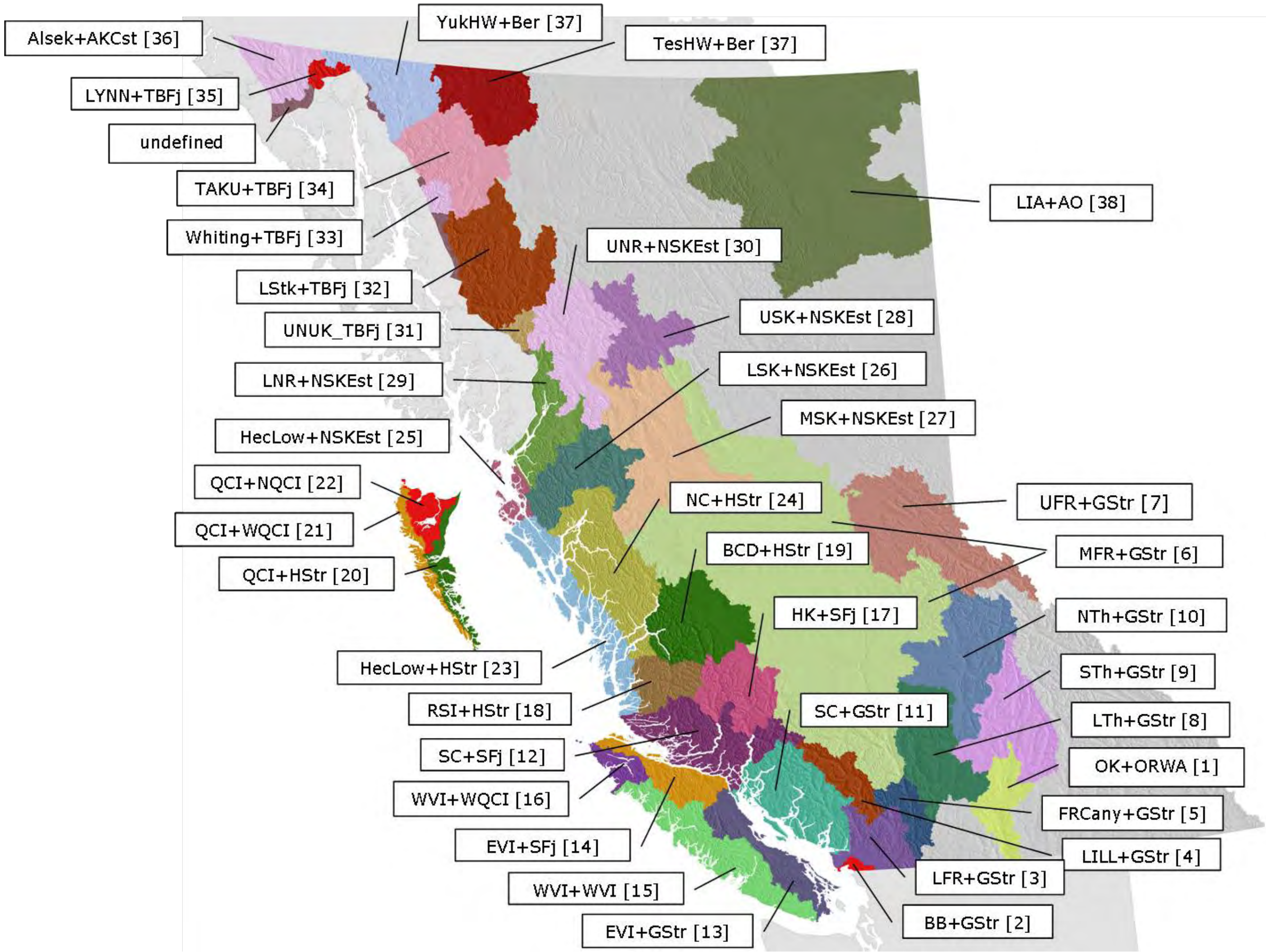


Figure 78. A map of the 39 Joint Adaptive Zones (JAZ) in British Columbia.

Appendix 4. Spawning dates of Pacific salmon populations

The SEDS database contains several fields that provide extensive information on the observed dates of spawning for Pacific salmon in BC. For each GFE_ID, a field identifies the "run type" as one of the following: type 1 (first of two runs), type 2 (second of two runs), [early Stuart, early Summer, Summer, Fall, Late], or unknown. The seasonal attributes (enclosed in []) apply only to Fraser River sockeye. For every GFE_ID there is a year-run type record of escapement that includes three fields identifying the start, peak and end of spawning but values are not always present in all of the fields. We first cross-tabulated the three timing fields species × GFE_ID × year × run-type. Where the run-type was 'unknown' run-type we recoded it to 'type 1'. In many Fraser River sockeye populations where there are two run-timing groups and two corresponding spawn-timings we encountered obvious coding errors in the run-timing field, which were subsequently confirmed as errors (pers. comm. E. Grundmann, PBS, Nanaimo). Where the error was obvious we corrected the run-timing designation. Where the date of peak spawning was not specified we entered the average of the beginning and end dates if they were present or discarded the record if not. The dates were then converted to the day-of-year with adjustments for leap-years and the average DOY across years was calculated for each species × GFE_ID × run-type cell of the cross-tabulation. The mean DOY of peak spawning was also seasonally classified following the classification scheme of Appendix 6.

There were spawning time records for nearly all of the GFE_ID in BC with the exception of the northern transboundary rivers where there were little or no data.

Appendix 5. Environmental variables used in the CU delineation

This appendix has been adopted with minor modifications from Ciruna and Butterfield (2005)

Hydrology

Flow Regime

The flow regime is a key environmental driver of the ecology of rivers and their associated floodplains (Naiman et al. 2002, Poff et al. 1997, Puckridge et al. 1998, Richter et al. 1997, Richter et al. 1996). Every river system has an individual or 'signature' flow regime with particular characteristics relating to magnitude, frequency, timing, duration and rate of change of flow events. Each of these hydrological characteristics has individual (as well as interactive) influences on the physical nature of river channels, sediment regime and water quality, biological diversity and key ecological processes sustaining freshwater ecosystems (Naiman et al. 2002). Consequently, the flow regime of a river ecosystem strongly influences the life history patterns of its resident Pacific salmon species (Beechie et al. 2006, Jager and Rose 2003).

Hydrometric gauge stations are sparsely located throughout BC. Given this lack of information on river hydrology, broad flow regime patterns for each river ecosystem were modeled using a thirty-meter grid of precipitation data acquired from Climate Source®[30]. Large-scale patterns in climate create patterns in hydrological and thermal regimes of river ecosystems. Precipitation and potential evapotranspiration control hydrological cycles including the seasonality and predictability of the overall flow pattern. Precipitation data from climate stations across the province were interpolated using a PRISM algorithm. Monthly mean precipitation was normalized by annual mean precipitation per river ecosystem. Monthly mean precipitation was grouped and totaled by season:

- Winter (December, January, February)
- Spring (March, April, May)
- Summer (June, July, August)
- Fall (September, October, November)

For each season, three classes of precipitation (high, intermediate, and low), were derived based on natural breaks in variability of third order watershed units within the BC Watershed Atlas for the entire province. A broad flow regime pattern based on seasonal flow patterns was created for each river ecosystem. The model was further refined by taking into consideration the following precipitation – temperature relationships:

- If mean minimum November, December, January or February temperatures were < 0°C, then the winter flow category for that river ecosystem unit was moved into lowest flow category (i.e., snow does not flow), spring flow was moved into the highest flow category, and summer flow was moved up into the next highest flow category from its original grouping;

[30] http://www.climatesource.com/

- If mean minimum October, November, December, January or February temperatures were between 0 – 5°C, then the flow category for fall and/or winter, depending on the month(s) in question, was moved into next lower flow category from its original grouping (i.e., rain on snow) , and spring was moved into the next highest flow category from its original grouping; and
- If mean maximum July temperatures were classified as warm, then the flow category for summer was moved into next lowest flow category from its original grouping based on predicted high evapotranspiration rates.

A total of seven flow regime patterns were identified across BC (following table).

Winter	Spring	Summer	Fall
1 = low flow, 2 = moderate flow, 3 = high flow			
1	3	1	1
1	3	1	2
1	3	2	1
1	3	2	2
2	3	1	2
3	2	1	2
3	3	1	2

Mean Annual Peak Flow

Mean annual peak flow is a measure of the highest flood flow on an annual basis. These flows are responsible for maintaining channel structure and ecological processes. Freshwater biota including Pacific salmon have evolved to rivers with specific flow events. Eaton et al. (2002) calculated mean annual peak flows per river ecosystem using known Water Survey of Canada gauge data and kriging a scale-independent runoff factor *K* for the mean annual flood. Five mean annual peak flow classes were derived from natural breaks in variability of third order watershed units within the BC Watershed Atlas for the entire province.

Water Temperature

Water temperature affects freshwater biota directly by controlling rates of feeding, metabolism, and growth (Brett 1979, Brett et al. 1982, Fry 1971, Hokanson et al. 1977, Murray and McPhail 1988, Selong et al. 2001, Velson 1987), or indirectly by mediating biotic interactions (Baltz et al. 1982, De Staso III and Rahel, Hinz Jr and Wiley 1998). As a result, spatial and temporal variation in river ecosystem temperatures are likely important factors contributing to the observed differences in species assemblages between river ecosystems. For example, water temperature has been shown to influence fish distribution (Torgersen et al. 1999, Welsh Jr et al. 2001), abundance (Holtby 1988), inter-specific competition (Reeves et al. 1987), and community composition (Wehrly et al. 2002).

Temperature is also important because it influences water chemistry. The rate of chemical reactions generally increases at higher temperatures, which in turn affects biological activity. An important example of the effects of temperature on water chemistry is its impact on oxygen. Warm water holds less oxygen than cool water, so it may be "saturated" with oxygen but still not contain enough for survival of freshwater biota.

Air temperature sets the potential thermal regime of river ecosystems. River ecosystems whose watersheds have cooler air temperatures have consequently cooler maximum water temperatures (Holtby 1988). In addition to seasonal variations in water temperature caused by changing air temperatures, many other physical aspects of a river ecosystem cause natural variation in temperature and, in particular, whether it flows from a glacier, a lake, or wetland.

Thermal regimes in river ecosystems have been traditionally described in terms of cold, cool and warm water categories based on the dominant fish species present. Numerous studies have described changes in species composition along longitudinal temperature gradients from cold headwater reaches to warm downstream reaches (Burton and Odum 1945, Cech et al. 1990, Hawkes 1975, Huet 1959, Hynes 1970, Moyle and Nichols 1973, Rahel and Hubert 1991). Recently, ecological assessment protocols have been developed that incorporate the influence of these broad-scale temperature categories on differences in expected species assemblage structure across sites (e.g., development of a coldwater index of biotic integrity (Lyons et al. 1996).

Water temperature was modeled using thirty meter grid air temperature data acquired from Climate Source®. Air temperature data from climate stations across the province were interpolated using a PRISM algorithm. Average maximum July air temperature over the past thirty years was calculated for each river ecosystem by averaging buffered grid cells to stream reaches for each river ecosystem. Mean maximum July air temperature was chosen based on current literature surrounding stream temperature classification (Lyons 1996, Magnuson et al. 1979, Nelitz 2006, State 1997, Stoneman and Jones 1996). Given the diverse physiography of BC, river ecosystems were subdivided into warm, cool and cold classes based on natural breaks in the range of variability of third order watershed units within the BC Watershed Atlas for the entire province. The following steps were taken to further refine the model by considering the effect of cold-water resource areas and lake/wetland systems on river ecosystem water temperature:

- If 10 – 100% of the river ecosystem is currently glacially influenced or exists within Alpine Tundra Biogeoclimatic Zone, then it was given a cold water designation;
- If 1 - 10% of the river ecosystem is currently glacially influenced or exists within Alpine Tundra BEC zone, then it was moved down one cooler temperature designation from its original grouping, i.e., from warm water to cool water;
- If 25 – 100% of the river ecosystem is connected to lakes and wetlands, then it was given a warm water designation; and

- If 10 - 25% of the river ecosystem is connected to lakes and wetlands, then it was moved up to one warmer temperature designation from its original grouping, i.e., from cold water to cool water.

Nutrients: Underlying Bedrock Geology

Watershed geology controls groundwater storage capacity and transmissivity (Bugliosi 1988, Siegel 1989). These are dominant influences on a river's base flow. Watershed geology is also the dominant controller of hydro-chemical processes, particularly at base flow (Walton 1970). Watershed geology also strongly influences erosion rate and sediment supply (Hack 1957).

Bedrock geology dataset from BC Energy and Mines was subdivided from seventy seven rock types into seven classes based on probable effects on infiltration and nutrient input. For each river ecosystem, the dominant nutrient class in all upstream watersheds (on an areal basis) was calculated and that class was assigned to the river. A summary of the properties of each nutrient class is shown in the following table.

Nutrient Class	Properties
Alluvium	Rainfall infiltration is high which tends to reduce flood frequency. There tends to be a high degree of surface water and ground water interaction. Base flows may be sustained be seepage or springs or may reduce in the downstream direction as water flows into the groundwater system. Water chemistry reflects the nature of the parent material.
Chemical sediments	Infiltration rate of rainfall is variable. High chemical sediment concentration. Variable substrate.
Carbonates	High rainfall infiltration. High degree of surface and groundwater interaction. High nutrient concentrations of calcium carbonate. Because of the relatively soft parent material suspended sediment concentrations tend to be high. In addition, substrates tend to be relatively fine.
Hard sedimentary rocks	Infiltration of rainfall is variable. Where geology is fractured, infiltration is high resulting in infrequent floods but sustained base flow. Low natural nutrient concentration. Low suspended sediment. Relatively coarse substrates (cobble, gravel, sands) depending on local morphology.
Soft sedimentary rocks	Low infiltration resulting in increased floods and low base flow. High natural phosphorous concentration. Because of the relatively soft parent material suspended sediment concentration tend to be high. In addition, substrates tend to be relatively fine (silts and mud).
Volcanic	This is a broad category within which considerable variation may exist. Phosphorous concentration tends to be high relative to other geology categories. Substrates tend to be finer and

Nutrient Class	Properties
	well packed.
Intrusives & Metamorphics	Infiltration of rainfall tends to be low. Low natural nutrient concentration. Low suspended sediment. Substrates tend to be bimodal, either large (boulder to cobble) or fine (sands) depending on local morphology.

The following table provides descriptions of all of the variables available to us in describing the freshwater habitats used by Pacific salmon, including the FIELD NAMES we used to identify the variables we used. The table was slightly modified from Ciruna and Butterfield (Ciruna and Butterfield 2005), which is referred to in the SOURCE field as "EAU BC". Other sources were:

1. WSA: the BC Watershed Atlas 1:50,000 (Spatial Vision Consulting 1996)
2. Climate Source: http://www.climatesource.com/
3. BC 25m DEM: Digital elevation map of British Columbia at 25m interval, http://www.photosat.ca/products/dem/bc_dem.shtml
4. QBEI_BC coverage from ARCWHSE: Digital map of Biogeoclimatic zones of British Columbia, BC Ministry of Forests & Range, http://www.for.gov.bc.ca/HRE/becweb/index.html
5. BC Ministry of Energy and Mines: Digital Geological map of British Columbia, http://www.em.gov.bc.ca/Mining/GeolsurvPublications/catalog/bcgeolmap.htm

Variable	DESCRIPTION	FIELD NAME	SOURCE
Watershed Unique ID	Unique watershed identifier based on WSA with flow class added	WSD_ID_FLO	WSA; EAU BC
Watershed Unique ID	Unique ID – another unique identifier	ID	EAU BC
Ecoregions and Ecological Drainage Units			
Freshwater Ecoregions	Placement of each watershed polygon within its freshwater ecoregion	FWECOREG	(Abell et al. 2000)
Ecological Drainage Units	Placement of each watershed polygon within its ecological drainage unit	EDU	EAU BC
Size of streams, drainage networks and watersheds			
Primary Drainage Network	Placement of each watershed polygon within its primary drainage network	PRIMARY_ID	EAU BC
Primary Drainage Network Total Link Magnitude	Total link magnitude (Shreve 1966) for each watershed polygon's primary drainage network	MAG_P_MAG	WSA; EAU BC
Magnitude	Maximum stream magnitude of watershed polygon calculated by cumulative number of first order streams to the mouth of the watershed polygon	MAG_MAX	WSA; EAU BC
Ratio of Stream Magnitude / Primary Drainage Network Magnitude	Ratio of each watershed polygon's maximum stream magnitude divided by its total primary drainage network magnitude	MAG_RATIO	WSA; EAU BC
Ratio of Stream Magnitude / Primary Drainage Network	Magnitude ratio classes per watershed polygon: 1 = headwater 2 = tributary 3 = mainstem	MAG_RATIO_CL	WSA; EAU BC

Variable	DESCRIPTION	FIELD NAME	SOURCE
Magnitude Classes			
Drainage Area	Accumulative drainage area per upstream drainage	SIZE_KM2	WSA; EAU BC
Actual accumulative precipitation yield	Accumulative precipitation yield per upstream drainage – surrogate for water yield	FLOW_MAX	ClimateSource; EAU BC
Outflow Order	Maximum stream order (Strahler) of watershed polygon	ORDER_MAX	WSA; EAU BC
Physiography			
Watershed ruggedness	Watershed ruggedness index (Melton's R) per watershed polygon	MELTONS_R	WSA; BC 25m DEM; EAU BC
Mean watershed elevation	Mean elevation of watershed polygon based on 25m DEM	ELEV_MEAN	BC 25m DEM; EAU BC
Standard deviation of watershed elevation	Standard deviation of watershed polygon elevation represented by 25m DEM	ELEV_STD	BC 25m DEM; EAU BC
Minimum watershed elevation	Minimum elevation of watershed polygon based on 25m DEM	ELEV_MIN	BC 25m DEM; EAU BC
Maximum watershed elevation	Maximum elevation of watershed polygon based on 25m DEM	ELEV_MAX	BC 25m DEM; EAU BC
Mean valley flat width	Mean valley flat width of watershed polygon measured perpendicular to the stream channel at point on either side of the channel where the slope becomes >7%	VFW_MEAN	BC Macroreaches; EAU BC
Mainstem gradient	Mainstem gradient classes per watershed polygon: 1 = steep 2 = moderate 3 = shallow	Mcl	WSA; EAU BC
Tributary gradient	Tributary gradient classes per watershed polygon: 1 = steep 2 = moderate 3 = shallow	Tcl	WSA; EAU BC

Variable	DESCRIPTION	FIELD NAME	SOURCE
River ecosystem gradient	Combination of mainstem and tributary gradient classes per watershed polygon: 11= steep mainstem, steep tributaries 12= steep mainstem, moderate tributaries 13= steep mainstem, shallow tributaries 21= moderate mainstem, steep tributaries 22= moderate mainstem, moderate tributaries 23= moderate mainstem, shallow tributaries 31= shallow mainstem, steep tributaries 32= shallow mainstem, moderate tributaries 33= shallow mainstem, shallow tributaries	MTcl	WSA; EAU BC
Stream Gradient:	Percentage of mainstem and tributary reaches of each watershed polygon in each of 6 gradient classes		
mean Mainstem gradient	Geometric mean gradient of mainstem calculated from the gradient classes	GRAD_M_MN	
< 0.02 Mainstem	Percent of river's mainstem with a gradient < 0.02	GRAD1_M	WSA & BC 25m DEM; EAU BC
0.02 – 0.08 Mainstem	Percent of river's mainstem with a gradient between 0.02 – 0.08	GRAD2_M	WSA & BC 25m DEM; EAU BC
0.08 – 0.12 Mainstem	Percent of river's mainstem with a gradient between 0.08 – 0.12	GRAD3_M	WSA & BC 25m DEM; EAU BC
0.12 – 0.16 Mainstem	Percent of river's mainstem with a gradient between 0.12 – 0.16	GRAD4_M	WSA & BC 25m DEM; EAU BC
0.16 – 0.20 Mainstem	Percent of river's mainstem with a gradient between 0.16 – 0.20	GRAD5_M	WSA & BC 25m DEM; EAU BC
> 0.20 Mainstem	Percent of river's tributaries with a gradient > 0.20	GRAD6_M	WSA & BC 25m DEM; EAU BC
mean Tributaries gradient	Geometric mean gradient of tributaries calculated from the gradient classes	GRAD_T_MN	
< 0.02 Tributaries	Percent of river's tributaries with a gradient < 0.02	GRAD1_T	WSA & BC 25m DEM; EAU BC
0.02 – 0.08 Tributaries	Percent of river's tributaries with a gradient between 0.02 – 0.08	GRAD2_T	WSA & BC 25m DEM; EAU BC
0.08 – 0.12 Tributaries	Percent of river's tributaries with a gradient between 0.08 – 0.12	GRAD3_T	WSA & BC 25m DEM; EAU BC
0.12 – 0.16 Tributaries	Percent of river's tributaries with a gradient between 0.12 – 0.16	GRAD4_T	WSA & BC 25m DEM; EAU BC
0.16 – 0.20 Tributaries	Percent of river's tributaries with a gradient between 0.16 – 0.20	GRAD5_T	WSA & BC 25m DEM; EAU BC

Variable	DESCRIPTION	FIELD NAME	SOURCE
> 0.20 Tributaries	Percent of river's tributaries with a gradient > 0.20	GRAD6_T	WSA & BC 25m DEM; EAU BC
Hydrology			
Actual accumulative precipitation yield	Accumulative precipitation yield per upstream drainage – surrogate for water yield	FLOW_MAX	ClimateSource; EAU BC
Accumulative precipitation yield (water yield) classes	Accumulative precipitation yield (water yield) classes per upstream drainage: 1 = low 2= moderate 3= high 4= very high	WATER_YIEL	ClimateSource; EAU BC
Mean Annual Peak Flow	Mean annual peak flow calculated for each watershed polygon	KFACTOR	(Eaton et al. 2002); pers. comm. Art Tautz
Mean Annual Peak Flow Classes	Mean annual peak flow classes for each watershed polygon: 1 = very low 2 = low 3 = moderate 4 = high 5 =very high	K_CL	EAU BC
Flow Regime	Combined winter, spring, summer and fall flow classes respectively per watershed polygon	FLOWREG_CL	ClimateSource; EAU BC
River ecosystem hydrology classes	Combined flow regime classes and mean annual peak flow classes per watershed polygon	HYDRO_CL	ClimateSource; EAU BC
Winter flow classes	Winter flow classes for each watershed polygon derived from total mean December, January, February precipitation and the effects of temperature on precipitation types 1 = low 2 = moderate 3 = high	WINTERCLR	ClimateSource; EAU BC
Spring flow classes	Spring flow classes for each watershed polygon derived from total mean March, April, May precipitation and the effects of temperature on precipitation types 1 = low 2 = moderate 3 = high	SPRINGCLR	ClimateSource; EAU BC
Summer flow classes	Summer flow classes for each watershed polygon derived from total June, July, August precipitation and the effects of temperature on evapotranspiration rates 1 = low 2 = moderate 3 = high	SUMMERCLR	ClimateSource; EAU BC

Variable	DESCRIPTION	FIELD NAME	SOURCE
Fall flow classes	Summer flow classes for each watershed polygon derived from total September, October, November precipitation 1 = low 2 = moderate 3 = high	FALLCLR	ClimateSource; EAU BC
Mean max July temp	Mean max July temp for reaches within each watershed polygon	MAX_TEMP	ClimateSource; EAU BC
Mean January precipitation	Mean January precipitation for each watershed polygon	PPT_JAN_M	ClimateSource; EAU BC
Mean February precipitation	Mean February precipitation for each watershed polygon	PPT_FEB_M	ClimateSource; EAU BC
Mean March precipitation	Mean March precipitation for each watershed polygon	PPT_MAR_M	ClimateSource; EAU BC
Mean April precipitation	Mean April precipitation for each watershed polygon	PPT_APR_M	ClimateSource; EAU BC
Mean May precipitation	Mean May precipitation for each watershed polygon	PPT_MAY_M	ClimateSource; EAU BC
Mean June precipitation	Mean June precipitation for each watershed polygon	PPT_JUN_M	ClimateSource; EAU BC
Mean July precipitation	Mean July precipitation for each watershed polygon	PPT_JUL_M	ClimateSource; EAU BC
Mean August precipitation	Mean August precipitation for each watershed polygon	PPT_AUG_M	ClimateSource; EAU BC
Mean September precipitation	Mean September precipitation for each watershed polygon	PPT_SEP_M	ClimateSource; EAU BC
Mean October precipitation	Mean October precipitation for each watershed polygon	PPT_OCT_M	ClimateSource; EAU BC
Mean November precipitation	Mean November precipitation for each watershed polygon	PPT_NOV_M	ClimateSource; EAU BC
Mean December precipitation	Mean December precipitation for each watershed polygon	PPT_DEC_M	ClimateSource; EAU BC
Mean annual precipitation	Mean annual precipitation for each watershed polygon	PPT_ANN_M	ClimateSource; EAU BC
Mean January air temperature	Mean January air temperature for reaches within each watershed polygon	TEMP_JAN_M	ClimateSource; EAU BC
Mean February air temperature	Mean February air temperature for reaches within each watershed polygon	TEMP_FEB_M	ClimateSource; EAU BC
Mean March air temperature	Mean March air temperature for reaches within each watershed polygon	TEMP_MAR_M	ClimateSource; EAU BC

Variable	DESCRIPTION	FIELD NAME	SOURCE
Mean April air temperature	Mean April air temperature for reaches within each watershed polygon	TEMP_APR_M	ClimateSource; EAU BC
Mean May air temperature	Mean May air temperature for reaches within each watershed polygon	TEMP_MAY_M	ClimateSource; EAU BC
Mean June air temperature	Mean June air temperature for reaches within each watershed polygon	TEMP_JUN_M	ClimateSource; EAU BC
Mean July air temperature	Mean July air temperature for reaches within each watershed polygon	TEMP_JUL_M	ClimateSource; EAU BC
Mean August air temperature	Mean August air temperature for reaches within each watershed polygon	TEMP_AUG_M	ClimateSource; EAU BC
Mean September air temperature	Mean September air temperature for reaches within each watershed polygon	TEMP_SEP_M	ClimateSource; EAU BC
Mean October air temperature	Mean October air temperature for reaches within each watershed polygon	TEMP_OCT_M	ClimateSource; EAU BC
Mean November air temperature	Mean November air temperature for reaches within each watershed polygon	TEMP_NOV_M	ClimateSource; EAU BC
Mean December air temperature	Mean December air temperature for reaches within each watershed polygon	TEMP_DEC_M	ClimateSource; EAU BC
Mean annual air temperature	Mean annual air temperature for reaches within each watershed polygon	TEMP_ANN_M	ClimateSource; EAU BC
Temperature			
Water temperature classes	Water temperature classes per watershed polygon based on mean maximum July air temperature and alpine tundra, glacier and lake/wetland influence: 1 = cold 2 = cool 3 = warm	W_TEMP	ClimateSource; WSA; EAU BC
Seasonal productivity classes	Seasonal productivity classes based on degree days above 0oC 1 = low 2 = moderate 3 = high	DDCLASS	ClimateSource; EAU BC

Variable	DESCRIPTION	FIELD NAME	SOURCE
River Ecosystem Water Temperature Classes	Combination of water temperature classes and seasonal productivity classes: 11 = cold, low ddays 12= cold, moderate ddays 13= cold, high ddays 21 = cool, low ddays 22 = cool, moderate ddays 23 = cool, high ddays 31 = warm, low ddays 32 = warm, moderate ddays 33 = warm, high ddays	WATTEMP_CL	ClimateSource; EAU BC
Mean max July temp	Mean max July temp for reaches within each watershed polygon	MAX_TEMP	ClimateSource; EAU BC
Percent watershed glaciated	Percentage of accumulative upstream drainage area that is currently glaciated	GLAC_PERC	WSA; EAU BC
Percent watershed in alpine tundra BEC zone	Percentage of accumulative upstream drainage area that is within alpine tundra	TUNDRA_PERC	WSA; EAU BC
Percentage of lake, wetland and reservoir area to watershed polygon area	Percentage of lake, wetland and reservoir area in each watershed polygon	L_W_RTOTAL	WSA; EAU BC
Percentage of lake area to watershed polygon area	Percentage of lake area in each watershed polygon	LAKE_PERC	WSA; EAU BC
Number of lakes	Number of lakes within each watershed polygon	LAKE_COUNT	WSA; EAU BC
Percentage of reservoir area to watershed polygon area	Percentage of reservoir area in each watershed polygon	RES_PERC	WSA; EAU BC
Number of reservoirs	Number of reservoirs within each watershed polygon	RES_COUNT	WSA; EAU BC
Percentage of wetland area to watershed polygon area	Percentage of wetland area in each watershed polygon	WET_PERC	WSA; EAU BC
Number of wetlands	Number of wetlands within each watershed polygon	WET_COUNT	WSA; EAU BC
Degree days above 0oC	Degree days above 0oC per watershed polygon		ClimateSource; EAU BC

Variable	DESCRIPTION	FIELD NAME	SOURCE
Biogeoclimatic zone			
Biogeoclimatic Zone:	Percentage of each watershed polygon within each of the 14 biogeoclimatic zones		
Alpine tundra	Percentage of watershed in Alpine tundra zone	AT	Qbei_bc coverage from ARCWHSE; EAU BC
Bunchgrass	Percentage of watershed in Bunchgrass zone	BG	Qbei_bc coverage from ARCWHSE; EAU BC
Boreal white and black spruce	Percentage of watershed in Boreal white and black spruce zone	BWBS	Qbei_bc coverage from ARCWHSE; EAU BC
Coastal Douglas fir	Percentage of watershed in Coastal Douglas fir zone	CDF	Qbei_bc coverage from ARCWHSE; EAU BC
Coastal western hemlock	Percentage of watershed in Coastal western hemlock zone	CWH	Qbei_bc coverage from ARCWHSE; EAU BC
Engelmann spruce – subalpine fir	Percentage of watershed in Engelmann spruce-subapline fir zone	ESSF	Qbei_bc coverage from ARCWHSE; EAU BC
Interior cedar hemlock	Percentage of watershed in Interior cedar-hemlock zone	ICH	Qbei_bc coverage from ARCWHSE; EAU BC
Interior Douglas fir	Percentage of watershed in Interior – Douglas fir zone	IDF	Qbei_bc coverage from ARCWHSE; EAU BC
Mountain hemlock	Percentage of watershed in Mountain hemlock zone	MH	Qbei_bc coverage from ARCWHSE; EAU BC
Montane spruce	Percentage of watershed in Montane spruce zone	MS	Qbei_bc coverage from ARCWHSE; EAU BC
Ponderosa pine	Percentage of watershed in Ponderosa pine zone	PP	Qbei_bc coverage from ARCWHSE; EAU BC
Sub-boreal pine-spruce	Percentage of watershed in Sub-boreal pine-spruce zone	SBPS	Qbei_bc coverage from ARCWHSE; EAU BC

Variable	DESCRIPTION	FIELD NAME	SOURCE
Sub-boreal spruce	Percentage of watershed in Sub-boreal spruce zone	SBS	Qbei_bc coverage from ARCWHSE; EAU BC
Spruce-willow-birch	Percentage of watershed in Spruce-willow-birch zone	SWB	Qbei_bc coverage from ARCWHSE; EAU BC
Nutrients			
Dominant nutrient class	Dominant nutrient class per upstream drainage of each watershed polygon	NUTRIENT_CL	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Alluvium, Till	Percentage of alluvium, till per upstream drainage of each watershed polygon	Alluvium	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Chemical sediments	Percentage of chemical sediments per upstream drainage of each watershed polygon	Chem_seds	BC Ministry of Energy & Mines at 1:250, 000; EAU BC
Carbonate sediments	Percentage of carbonate sediments per upstream drainage of each watershed polygon	Carb_seds	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Hard sedimentary rock	Percentage of hard sedimentary rock per upstream drainage of each watershed polygon	Hard_seds	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Soft sedimentary rock	Percentage of soft sedimentary rock per upstream drainage of each watershed polygon	Soft_seds	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Volcanic rock	Percentage of volcanic rock per upstream drainage of each watershed polygon	Volcanic	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Instrusive & Metamorphic rock	Percentage of intrusive and metamorphic rock per upstream drainage of each watershed polygon	Int&Meta	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Geology:	Percentage of accumulative upstream drainage in each of the 19 geology classes		

Variable	DESCRIPTION	FIELD NAME	SOURCE
Sediments, Undivided	Percentage of watershed in Sediments, Undivided	GEO1	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Sediments, Chemical sediments	Percentage of watershed in Sediments, Chemical sediments	GEO2	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Sediments, Fine clastics (shale, mudstone)	Percentage of watershed in Sediments, Fine clastics (shale, mudstone)	GEO3	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Sediments, Sandstones	Percentage of watershed in Sediments, Sandstones	GEO4	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Sediments, Coarse clastics	Percentage of watershed in Sediments, Coarse clastics	GEO5	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Sediments, Carbonates	Percentage of watershed in Sediments, Carbonates	GEO6	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Sediments, Interbedded limestone / shale	Percentage of watershed in Sediments, Interbedded limestone / shale	GEO7	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Volcanics, Undivided	Percentage of watershed in Volcanics, Undivided	GEO8	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Volcanics, Intermediate to felsic	Percentage of watershed in Volcanics, Intermediate to felsic	GEO9	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Volcanics, Mafic	Percentage of watershed in Volcanics, Mafic	GEO10	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Volcanics, Bimodal (mafic / felsic)	Percentage of watershed in Volcanics, Bimodal (mafic / felsic)	GEO11	BC Ministry of Energy & Mines at 1:250,000; EAU BC

Variable	DESCRIPTION	FIELD NAME	SOURCE
Volcanics, Mixed sediments and volcanics	Percentage of watershed in Volcanics, Mixed sediments and volcanics	GEO12	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Intrusives, Undivided	Percentage of watershed in Intrusives, Undivided	GEO13	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Intrusives, Intermediate to felsic	Percentage of watershed in Intrusives, Intermediate to felsic	GEO14	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Intrusives, Mafic	Percentage of watershed in Intrusives, Mafic	GEO15	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Intrusives, Ultramafic	Percentage of watershed in Intrusives, Ultramafic	GEO16	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Intrusives, Alkalic	Percentage of watershed in Intrusives, Alkalic	GEO17	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Metamorphics, Undivided	Percentage of watershed in Metamorphics, Undivided	GEO18	BC Ministry of Energy & Mines at 1:250,000; EAU BC
Alluvium, Till	Percentage of watershed in Alluvium, Till	GEO19	Same as above

Appendix 6. Seasonal classification of dates

Confusion continually arises over the use of seasonal terms such as summer and fall since the dates referred to are seldom stated. The following table is a suggestion for a uniform treatment of dates and seasons. February 29th would be day 59.25 in late winter (LWIN).

Season	sub-season	DOY	dates
Spring	early spring (ESPR)	80-109	Mar. 21 – Apr. 19
	mid-spring (MSPR)	110-139	Apr. 20 – May 19
	late-spring (LSPR)	140-171	May 20 – Jun 20
Summer	early summer (ESUM)	172-201	Jun 21 – Jul 20
	mid-summer (MSUM)	202-231	Jul 21 – Aug. 29
	late summer (LSUM)	232-263	Aug. 30 – Sep.20
Fall	early-fall (EFALL)	264-293	Sep. 21 – Oct. 20
	mid-fall (MFALL)	294-323	Oct. 21 – Nov. 19
	late-fall (LFALL)	324-354	Nov. 20 – Dec. 20
Winter	early-winter (EWIN)	355-18	Dec.21 – Jan. 18
	mid-winter (MWIN)	19-48	Jan. 19 – Feb. 17
	late-winter (LWIN)	49-79	Feb. 18 – Mar. 20

Appendix 7. Glossary

The glossary has been compiled from a large number of online and published sources. Online sources are numbered and listed at the end of the appendix. Published sources are cited in the glossary entry. Where no source is indicated, the definition came either from the Wild Salmon Policy glossary or from the authors. The notation *q.v.* stands for the Latin phrase *quod vide* that literally means "which see." It is used when the word or phrase referred to is also in the glossary.

Adaptation. Changes in an organism's physiological structure, function or habits that allow it to survive in new surroundings. (11). Change in a organism resulting from natural selection; a structure which is the result of such selection. (12)

AEW. See Annual Escapement Waterbody.

Age of maturity. The age when 50% of the fish of a given sex are considered to be reproductively mature. (1)

Allele. Alternative forms of a gene resulting in different gene products and (potentially) different phenotypes. In sexually reproducing organisms, a single allele for each autosomal (*q.v.*) gene is inherited separately from each parent. An organism is homozygous for a gene if the alleles are identical, and heterozygous if they are different. (3)

Alevin. A larval salmonid that has hatched but has not fully absorbed its yolk sac, and generally has not yet emerged from the spawning gravel. Absorption of the yolk sac, the alevin's initial energy source, occurs as the larva develops its mouth, digestive tract and excretory organs and otherwise prepares to feed on natural prey. (14)

Allozyme. One of multiple forms of an enzyme that is coded for by different alleles (*q.v.*) of one gene (*q.v.*). The mixture of allozymes in a population has been used to characterize genetic diversity.

Anadromous trout. In Canada, species in the genus *Oncorhynchus* that are not Pacific salmon, namely steelhead (*O. mykiss*) and cutthroat (*O. clarki*).

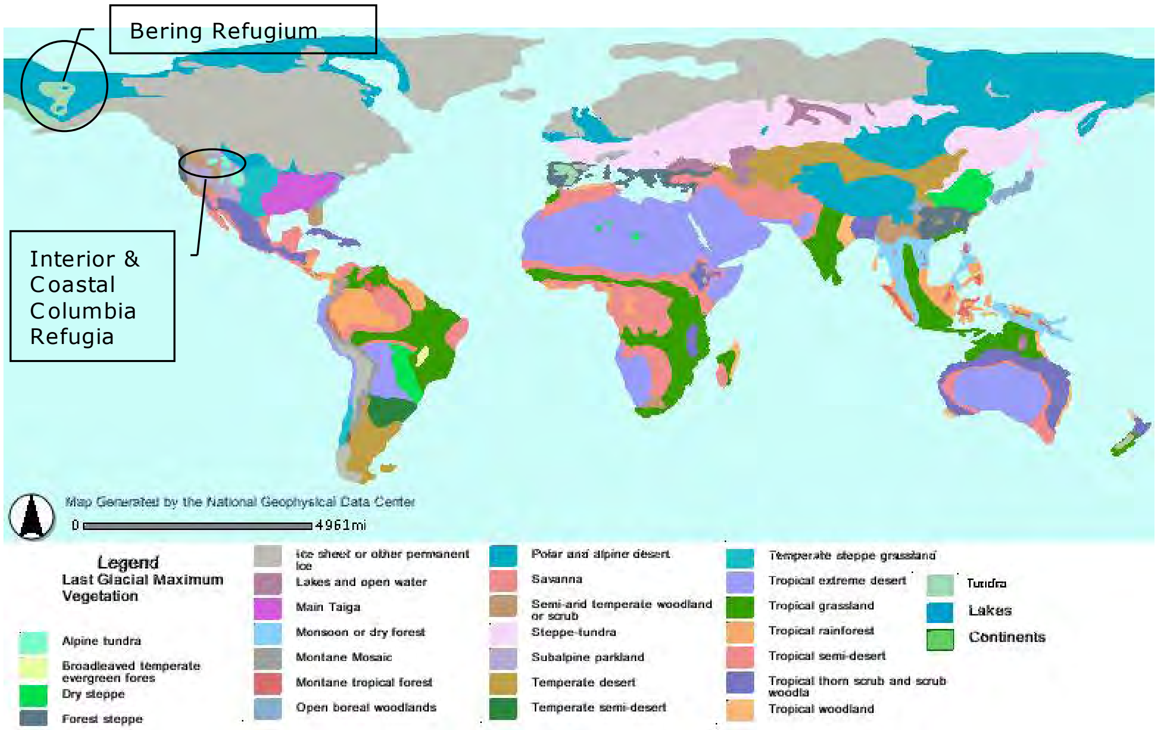
Anadromous species. Fish that spend their adult life in the sea but swim upriver to freshwater spawning grounds to reproduce. (1)

Annual Escapement Waterbody (AEW). A name given to a set of waterbodies (stream, lake, slough or segments thereof) that is used in SEDS (*q.v.*) for escapement summaries. Each AEW is associated with a GFE_ID (*q.v.*).

Autosomal. Pertaining to an autosome, which is a chromosome that is not involved in the determination of gender. (4)

Benchmark. See Biological Reference Point.

Bering Refugium. Large area in what is now Alaska and the Bering Sea that was free of ice sheets during the last glacial period. Some species of salmon are believed to have persisted in this refugium. See the following map showing terrestrial ecozones during the last glacial period. (5)



Biogeography. The study of the distribution of biodiversity over space and time. It aims to reveal where organisms live, at what abundance, and why. (6)

Biodiversity. The full range of variety and variability within and among living organisms and the ecological complexes in which they occur. Biodiversity encompasses diversity at the ecosystem, community, species, and genetic levels and the interaction of these components. In the context of the Wild Salmon Policy, biodiversity is infraspecific (*q.v.*) and its major components are geographic or spatial diversity and temporal diversity. Both are result of the expression of genetic diversity interacting with the environment.

Biodiversity continuum. All organisms on Earth are related to one another through the biodiversity continuum or the tree of life. The biodiversity continuum is a hierarchical scheme for representing that continuum. The species (*q.v.*) is one level in the hierarchy and has been the focus for biological research since the Enlightenment. Biologists are increasingly aware of the importance of infraspecific diversity to the continuation of life. (5)

Biological diversity. See biodiversity.

Biological reference point. A biological benchmark against which the abundance of a stock or its fishing mortality rate can be measured to determine its status. These reference points can be used as limits or targets, depending on their intended usage. For further information see Caddy and Mahon (1995), and Caddy (2002, 2004).

Broodline. In a semelparous species such as the Pacific salmon, if the age of reproduction is fixed or nearly so then all (or nearly all) of the fish spawning in a particular year are the offspring of fish that spawned in a single year and the fish spawning in sequential generations are called broodlines. Broodlines are usually referred to by a significant year in the past. For example, survival of coho salmon in the Skeena River was very low for smolts that entered the ocean in 1996. Since most of the coho salmon are three-years old at maturity (aged 1.1, see Fish Ages), very few coho returned to spawn in the fall of 1997. The lack of spawners in the 1997 broodline was detectable in 2000 and in 2003. In pink salmon, all of the fish are two-years old at maturity (age 0.1) and so there are even-year and odd-year broodlines in most rivers.

Cavalli-Sforza and Edwards (1967) chord distance. A geometric measure of the distance between multi-dimensional points on a hypersphere (a sphere with > 3 dimensions). For example, if there are two sites, *S*1 and *S*2, where the allelic frequencies at a single locus (*q.v.*) have been determined then the chord distance (D_{C-Sf}) where there are *k* alleles is defined as $D_{C-Sf} = \sqrt{2 - 2\mathrm{Cos}(\varphi)}$ where $\mathrm{Cos}(\varphi) = \sum_{i=1}^{k} \sqrt{s1_i s2_i}$ and $s1_i$ is the frequency of the *i*=1 to *k* allele at the first site, S1.

Climate. The average weather (usually taken over a 30-year time period) for a particular region and time period. Climate is not the same as weather, but rather, it is the average pattern of weather for a particular region. Weather describes the short-term state of the atmosphere. Climatic elements include precipitation, temperature, humidity, sunshine, wind velocity, phenomena such as fog, frost, and hail storms, and other measures of the weather. (11)

Cline. A systematic relation between location and the frequencies of phenotypes, genotypes, etc. Lines connecting points of equal frequency are termed isoclines, and the direction of the cline at any point is at right angles to an isocline. (4)

Closed population. A group comprising one or more populations that is almost completely isolated from other such groups ($N_e m<1$; *q.v.*) such that its genetic diversity is at risk through random genetic drift when reduced to low abundance. This is the smallest unit the IUCN (*q.v.*) considers for Red Book Listing (Baillie and Groombridge 1996, IUCN 2001), as proposed by Mace and Lande (1991).

Clustering. The classification of objects into different groups, or more precisely, the partitioning of a data set into subsets (clusters), so that the data in each subset (ideally) share some common trait–often proximity according to some defined distance measure. There are a large number of distance measures (e.g. Cavalli-Sforza and Edwards chord distance (*q.v.*) and algorithms for forming the clusters. (5)

Coded-wire tag. A small piece (0.25 x 0.5 or 1.0 mm) of stainless steel wire that is injected into the snouts of juvenile salmon and steelhead (Jefferts et al. 1963). Each tag is etched with a binary code that identifies a tag group. Tags are applied and recovered over most of the west coast of North America in a program coordinated by the Pacific Salmon Commission. Information derived from the program includes catch composition, exploitation rates, marine survival, and ocean distributions.

Columbian Refugium. During the last glacial period, an area to the south of the Cordilleran ice sheet (*q.v.*). All species of Pacific salmon persisted through the last glacial period in this refugium. For a map showing glacial coverage during the last glacial period see Bering Refugium. Also called the Cascadian Refugium. (5)

Common-garden experiment. An organism's phenotype (*q.v.*) results from the expression of its genotype (*q.v.*) interacting with its environment. To distinguish between genotypic and environmental effects, phenotypes are examined in organisms reared in identical environments, i.e., a common-garden.

Connectedness. Degree to which organisms can move between sites, populations, etc. See lateral connectivity and longitudinal connectivity.

Conservation status. The state of a species or in the context of the WSP, a CU, relative to reference points or benchmarks related to extinction risk.

Conservation Unit. A group of wild salmon sufficiently isolated from other groups that, if extirpated, is very unlikely to recolonize naturally within an acceptable timeframe.

Conservation. The protection, maintenance, and rehabilitation of genetic diversity, species, and ecosystems to sustain biodiversity and the continuance of evolutionary and natural production processes. The Wild Salmon Policy refers the reader to Grumbine (1994), Olver et al. (1995), and Mangel et al. (1996) for additional information. An exchange of comments following Olver et al. (1995) provides an indication of how difficult it has proven to provide a definition of conservation that is satisfactory to all (Crawford and Morito 1997, Shuter et al. 1997).

Cordilleran ice sheet. The Cordilleran ice sheet was a major ice sheet that covered, during glacial periods of the Quaternary, a large area of western North America, including all of British Columbia, northern Washington . down to about Seattle and Spokane, Washington, the southwestern third or so of Yukon territory, all of the Alaska Panhandle, South Central Alaska, the Alaska Peninsula, and almost all of the continental shelf north of the Strait of Juan de Fuca. At its eastern end the Cordilleran ice sheet merged with the Laurentide ice sheet at the Continental Divide., forming an area of ice that contained one and a half times as much water as the Antarctic ice sheet does today. At its western end, several small glacial refugia may have existed during the last glacial maximum below present sea level in now-submerged Hecate Strait and on the Brooks Peninsula in northern Vancouver Island. However, evidence of ice-free refugia above present sea level north of the Olympic Peninsula has been refuted by genetic and geological studies since the middle 1990s. The ice sheet faded north of the Alaska Range because the climate was too dry to form glaciers. Unlike the Laurentide ice sheet, which may have taken as many as eleven thousand years to fully melt, it is believed the Cordilleran ice sheet, except for areas that remain glaciated today, melted very quickly, probably in four thousand years or less. (5)

Cross-tabulation. A cross tabulation (often abbreviated as cross tab) displays the joint distribution of two or more variables. They are usually presented as a contingency table in a matrix format. Whereas a frequency distribution provides the distribution of one variable, a contingency table describes the distribution of two or more variables simultaneously. Each cell shows the number of samples that have a specific combination of values or levels of each variable. Each cell contains a single cross tabulation. Cross tabs are frequently used because: they are easy to understand and construct; they can be used with any level of data: nominal, ordinal, interval, or ratio—cross tabs treat all data as if it is nominal; and they can provide greater insight than single statistics. In Microsoft EXCEL cross tabs are called Pivot Tables. (5)

Cross-walk. See Cross-tabulation.

CU. See Conservation Unit.

Deme. An interbreeding group of organisms (without genetic connotations). There are three different types of demes. A **topodeme** is a deme occurring in a particular geographic area. An **ecodeme** is a deme occurring in a particular habitat. A **phenodeme** is a deme distinguished by phenotypic characters. (Wood and Holtby 1998)

Demographic rate. The rate of change of some property of a population, usually due to a specific process such as birth, death or migration.

Demography. The statistical study of all populations. It can be a very general science that can be applied to any kind of dynamic population, that is, one that changes over time or space (see population dynamics). It encompasses the study of the size, structure and distribution of populations, and spatial and/or temporal changes in them in response to birth, death, migration and aging. (5)

Dendrogram. A tree diagram frequently used to illustrate the arrangement of the clusters produced by a clustering algorithm. Dendrograms are often used in computational biology to illustrate the clustering of genes. From Greek dendron "tree", and gramma "drawing". (5)

Designatable Unit (DU). Infraspecific (*q.v.*) entities for assignment of conservation status. DUs are determined during the process of resolving a species' conservation status using a procedure that asks whether putative DUs are distinguishable based on a reliably established taxonomy or a well-corroborated phylogeny, compelling evidence of genetic distinction, range disjunction, and/or biogeographic distinction as long as extinction probabilities also differ. (COSEWIC 2005, Green 2005)

Detritus. Any loose material produced directly from disintegration processes. Organic detritus consists of material resulting from the decomposition of dead organic remains. (11)

Discriminant analysis. A statistical procedure for finding the linear combination of features which best separate two or more classes of objects or events. The resulting combination may be used as a linear classifier or for dimensionality reduction before later classification. Linear discriminant analysis (LDA) is closely related to ANOVA (analysis of variance) and regression analysis, which also attempt to express one dependent variable as a linear combination of other features or measurements. In ANOVA and regression the dependent variable is a numerical quantity, while for LDA it is a categorical variable (i.e., the class label). (5)

Diversity. See biodiversity.

Drainage density. The total length of all the streams and rivers in a drainage basin divided by the total area of the drainage basin. This can effect the shape of a river's hydrograph (*q.v.*). Rivers that have a high drainage density will often have a more 'flashy' hydrograph with a steep falling limb. High drainage densities are also associated with a greater flood risk. (5)

DU. See Designatable Unit.

Early migrant type. A life history type of coho salmon in which fry smolt soon after emergence and migrate to estuaries and coastal waters.

Ecological adaptive zone. An area within which individuals of the same taxon are ecologically interchangeable (*q.v.*) or within which such interchangeability is presumed possible because of the similarity of the abiotic and biotic environments.

Ecological time frame (or time scale). The period of time over which there can be significant changes in the function or structure of an ecosystem due to evolutionary processes–tens of generations or less (Carroll et al. 2007).

Ecological interchangeability. Two taxa would be ecologically interchangeable if on the substitution of one for the other, the substitute persisted in the ecosystem, fully performed the functional and structural roles of the replaced taxon, and there was no significant change to ecosystem state.

Ecology. From Greek: οίκος, oikos, "household"; and λόγος, logos, "knowledge", is the scientific study of the distribution and abundance of life and the interactions between organisms and their environment. The environment of an organism includes physical properties, which can be described as the sum of local abiotic factors such as insolation (sunlight), climate, and geology, and biotic factors, which are other organisms that share its habitat. (5)

Ecosystem. A natural unit consisting of all plants, animals and micro-organisms (biotic factors) in an area functioning together with all of the non-living physical (abiotic) factors of the environment.(5). The dynamic and interrelating complex of plant and animal communities and their associated non-living environment (14). A biotic community and its abiotic environment, considered together as a unit. Ecosystems are characterized by a flow of energy that leads to trophic structure and material cycling. (11)

Ecosystem state. Any of various conditions characterized by definite quantities usually combined into a multi-attribute index. A great variety of indices have been developed but all include measures of process or function (see Ecosystem). Measures or characterizations of structure only are termed ecotypologies.

Ecotypology. A characterization of the structure of an ecosystem without reference to dynamic processes. Typologies often include measures of both abiotic and biotic ecosystem components.

Ecological unit. See ecological adaptive zone.

Ecotypic characterizations. See ecotypology.

Effective population size (N_e). In population genetics, "the number of breeding individuals in an idealized population that would show the same amount of dispersion of allele frequencies under random genetic drift or the same amount of inbreeding as the population under consideration". It is a basic parameter in many models in population genetics. The effective population size is usually smaller than the absolute population size (N). (Wright 1938)

Emergence. Departure of fry from the incubation gravel into the water column. See alevin and fry.(4)

Empirical. Pertaining to, or founded upon, experiment or experience; depending upon the observation of phenomena; versed in experiments (4). Empirical research is any research that bases its findings on direct or indirect observation as its test of reality (5). Alternatively, an empirical model depends upon experience or observation alone, without due regard to science and theory. A notable proponent of empirical as opposed to theoretical approaches in ecology was the Canadian ecologist Frank Rigler (1982).

Environmental regime. A relatively stable environmental or ecosystem state (*q.v.*) A rapid change from one state or regime to another has been termed a regime shift (*q.v.*)

Environmental typology. See ecotypology.

Escapement. The number of mature salmon that pass through (or escape) fisheries and return to fresh water to spawn.

ESU. See Evolutionarily Significant Unit.

Euryhaline. Able to adapt to a wide range of salinities. Euryhaline organisms are commonly found in habitats such as estuaries and tide pools where the salinity changes regularly. However, some organisms are euryhaline because their life cycle involves migration between freshwater and marine environments, as is the case with salmon and eels. The opposite of euryhaline organisms are stenohaline ones, which can only survive within a narrow range of salinities.

Evolutionarily Significant Unit (ESU). A term used by Waples (1991b) to define "distinct population segment," for the purposes of applying the US Endangered Species to Pacific salmon. An ESU must: (1) be substantially reproductively isolated from other conspecific populations, and (2) represent an important component in the evolutionary legacy of the biological species.

Exploitation rate. In salmon, the proportion of adult fish that are killed by all fisheries. A simple exploitation rate assumes that there is no natural mortality after fish enter the fishery. In some instances, exploitation rates are adjusted for natural mortality.

Extirpation. The local extinction of a species. In the Wild Salmon Policy, the term is usually used in reference to a Conservation Unit.

FAZ. See Freshwater Adaptive Zone.

Fish ages. There are three systems for indicating the age of an anadromous fish, with two in common use. All of the systems refer to the number of annuli (singular annulus (*q.v.*)) found on a morphological structure (usually a scale) used to age the individual. The first commonly used method is that of Gilbert and Rich (1927) in which age is written as total age$_{\text{freshwater age}}$, e.g. 5_3. In this example the fish is in its fifth year of life (i.e., there are four annuli) and it entered the ocean in its third summer (i.e., there are two annuli prior to entering the ocean.) The second commonly used system is called the European method (Koo 1962) and age is written as #fresh water annuli.#ocean annuli. The example fish would be aged 2.2. The third system is not in common use. In it the age is written as #annuli$_{\text{\#freshwater annuli}}$ and the example fish would be aged 4_2. The European system is useful because freshwater and marine ages can be referred to unambiguously (i.e., age 2. or age .2 in the example). In the European system an age designation of 0^+, for example, means that the fish was in its first summer of life after emergence and was in freshwater when aged. A pink salmon in the ocean in its first summer of life would be aged 0.0^+. (2)

Fish habitat. Spawning grounds and nursery, rearing, food supply, and migration areas on which fish depend directly or indirectly to carry out their life processes.

Fluvial geomorphology. A branch of geology that studies the effects of precipitation and runoff on the form and pattern of riverbeds and river channels. (11)

Fraser glaciation. Also called the Pinedale glaciation, it was the last glacial period in western North America in which glaciers arising in the Rocky Mountains merged into the Cordilleran ice sheet (*q.v.*) The Fraser glaciation lasted from approximately 30,000 to 10,000 years ago and was at its greatest extent between 23,500 and 21,000 years ago. (5)

Freshwater adaptive zone (FAZ). See ecological adaptive zone.

Fry. Salmon that have emerged from gravel, completed yolk absorption, remained in freshwater streams, and are less than a few months old. If fry remain in fresh water they become "parr" (*q.v.*). If they leave fresh water to enter the ocean they become "smolts" (*q.v.*)

Gene. An ordered sequence of nucleotides located in a particular position (locus) on a particular chromosome that encodes a specific functional product (the gene product, i.e. a protein or RNA molecule). It includes regions involved in regulation of expression and regions that code for a specific functional product. (3)

Gene flow. The movement of alleles from one population to another by way of interbreeding of individuals in the two populations. (9). Gene flow has, therefore, three components. First, there is the physical movement of mature individuals from a source population to a receiving population. Second, the migrants must interbreed with members of the receiving population. Third, the migrants must reproduce successfully, which means that their offspring must survive to reproduce. If there is movement but no interbreeding, then the two populations are behaving like separate species. If there is interbreeding but no offspring survive to reproduce then none of the novel alleles that may be carried by the migrant are introduced into the receiving population and there is no gene flow.

Gene frequency. The frequency of occurrence or proportions of different alleles of a particular gene in a given population. More properly called allelic frequency. (4)

Genetic diversity. Variation in allelic frequencies at the level of individual genes, and provides a mechanism for populations to adapt to their ever-changing environment. It refers to the differences in genetic make-up between distinct species and to genetic variations within a single species.

Genetic drift. In population genetics, genetic drift (or more precisely allelic drift) is the evolutionary process of change in the allele frequencies (or gene frequencies) of a population from one generation to the next due to purely chance events determining which alleles (variants of a gene) within a reproductive population will be carried forward while others disappear. Especially in the case of small populations, the statistical effect of sampling error during random sampling of certain alleles from the overall population may result in an allele, and the biological traits that it confers, to become more common or rare over successive generations, and result in evolutionary change over time. Genetic drift is distinct from natural selection, a non-random evolutionary selection process in which the tendency of alleles to become more or less widespread in a population over time is due to the alleles' effects on reproductive success. (5)

Genetically effective population size. See effective population size.

Genodeme. The smallest detectable unit of genetic population structure. It may comprise non-differentiated topodemes (*q.v.*) Gene flow (*q.v.*) between genodemes is large such that genetic drift and/or migration preclude local adaptation within the genodeme. (Wood and Holtby 1998)

Genome. All the genetic material in the chromosomes of a particular organism; its size is generally given as its total number of base pairs. (7)

Genotype. The genetic constitution of an organism, as distinguished from its physical appearance (its phenotype *q.v.*). (7)

Geographic cline. See cline.

Geographic diversity. Phenotypic variability observed within a species over space (geography). This variation may have a genetic basis or may result from an interaction between the organism's genotype (*q.v.*) and its environment.

GFE_ID. A unique index value (integer) assigned to an Annual Escapement Waterbody in SEDS.

Gill raker. A bony, finger-like projection of the gill arch filaments of fish, used for food retention in some species. (8)

Glacial rebound. During continental glaciation, the weight of the ice, which was several kilometers thick, depressed the earth's crust or lithosphere. The land has been rebounding from these depressions since the ice melted. Studies have shown that the uplift has taken place in two distinct stages. The initial uplift following deglaciation was rapid (called "elastic"), and took place as the ice was being unloaded. After this "elastic" phase, uplift proceed by "slow viscous flow" so the rate decreased exponentially after that. Today, typical uplift rates are of the order of 1 cm/year or less. Studies suggest that rebound will continue for about at least another 10,000 years. The total uplift from the end of deglaciation depends on the local ice load and could be several hundred meters near the center of rebound. (5)

Glaciation. See Ice Age

Great Plains Refugium. During the last glacial period, the ice-free region to the south and east of the Continental Divide (McPhail 1998) and comprising the Missouri Regium in the west and the Mississippi Refugium in the east.

Habitat integrity. The extent to which human activities have altered the structure and function of habitat. For running waters four classes of criteria have been suggested for evaluating habitat integrity: (1) discharge regime; (2) physical structures; (3) lateral connectivity (*q.v.*); and (4) longitudinal connectivity (*q.v.*) (Muhar and Jungwirth 1998)

Harvestable surplus. The number of individuals that can be harvested from a population without affecting long term stability, or average population size. (5)

Hierarchical scheme (hierarchy). A hierarchy (in Greek: Ἱεραρχία, derived from ἱερός — hieros, 'sacred', and ἄρχω —arkho, 'rule') is a system of ranking and organizing things where each element of the system (except for the top element) is a subordinate to a single other element. The only direct links in a conventional hierarchy are to one's immediate superior (or “parent”) or to one of one's subordinates (or “children”). All parts of the hierarchy that are not vertically linked to one another can nevertheless be "horizontally" linked by traveling up the hierarchy to find a common direct or indirect superior, and then down again. In biology, the study of taxonomy is one of the most conventionally hierarchical kinds of knowledge, placing all living organisms in a nested structure of divisions related to their probable evolutionary descent. Most evolutionary biologists assert a hierarchy extending from the level of the specimen (an individual living organism — say, a single fish), to the species of which it is a member (perhaps chinook salmon), outward to further successive levels of genus, family, order, class, phylum, and kingdom. (A chinook is a kind of salmonid (family), and all salmonids are types of bony-rayed fishes (class), which are all types of vertebrates (phylum).) Essential to this kind of reasoning is the proof that members of a division on one level are more closely related to one another than to members of a different division on the same level; they must also share ancestry in the level above. Thus, the system is hierarchical because it forbids the possibility of overlapping categories. For example, it will not permit a 'family' of beings containing some examples that are amphibians and others that are reptiles—divisions on any level do not straddle the categories of structure that are hierarchically above it. (Such straddling would be an example of heterarchy.) (5)

Hydrograph. A plot of the discharge of a river as a function of time. A storm hydrograph has three parts, the rising limb as discharge increases during or after a storm, peak discharge, and the falling limb as discharge decreases to the base flow. In a “flashy” stream, the storm hydrograph shows rising and descending limbs of short duration and large peak discharges compared to the storm hydrograph of a stable stream. (5)

Ice Age. The Quaternary glaciation, also known as the Pleistocene glaciation or simply the ice age, refers to the period of the last few million years (2.58 Ma to present) in which a permanent ice sheet was established in Antarctica and probably Greenland, and fluctuating ice sheets have occurred elsewhere (e.g. the Laurentide). During the Quaternary Period, the total volume of land ice, sea level and global temperature has fluctuated initially on 41,000- and more recently on 100,000-year time scales. There have been approximately 80 glacial cycles over this time. All of this time is referred to as an ice age because at least one permanent large ice sheet–Antarctica–has existed continuously. There is uncertainty over how much of Greenland was present during the previous and earlier interglacials. During the colder episodes–referred to as glacial periods–large ice sheets also existed in Europe, North America, and Siberia. The shorter and warmer intervals between glacials are called interglacials.

Interglacial. Within an ice age (*q.v.*), warmer periods during which continental ice sheets withdraw.

Infraspecific. Pertaining to a taxon at a rank lower than species. Usage: only in botany, not in zoology and bacteriology (8). In using the term to define a Designatable Unit (*q.v.*), Green (2005) appears to have widened the usage of this term beyond plants.

Intraspecific. Arising or occurring within a species; involving the members of one species. (4)

Intraspecific diversity. Diversity, usually genetic, within a species.

Isozyme. One of multiple forms of an enzyme whose synthesis is controlled by more than one gene.

Iteroparous. Reproducing more than once in a lifetime. The two anadromous trout in the genus *Oncorhynchus*, steelhead (*O. mykiss*) and cutthroat (*O. clarkii*) are iteroparous. (8)

IUCN. The International Union for the Conservation of Nature and Natural Resources or as it is now known, the World Conservation Union, is the world's largest and most important conservation network. The Union brings together 83 States, 110 government agencies, more than 800 non-governmental organizations (NGOs), and some 10,000 scientists and experts from 181 countries in a unique worldwide partnership. The Union's mission is to influence, encourage, and assist societies throughout the world to conserve the integrity and diversity of nature and to ensure that any use of natural resources is equitable and ecologically sustainable. Its headquarters are in Gland, Switzerland. (15)

JAZ. See Joint Adaptive Zone.

Joint Adaptive Zone. Zones formed by the intersection of Freshwater and Marine Adaptive Zones (*q.v.*). These zones are the basis for the ecotypic classification used to describe Conservation Units (*q.v.*). See ecological adaptive zone.

Kokanee. The obligate freshwater form of sockeye salmon (*Oncorhynchus nerka*).

River/ocean-types of sockeye. A life-history type of sockeye salmon whose juveniles are adapted to rearing in flowing water instead of lakes, which is the norm for the species.

Lake-type. A life-history type with a suite of adaptations for living in lakes. An example for coho salmon can be found in Swain and Holtby (1989).

Lateral connectivity. In fluvial geomorphology, refers to the transport of materials into or out of the stream through riparian and hillslope processes (Brierley et al. 2006, Fryirs et al. 2007). In salmon ecology, refers to the seasonal movements of parr into off-channel habitats (Brown and Hartman 1988, Hartman and Brown 1987). In a salmon metapopulation (*q.v.*), refers to the movement of juveniles or adults between its component groups (usually topodemes (*q.v.*) or subpopulations (*q.v.*)) (Wood and Holtby 1998).

Laurentide Ice Sheet. The Laurentide ice sheet covered most of Canada and a large portion of the northern United States, between c. 95,000 and c. 20,000 years before the present day. Its southern margin included the modern sites of New York City and Chicago, and then followed quite precisely the present course of the Missouri River up to the northern slopes of the Cypress Hills, beyond which it merged with the Cordilleran Ice Sheet (*q.v.*). (5)

Life history. A system of interrelated adaptive traits forming a set of reproductive tactics (10)

Life-history type. A phenotype associated with a particular habitat type, ecological zone or niche. One of a group of alternative life histories found in a species.

Local adaptation. Adaptation on a spatial or temporal scale less than that occupied by the species.

Local population. A group comprising one or more subpopulations (*q.v.*) that is relatively isolated from other such groups and that is probably locally adapted to its habitat. (Wood and Holtby 1998)

Locus. The physical location of a gene or other significant sequence such as a microsatellite (*q.v.*) on a chromosome. (5)

Longitudinal connectivity. In fluvial geomorphology, refers to the transport of materials down a stream through fluvial transport processes (Brierley et al. 2006, Fryirs et al. 2007), which can be interrupted by barriers. Similarly, barriers such as landslides and dams can block the movement of salmon and disrupt the connections between freshwater habitats and the ocean. Longitudinal connectivity can also refer to connections through time.

Marine Adaptive Zone. See ecological adaptive zone.

MAZ. See Marine Adaptive Zone.

Microsatellite locus. See locus.

Microsatellite. Also called Simple Sequence Repeats (SSRs), microsatellites are polymorphic loci present in nuclear DNA and organellar DNA that consist of repeating units of 1-4 base pairs in length. They are typically neutral (*q.v.*) and are used as molecular markers which have wide-ranging applications in the field of genetics, including kinship and population studies. Microsatellites are a subclass of Short Tandem Repeats or STRs (*q.v.*) (5)

Minimum viable population (MVP). The smallest possible size at which a biological population can exist without facing extinction from natural disasters or demographic, environmental, or genetic stochasticity (Shaffer 1981).

Mississippi Refugium. The eastern half of the Great Plains Refugium (*q.v.*)

Missouri Refugium. The western half of the Great Plains Refugium (*q.v.*)

Mixed-stock fisheries. Fisheries in which the catch comprises individuals from more than one stock (*q.v.*) Mixed-stock fisheries are often difficult to manage because of differences in the productivities of the component stocks. Most fisheries for Pacific salmon are on mixed stocks to at least some degree. Most of the hook-and-line fisheries for coho and chinook salmon are considered highly mixed-stock because of the large number of stocks that are typically exploited.

Molecular genetics. The study of macromolecules important in biological inheritance. (7). The study of the flow and regulation of genetic information between DNA, RNA, and protein molecules (4).

Morphometric characters. Any anatomical feature used in morphometrics (*q.v.*).

Morphometrics. Generally, morphometrics (from the Greek: "morph," meaning shape or form, and "metron", meaning measurement) comprises methods of extracting measurements from shapes. In most cases, the term is applied to biological topics in the widest sense. Morphometrics studies the "form follows function" aspect of biology, mapping the changes in an organism's shape in regards to its function. Schools of morphometrics are characterized by what aspects of biological "form" they are concerned with, what they choose to measure, and what kinds of questions they ask of the measurements once they are made. In many cases involves calculating angles, areas, volumes and other quantitative data from landmark and segmentation data. (5)

Natural selection. Natural selection is the process by which favorable heritable traits become more common in successive generations of a population of reproducing organisms, and unfavorable heritable traits become less common. Natural selection acts on the phenotype, or the observable characteristics of an organism, such that individuals with favorable phenotypes are more likely to survive and reproduce than those with less favorable phenotypes. If these phenotypes have a genetic basis, then the genotype associated with the favorable phenotype will increase in frequency in the next generation. (5)

N_em. N_e (*q.v.*) is the effective population size while m is the proportion of N_e that has migrated into the population in some specified unit of time, usually one generation. The product, N_em, is thus the migration rate with units migrants per unit time

Nest site. See redd.

Neutral gene. Any gene where allelic frequencies are not determined by natural selection (*q.v.*) For example, microsatellite genes are not expressed and do not affect the phenotype of an organism. They are, therefore, invisible to natural selection that acts on the phenotype and not the genotype. The frequency of microsatellite alleles is determined by mutation rates (the rate at which new alleles appear, which is thought to be very high in microsatellites), immigration rates (the rate at which potentially novel alleles are introduced into the population, and genetic drift (the rate at which allelic frequencies change due to chance events).

Northern transboundary rivers. A general name for rivers originating in Canada to the north of the Nass River and terminating in the Alaskan Panhandle region. The major transboundary rivers are the Unuk, Stikine, Whiting, Taku, Chilkat and Alsek Rivers.

Oncorhynchus. The genus of the Pacific salmon (*q.v.*)

Pacific Refugium. During the last glacial period, the ice-free region to the south and west of the Continental Divide. Also called the Columbia Refugium (*q.v.*) (McPhail 1998).

Pacific salmon. Salmon of the Pacific Ocean regions, with the following taxonomic classification: **Class:** Actinopterygii (ray-finned fishes) ⇨ **Order:** Salmoniformes (salmons) ⇨ **Family:** Salmonidae (Salmonids) ⇨ **Subfamily**: Salmoninae ⇨ genus *Oncorhynchus*. The genus includes seven species of anadromous Pacific salmon, of which five occur in Canada and are addressed in the Wild Salmon Policy. They are sockeye (*O. nerka*), pink (*O. gorbuscha*), chum (*O. keta*), coho (*O. kisutch*) and chinook (*O. tshawytscha*). The two other Pacific salmon, cherry (2 subspecies *O. masou masou* & *O. masou macrostomus*) and *O. rhodorus* are found in Japan. The genus includes two anadromous trout that are found in BC, the steelhead (*O. mykiss*) and cutthroat trout (*O. clarkii*). The remaining species are trouts found in restricted areas of the US Southwest and northwest Mexico (*O. aguabonita, O. apache, O. chrysogaster, & O. gilae*) or Japan (*O. iwame*). There is also a freshwater subspecies of the cherry salmon (*O. masou formosanus*) on the island of Formosa.

Parr. Juvenile salmon in fresh water, usually several months old. Most species of salmon and trout have parr marks while in fresh water, which are vertical bars of dark pigment on their sides. Parr marks are thought to serve as camouflage and may play are role in behavioral signaling. Their number, position and size vary among species.

Phenotype. A phenotype describes any observable quality of an organism, such as its morphology, development, or behavior, as opposed to its genotype–the inherited instructions it carries, which may or may not be expressed. This genotype-phenotype distinction was proposed by Wilhelm Johannsen in 1911 to make clear the difference between an organism's heredity and what that heredity produces. (5)

Phylogenetics. In biology, phylogenetics (Greek: phyle = tribe, race and genetikos = relative to birth, from genesis = birth) is the study of evolutionary relatedness among various groups of organisms (e.g., species, populations). Also known as phylogenetic systematics or cladistics, phylogenetics treats a species as a group of lineage-connected individuals over time. Taxonomy (*q.v.*) has been richly informed by phylogenetics but remains methodologically and logically distinct. (5)

Phylogeny. The evolutionary relatedness among groups of organisms that results from

Physiography. Physical geography (6)

Pleistocene. Approximately the last one million years, a period in geologic history when ice sheets covered large sections of the Earth's land surface not now covered by glaciers. (6)

Putative Conservation Unit. A CU that is assumed to exist with an ecological adaptive zone (*q.v.*)

Recorded history. History that has been written down or recorded by the use of language, whereas history is a more general term referring simply to information about the past. It starts in the 4th millennium BC, with the invention of writing, so the duration of recorded history is about 6000 years. (5)

Redd. Nest made in gravel, consisting of a depression dug by a fish for egg deposition (and then filled) and associated gravel mounds. In Pacific salmon redds are constructed for the most part by the female. A single female might dig several redds. (4)

Refugium. During glacial periods, an area free of ice sheets in which terrestrial organisms persisted.

Regime shift. A rapid reorganization of an ecosystem from one relatively stable state to another. In the marine environment, regimes may last for several decades and shifts often appear to be associated with changes in the climate system. In the North Pacific, climate regimes are typically described using the concept of Pacific Decadal Oscillation. (5)

Reproductive isolation. Two groups of the same species or sister species are reproductively isolated if gene flow between them is restricted or absent. Isolation can be physical, i.e., there is no interbreeding, ecological, there is interbreeding but the hybrids survive poorly or not at all in the wild, or genetic, i.e., there is interbreeding but the hybrids are not viable. Isolation can range from complete, i.e., there has been no gene flow on an ecological time scale to partial.

Salmon Escapement Database System. A database maintained by the Salmon Assessment Group at the Pacific Biological Station that contains escapement records for Pacific salmon in Western Canada and information associated with those records. For most AEW escapement records begin in the early 1950's, although for some Fraser River sites records are available from the 1930's to present.

Salmonid. A group of fish that includes salmon, trout, and char, belonging to the taxonomic Family Salmonidae.

SEDS. See Salmon Escapement Database System.

Selection. See Natural Selection.

Semelparous. Reproducing only once in a lifetime. All of the Pacific salmon are semelparous and die immediately after they have spawned. In contrast, the trout in the genus *Oncorhynchus* (*q.v.*) are iteroparous (*q.v.*) (8)

Sexual dimorphism. Body morphology (size, color, shape, etc.) differ between the sexes. Dimorphism occurs in all Pacific salmon to some extent and is most profound in pink salmon.

Short Tandem Repeat (STR). A short tandem repeat (STR) in DNA is a class of polymorphisms that occurs when a pattern of two or more nucleotides are repeated and the repeated sequences are directly adjacent to each other. The pattern can range in length from 2 to 10 base pairs (bp) (for example (CATG)n in a genomic region) and is typically in the non-coding intron region, making it "junk" DNA. By examining enough STR loci and counting how many repeats of a specific STR sequence there are at a given locus, it is possible to create a unique genetic profile of an individual. There are currently over 10,000 published STR sequences in the human genome. STR analysis has become the prevalent analytical method for determining genetic profiles (fingerprints) in forensic cases and for stock identification in fishes. (5)

Smolt. A juvenile salmon that has completed rearing in freshwater and migrates into the marine environment. A smolt becomes physiologically capable of balancing salt and water in the estuary and ocean waters. Smolts vary in size and age depending on the species and population of salmon.

Smolt age. See Fish ages.

Species. A group of actually or potentially interbreeding populations that is reproductively isolated from other such groups. This is the usual textbook definition of a species and is called the Biological Species. It is but one of over a dozen species definitions in common use. The difficulty in fashioning a definition of a species that adequately accounts for the immense complexities of the biodiversity continuum (*q.v.*) is called the Species Problem, and is one of the most fascinating and profound problems in biological science. (5).

Stock concept. A stock is an infraspecific taxon that is characterized by local adaptation to its environment. The term was first coined by Moulton (1939) but the existence of geographic variants in salmon had been recognized much earlier (Quinn 1999). The stock concept was articulated by Ricker (1972) and underlies much of the research into the conservation and management of salmonids.

Subpopulation. A group comprising one or more genodemes (*q.v.*) that is partially isolated from other such groups. Local adaption may exist if the effective population size and the selection coefficient are sufficiently large. (Wood and Holtby 1998)

Sustainable use. The use of resources in a way and at a rate that does not lead to their long-term decline, thereby maintaining the potential for future generations to meet their needs and aspirations. Sustainable use refers to consumptive uses of biological resources.

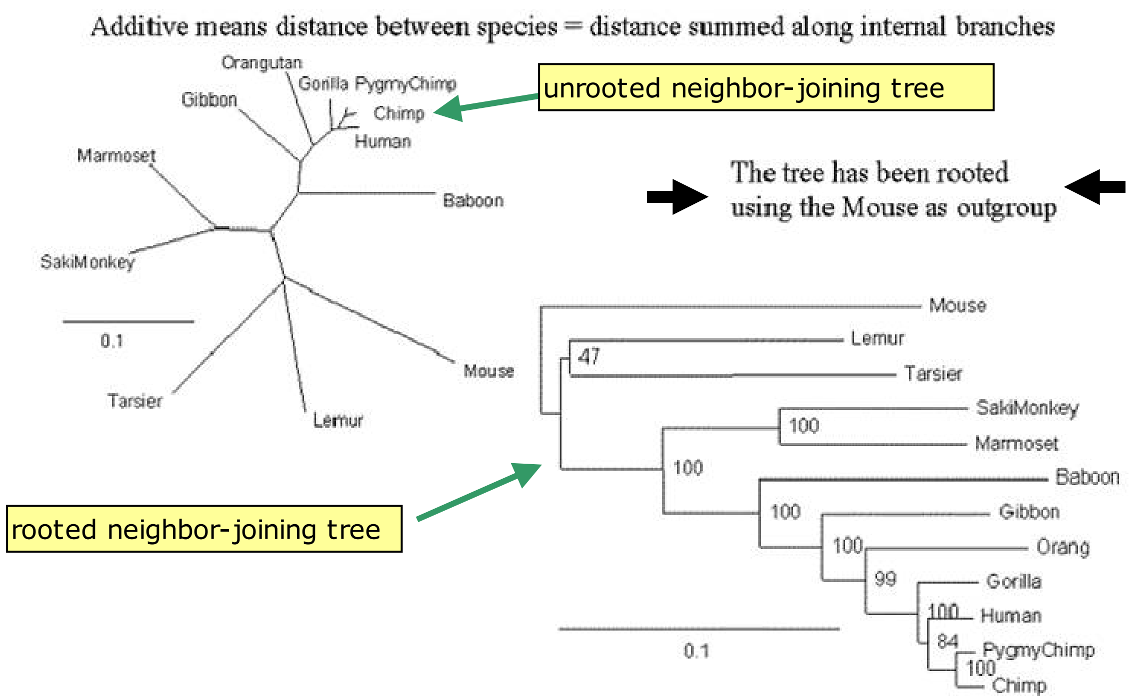
Taxonomy. Taxonomy, sometimes alpha taxonomy, is the science of finding, describing and categorizing organisms, thus giving rise to taxonomic groups or taxa (singular: taxon), which may then be named. The relationship between "taxonomy" and "systematics" is a potential source of confusion. These words have a similar history and over time, these terms have been used as synonyms, as overlapping or as completely complementary. In today's usage, taxonomy (as a science) deals with finding, describing and naming organisms, while systematics (as a science) deals with the relationships between taxa, especially at the higher levels. Modern systematics is greatly influenced by data derived from nuclear and organellular DNA. This is sometimes known as molecular systematics. (5)

Temporal diversity. Variations of phenotype (*q.v.*) in time.

Thermal requirements. The preferred and tolerated temperature limits of an organism (Brett 1956) or the ecological effects of temperature on growth, survival and ecology of an individual, population or species (Holtby and Scrivener 1989, Selong et al. 2001).

Topodeme. See deme.

Unrooted neighbor-joining tree. Neighbor-joining is a clustering algorithm that produces an additive tree that approximates to the data matrix. The data matrix comprises the pair-wise distances between all of the samples. The tree is additive because the sum of the branch lengths of the tree joining two samples approximates to the distance between them. The tree is unrooted because any one of the samples can be used to root the tree, i.e., serve as the starting point for the bifurcation of the branches. This is illustrated in the following diagram. (13, including diagram)



Viable population. See minimum viable population

Wild Salmon Policy. Canada's Policy for Conservation of Wild Pacific Salmon is published by Fisheries and Oceans Canada, 401 Burrard Street, Vancouver, BC V6C 3S4, with cataloguing information: ISBN 0-662-40538-2 & Cat. No. Fs23-476/2005E

Wisconsin glaciation. The Wisconsin Glacial Episode was the last major advance of continental glaciers in the North American Laurentide ice sheet (*q.v.*). This glaciation is made of three glacial maxima (commonly called ice ages) separated by interglacial periods (such as the one we are living in). These ice ages are called, from oldest to youngest, Tahoe, Tenaya and Tioga. The Tahoe reached its maximum extent perhaps about 70,000 years ago. Little is known about the Tenaya. The Tioga was the least severe and last of the Wisconsin Episode. It began about 30,000 years ago, reached its greatest advance 20,000 years ago, and ended about 10,000 years ago. At the height of glaciation the Bering land bridge permitted migration of mammals and humans to North America from Siberia. (5)

WSP. See Wild Salmon Policy.

Zoogeography. Zoogeography is the study of the patterns of the past, present, and future distribution of animals (and their attributes) in nature and the processes that regulate these distributions, and it's the scientific analysis of the patterns of biodiversity regarding time and space. Zoogeography is a branch of the science of biogeography (*q.v.*) (5)

Additional Sources

(1) FAO Fisheries Glossary, part of the UN Atlas of the Oceans http://www.oceansatlas.org/

(2) Citations given in definition

(3) Birgid Schlindwein's Hypermedia Glossary Of Genetic Terms http://hal.wzw.tum.de/genglos/asp/genreq.asp?list=1

(4) Biology Online dictionary http://www.biology-online.org/dictionary/

(5) Wikipedia: http://en.wikipedia.org/wiki

(6) Glossary of geography: http://usinfo.state.gov/products/pubs/geography/glossary.htm

(7) Glossary of the Human Genome Project: http://www.ornl.gov/sci/techresources/Human_Genome/glossary/

(8) Wiktionary: http://en.wiktionary.org/wiki/semelparous

(9) EverythingBio glossary: http://www.everythingbio.com/glos/index.php

(10) Glossary of terms for use in avian conservation biology: http://www.npwrc.usgs.gov/resource/literatr/avian/glossary.htm

(11) US Environmental Protection Agency Terminology Reference Section: http://www.epa.gov/trs/

(12) University of California of Paleontology glossary: http://www.ucmp.berkeley.edu/glossary/glossary.html

(13) From lecture notes of Dr. H.C. Paul Lee, University Chair Professor of Biophysics, Graduate Institute of Systems Biology and Bioinformatics, Department of Physics/ Graduate Institute of Biophysics, Center for Complex Systems, National Central University, Chungli 320, Taiwan: (phylogeny lecture #3), http://sansan.phy.ncu.edu.tw/~hclee/lectures/lectures.html

(14) Biotech Life Sciences Dictionary: http://biotech.icmb.utexas.edu/search/dict-search.html

(15) The World Conservation Union: http://www.iucn.org/en/about

Appendix 8. Consultations Undertaken.

author: Raymond Lauzier, DFO, PBS

Introduction

As described in DFO (2004), Fisheries and Oceans Canada (DFO) is obligated to "undertake consultations in order to improve departmental decision-making processes, promote understanding of fisheries, oceans and marine transport issues, and strengthen relationships". DFO committed to an open process with WSP implementation (Principle 4 - open and transparent decision-making) including consultations with local First Nations in accordance with its consultation obligations (Principle 2 – honour obligations to First Nations). The identification of CUs, and the methodology to do so, are clearly important steps in WSP implementation worthy of consultation.

This Appendix documents non-DFO CU related consultations and information exchanges that took place during the latter half of 2006 and the early part of 2007. There were various internal DFO staff briefings and communications, both in person, and by e-mail that are not described.

The primary purposes of the non-DFO consultation/information sessions were to:

- Outline the proposed methodology for CU identification and solicit feedback on it.
- Review preliminary lists of CUs for errors, omissions, and misinformation.

Presentations

The following were provided at most sessions:

- Power Point presentation entitled "The Identification of Conservation Units"[31]
- Posters outlining the proposed methodology
- Posters delineating preliminary CUs and showing the freshwater location where the fish spawn and/or rear.
- Six-page narrative "Outline of method for identifying salmon Conservation Units under the Wild Salmon Policy"
- Four to six binders (depending on the size of the audience) that listed the proposed CUs and their constituent rivers, streams and lakes.

Following the Power Point presentations and a question and answer period, participants were provided with "Post-It" notes and felt pens, and invited to provide their comments and input either on the wall posters or in the binders. The notes were gathered at the end of each information session and subsequently collated by area. In addition, binders were left in the communities for further input with instructions on how to return them so their feedback and information could be considered and integrated into a revised CU list. All participants were asked to identify themselves with contact information, so any feedback and advice they provided could be verified, confirmed or corroborated.

[31] Note that this was just one of 4 WSP presentations given at most sessions.

After the meetings, we reviewed all feedback and made changes to CUs as appropriate. We are in the process of documenting these comments and our responses.

Participants and stakeholder representatives

Participation at First Nations CU information exchanges included First Nations Fisheries Technical Committees, tribal councils, band councillors and chiefs, as well First Nations individuals. First Nations Fisheries Technical Committees are scientific and technical advisers to First Nations on fisheries issues. They provide advice on proposals, enhancement projects, feasibility studies, management and assessment plans. First Nations Fisheries Technical Committees that participated in the information exchange on CUs included the Haida Fisheries Commission in Skidegate, Skeena Fisheries Commission in Smithers, Secwepemc Fisheries Commission in Merritt, and Uu-a-thluk in Port Alberni. Tribal councils and umbrella groups that participated with the CU discussions included: Nuu-chah-nulth Tribal Council, Okanagan Nation Alliance, Shuswap Nation Tribal Council, Tsilhqot'in National Government, Upper Fraser Fisheries Conservation Alliance, Cowichan Tribes, and Nicola Tribal Association. In all, members of over 55 First Nations attended 9 information exchange/consultation sessions on CUs proposed with the Wild Salmon Policy (Table 1).

There were representatives from the commercial fishing sector, recreational sector, environmental groups, labour unions, community groups, as well as private sector consultants at the multi-stakeholder information exchange/consultation sessions. Commercial fishing interests included representatives from the Canadian Fishing Corporation, Northern Native Fishing Corporation, and Native Brotherhood of BC. Recreational fishing interests included representatives from the Sport Fishing Institute and the Sport Fish Advisory Boards. Environmental interests included representatives from the David Suzuki Foundation, Sierra Legal Defence Fund, Pacific Streamkeepers Federation, T. Buck Suzuki Environmental Foundation, and over 15 other community and environmental groups.

In addition to the formal presentations made to the First Nations groups and multi-stakeholder groups, Community Open House dialogue sessions were held for the general public in Prince Rupert, Prince George, Bella Coola, Kamloops, Nanaimo, Port Alberni, Penticton, and Vancouver during the fall 2006.

Timetable

Some First Nations groups were presented with an early draft of the CU methodology and CU lists during the spring and summer of 2006:

- First Nations Visions Conference – Merritt 29 March 06;
- Nass Joint Technical Committee - Overview and Next Steps – Prince Rupert - 18 April 2006;
- Nass Joint Fisheries Management Committee – Prince Rupert - 19 April 2006

The majority of the presentations were made to First Nations, stakeholder groups and the general public during the DFO Community Dialogue sessions held annually during the fall throughout B.C. (Table 1).

Table 1. Dates and locations of CU consultation/ information exchange sessions held in 2006-2007

Location	Participants	Date
Bella Coola	Local First Nations	July 20, 2006
Smithers	Skeena Fisheries Commission	July 27, 2006
Skidegate	Council of Haida Nations	August 29,2006
Prince Rupert	Community Open House	October 3, 2006
	First Nations	October 5, 2006
	Multi-stakeholder	October 5, 2006
Prince George	First Nations	October 13, 2006
	Community Open House	October 13, 2006
Penticton	Open House	October 16, 2006
		Oct 17
	First Nations	Nov 21
Bella Coola	Community Open House	October 20, 2006
	Multi-stakeholder	October 21, 2006
Victoria	BC Ministry of Environment	October 23, 2006
Merritt	First Nations	October 27, 2006
Kamloops	Community Open House	October 27, 2006
	Multi-stakeholder	October 28, 2006
Nanaimo	Community Open House	November 6, 2006
	Multi-stakeholder	November 7, 2006
	First Nations	November 8, 2006
Chilliwack	First Nations	November 15, 2006
Vancouver	Community Open House	November 16, 2006
	Multi-stakeholder	November 17, 2006
Port Alberni	First Nations	November 9, 2006
	Community Open House	November 22, 2006
	Multi-stakeholder	November 23,2006
Alert Bay	Namgis FN	January 29, 2007
Vancouver	Sport Fish Advisory Board-Main	February 2007
Victoria	Sport Fish Advisory Board-Southern	April 1, 2007
Prince Rupert	Sport Fish Advisory Board-Northern	April 13, 2007

Overview of general feedback from consultation/information exchange sessions

As indicated earlier, detailed feedback and responses are currently being assembled. The following is a general summary.

Most feedback and comments were positive. We received feedback that included general oral comments, inquiries on the process, political statements on various subjects, and oral and written suggestions on the appropriate size and composition of specific CUs.

Many commented that the CU identification methodology appeared to be sound, inclusive and logical. Presenters were often complemented on the thoroughness and clarity of the process of CU identification. Many concerns were alleviated by a more detailed explanation of the process, or with an expanded discussion on the significance and impacts of CUs. At one presentation, was there a minor disagreement on the concept of glacial refugia. In a few cases, there was concern that either the freshwater ecological zones or the marine ecological zones were too large, and did not capture or reflect unique local features or conditions. At an information exchange meeting with B.C. Ministry of Environment fisheries staff, it was realized there was very good agreement on the DFO salmon CUs and the B.C. MOE steelhead trout CUs.

Concerns were expressed by some stakeholders and the general public on what would be done with the local knowledge input provided to DFO, and that it should be two-way communication. The same concerns were expressed at the First Nations sessions, where there is apprehension about revealing Aboriginal Traditional Ecological Knowledge (ATEK). Concerns were expressed at not only how to gather and assess ATEK, but the weighting of ATEK compared to scientific knowledge. First Nations participants often felt that ATEK was superior to scientific knowledge. First Nations participants also raised concerns on the potential impact of CUs on their aboriginal right to harvest at long-standing traditional harvesting sites or particular areas. At many First Nations and multi-stakeholder presentations, concerns were expressed on the location or presence of marine salmon net pen aquaculture facilities and how that would affect the viability of CUs. Concerns were also raised about DFO increasingly depending on volunteer and community groups to provide advice and input on what they perceived to be short-funded initiatives. These groups are experiencing volunteer burn-out, and it was pointed out several times that DFO needs to realistically consider the costs of volunteer time and effort in participating in consultation/information exchange sessions.

At several multi-stakeholder presentations, concerns were expressed that some of the proposed CUs were too large, and as a result some small unique or compromised populations will not get the attention needed for restoration and maintenance. At several presentations, concerns were raised on how to protect different populations within large CUs that have geographical barriers to straying or re-colonizing. However representatives of commercial harvesters sometimes expressed the opposite view, that there were too many CUs or the CUs were not large enough. As a result, it would be increasingly difficult to manage the resource and this will have a serious and significant impact by reducing harvesting opportunities.

In summary, most criticism was constructive, and based on local knowledge. This result was the intent of the information exchange/consultation sessions, which was to correct any errors or omissions, and to provide any additional information from local knowledge or ATEK. There were considerably fewer than anticipated suggested changes to CU identification, delineation and composition.

References

DFO. 2004. Consultation Framework for Fisheries and Oceans Canada. Fisheries and Oceans Canada, Ottawa. DFO/2004-66. 37pp + ix.

Appendix 9. PSARC Request for Working Paper[32]

Date Submitted: May 2007

Regional sector requesting advice: Science
(FAM, OHEB, Policy, Science)

Proposed PSARC Presentation Date: June 13 2007

Subject of paper (title if developed): Title of Working Paper: **"**Conservation Units for Pacific salmon under the Wild Salmon Policy"

Science lead author: Blair Holtby

Resource Management lead author: NA

Rationale for request:
(What is the issue, what will it address, importance, etc.)

Conservation Units (CU) under the Canada's Policy for Conservation of Wild Pacific Salmon , otherwise known as the Wild Salmon policy (WSP) are defined as …"*a group of wild salmon sufficiently isolated from other groups that, if extirpated is very unlikely to recolonize naturally within an acceptable timeframe, such as a human lifetime or a specified number of salmon generations."* The WSP specifies (Strategy 1, Action Step 1.1) that the science basis for identifying CUs will be assessed through peer review (via the Pacific Scientific Advice Review Committee, PSARC).

Objective of working paper including assessment of environment/climate impacts:
(To be developed by FAM, OHEB, Policy, Science)

The objective of the working paper is to present a methodology for PSARC review that will be used to identifying individual Conservation Units (WSP Strategy 1, Action Step 1.1) for all species of wild Pacific salmon. This is in support of Objective 1 of the WSP; that of maintaining the genetic and habitat diversity of wild Pacific salmon through the protection of CUs.

Question(s) to be addressed in the working paper:
(To be developed by initiator)
The details of the advice is developed in the WSP Strategy 1, Action Step 1.1 "*The delineation of CUs will be based on biological information, including genetic traits (e.g. DNA variants), polygenic traits (e.g. run timing, life history traits, ocean distribution, etc,), and ATK where available.*"

Stakeholders affected: all sectors

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[32] Science – append approved RFWP to working paper.
Sector initiator – send approved RFWP to PSARC after sign off, and before significant work begins on the paper.

How advice may impact the development of a fishing/recovery plan:
The biological status of CUs will be the primary basis for assessing the performance of fishing/recovery plans. Fishing/recovery plans will therefore need to account for their impacts on the status of CUs.

Timing issues related to when advice is necessary:
The PSARC methodology review is part of a long term plan to implement the WSP. The advice will form the basis for identifying and monitoring individual CUs. There is no specific or immediate timing issues related to when the advice is necessary.

Initiating sector approval:

Regional Director/Designated Authority: ________________________

Date:______________________