Genetic composition of Pacific trout species in relation to landscape features in the upper Snoqualmie River watershed, WA

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Abstract

The upper Snoqualmie River watershed (USRW) is located above an 82 m vertical barrier to anadromous fishes. Main stem rivers and tributaries in the USRW contain wild populations of coastal and westslope cutthroat trout, rainbow trout, and hybrids among these species. Releases of hatchery-raised strains of Pacific trout were widespread throughout the watershed between 1930's and 1990's and continue in alpine lakes that drain into tributaries and main stem rivers. Trout identified in the field as rainbow, coastal cutthroat, westslope cutthroat, and hybrids were sampled in main stem and tributary habitats in the USRW and analyzed to describe the various species and lineages inhabiting the watershed and the magnitude of introgression by hatchery strains of Pacific trout. Fish were genotyped at seven microsatellite DNA loci and 96 single nucleotide polymorphism loci (SNPs) and results differentiated between putative native and hatchery strains of coastal and westslope cutthroat, rainbow and hybrids between all of these species. Hybrids were composed of first generation types (F1) and descendants of hybrids (beyond F1 or introgressed). Many samples contained a mixture of native and hatchery strains indicating that hatchery-raised trout have introgressed into the populations and even dominate the genetic structure in discrete segments of the watershed. Dominant lineages (native or hatchery ancestry) were generally homogenous within each fork but varied between the forks, indicating that some native subpopulations were probably more vulnerable to displacement by hatchery-raised species or the area was unoccupied prior to hatchery introductions. Current spatial distribution of the genetic composition of Pacific trout revealed possible causal mechanisms of the distribution of salmonids during and after the last glacial recession (c. 10,000 to 15,000 years before present).

Introduction

The Snoqualmie River Game Fish Enhancement Plan (Plan) is a comprehensive inventory and ecological study of the fishery resources in the upper Snoqualmie River watershed (USRW). The USRW consists of all waters draining the Snoqualmie River basin upstream of the Snoqualmie Falls Hydroelectric Project at Snoqualmie Falls, which is owned and operated by Puget Sound Energy (PSE). In 2004 the Federal Energy Regulatory Commission (FERC) issued a new license for the hydroelectric project. Article 413 of the license required PSE to file a final Plan to the FERC for approval and allocate funds to implement the Plan. PSE developed the final Plan in consultation with the Washington Department of Fish and Wildlife (WDFW) and submitted it to the FERC (Puget Sound Energy 2005). The Plan was approved by the FERC in December 2006 and in 2007 PSE contracted WDFW to conduct the Plan (Thompson et al. 2011).

One of the goals of the Plan was to determine trout species composition and distribution in the watershed. Pacific trout species known to inhabit the USRW include coastal cutthroat (CCT: *Oncorhynchus clarki clarki*), rainbow (RBT: *O. mykiss*), westslope cutthroat (WCT: *O. clarki lewisi*), and hybrids among these species (Onxx). Bull trout (*Salvelinus confluentus*) is the only char species endemic to the inland Central Puget Sound region, but none were found during this study (Thompson et al. 2011). Over the years anglers have reported sightings of bull trout in the USRW; however, none were observed during a previous study designed specifically to detect their presence in the USRW (Berge and Mavros 2001).

Coastal cutthroat and rainbow trout are the most likely native trout species in the USRW, as westslope are known to be native only in drainages east of the Cascade Mountains. Various species of hatchery-raised trout (CCT, RBT, and WCT) were released into water bodies of the USRW between the 1930's and 1990's (Table 1). It is likely that additional trout were stocked prior to 1930 (Bob Pfeifer, personal communication). Plants of hatchery-raised CCT and RBT continue presently, but are limited to alpine lakes or water bodies that do not connect directly with main stem rivers (Table 1). Coastal cutthroat are the most abundant species of Pacific trout in the USRW followed by RBT, and Onxx. Accurate field differentiation between CCT, RBT, and Onxx is difficult in discrete segments of the USRW (Thompson et al. 2011). Genetic analysis of individuals sampled throughout the watershed can help field biologists describe species composition and can help identify the extent of introgression or hybridization with putative native species. Analysis of genetic samples collected on a landscape scale can help managers identify where various lineages (native or hatchery) occur so appropriate management actions can be prioritized in specific reaches.

The objectives of this study were to identify the various Pacific trout species and to describe species and lineage composition of Pacific trout on a large spatial scale in the USRW. Genetic samples were spatially distributed among main stem rivers and tributaries in the USRW to facilitate a watershed-scale understanding of species composition.

Study Area

Upper Snoqualmie River Watershed

The USRW is composed of the headwater portions of the Snoqualmie River above Snoqualmie Falls, an 82 m vertical barrier that limits anadromous fish distribution to the lower watershed. The Snoqualmie River below Snoqualmie Falls converges with the Skykomish River near the city of Monroe to form the Snohomish River, the second largest river system flowing into the Puget Sound (Figure 1). Major river systems of the USRW include the North, Middle and South forks, and the mainstem of the Snoqualmie River above Snoqualmie Falls. Each of the Snoqualmie forks originates on the west slopes of the Cascade Mountains, flowing in a general westerly direction through varied landscapes until they converge as the mainstem Snoqualmie River. The mainstem Snoqualmie continues downstream for about 6 km before plunging over Snoqualmie Falls (Figure 2).

The headwater portions of each fork originate high on the Cascade Crest in the Alpine Lakes Wilderness Area. In a landscape sculpted by alpine glaciers (c. 20,000 ybp), headwaters consist of confined, turbulent, high gradient habitats with geologic barriers that isolate fish into sub-populations (Figure 2). Downstream of headwaters the steep stream channels converge with more moderate gradient terraced u-shaped montane valley bottoms. Gradient is heterogeneous along montane valley bottoms as low gradient segments yield to exposed bedrock or boulder-cascade reaches that isolate fish (e.g., Big Creek Falls in the North Fork and Weeks Falls in the South Fork). Each fork is low to moderate gradient downstream of the most major geologic barriers (Black Canyon in the North Fork, Twin Falls in the South Fork, and Dingford Canyon in the Middle Fork).

Prior to the most recent glaciation (c. 14,000 ybp) the upper Cedar River basin drained into the Snoqualmie basin. However, the Cedar River was diverted south and the major geologic barriers in each fork of the Snoqualmie were formed after the most recent encroachment and retreat of the Vashon Lobe of the Cordilleran Ice Sheet, as glacial moraines (e.g., Grouse Ridge) were formed creating lakes behind large ‘earthen dams’ and bedrock outcroppings (e.g., Twin Falls) were exposed. The Vashon Lobe blocked the pathway of the Snoqualmie River and a large ice-marginal lake occupied the lower portion of the basin just upstream of Snoqualmie Falls as the Vashon Lobe slowly retreated. This lake received streamflows from most, if not all, northern and central Puget Sound basins (Skagit, Stillaguamish, Skykomish, etc.) as they converged with and flowed south along the eastern border of the ice sheet. The original outlet for the ice marginal lake was through the Cedar Channel near Rattlesnake Lake, but as the Vashon Lobe retreated the lake level dropped and the Snoqualmie River carved a new channel that flowed over Snoqualmie Falls (Figure 2).

Each fork and the mainstem Snoqualmie River were divided into river segments (Figure 3). River segments corresponded with discrete channel types (sediment transport or deposition), geography, trout abundance, and trout species composition (Thompson et al. 2011). Sample reaches were located within river segments and spatially explicit trout genetic composition was analyzed by comparing trout genetics between river segments.

Materials and Methods

Data collection

Sample reaches were distributed across river segments (Figure 3) and fish were sampled randomly from length groups in sample reaches (0–99, 100–149, 150–229, 230–299, 300–379, 380+ mm total length - TL). Size of sample reach ranged between 50 m and 8 km in length and from shallow margins to the entire wetted width depending on habitat size. Fish were captured between June 2009 and October 2010 using one of two methods: 1) single pass backpack electrofishing without blocknets (*sensu* Bateman et al. 2005); or 2) wade- or float-based angling. Wade-based angling was used in conjunction with backpack electrofishing in reaches containing habitats too deep for effective backpack shocking. Captured fish were held in containers of cold, fresh, aerated water with cover to reduce stress. Fish were anesthetized using 6 ml of 10g:1 L solution MS 222 in 7.5 L of fresh water, and were identified to species, measured for total and fork lengths (mm), and weighed (0.1 g). Lower caudal fin samples were distributed proportionally among length frequency groups, and egg and alevin samples were retained during spawning surveys in main stems and tributaries during winter and spring of 2010. Tissue samples for DNA extraction were placed directly in vials containing 95% ethanol. Samples were grouped into two collections with WDFW codes 09IJ and 09IK but field collections were not segregated by these codes consistently (field identifications presented in Table 7). Most of the cutthroat trout were in collection 09IJ and most of the rainbow trout were in collection 09IK, but each collection contained both species types. To help us distinguish descendants of introduced hatchery cutthroat trout from possible native cutthroat trout we included samples of two of the hatchery cutthroat trout collections [Lake Whatcom broodstock (coastal cutthroat trout) housed at Tokul Creek Hatchery (WDFW code 01NZ); Twin Lakes broodstock (westslope cutthroat trout) housed at Twin Lakes Hatchery (WDFW code 99GB)] as well as a native coastal cutthroat trout collection from Cedar River in South Puget Sound (WDFW code 05BB).

To further identify trout origins, we compared the USRW trout to archived trout data from WDFW. The archived data had five microsatellite loci in common with contemporary data. Analyses were conducted to pursue signals indicating that some of the Snoqualmie trout samples may have had ancestry in hatchery rainbow trout broodstocks that were not represented in the baseline samples (listed above) that had been genotyped with microsatellites and SNPs. The archived data included rainbow trout from the Puget Sound basin (Puyallup, Cedar, Green rivers and Chester Morse Lake) and hatchery rainbow trout broodstocks planted throughout Washington State (Eells Springs, South Tacoma, Goldendale, and Spokane hatcheries). The archived data also included coastal cutthroat trout from Puget Sound (Bear and Minter creeks and a collection from Lake Washington) and westslope cutthroat trout from Pend Oreille basin (Sullivan Lake, Sullivan and Gold creeks).

Laboratory analyses

Genomic DNA was extracted from tissue samples using Clone-tech® extraction kits. Trout samples were genotyped at seven microsatellite loci (One-108, Ots-103, Omy-77, Ots-1, Ots-3M, Ogo-3, and Omm-1138) which had large differences in allelic distributions between cutthroat trout and rainbow trout in Marshall et al. (2006). Microsatellite alleles were PCR-amplified using fluorescently labeled primers. PCRs were conducted in 96 well plates in 10 µl volumes employing 1 µl template with final concentrations of 1.5 mM $MgCl_{2,}$ 200µM of each dNTP, and 1X Promega PCR buffer. The following microsatellite loci were used at the following concentrations (concentration in µM after locus name): One-108 [0.075], Ots-103 [0.037], Omy-77 [0.075], Ots-1 [0.08], Ots-3M [0.05], Ogo-3 [0.07], and Omm-1138 [0.08]). After initial two minute denature at 94°, there were 3 cycles consisting of 94° denaturing for 30 seconds, 60° annealing for 30 seconds, at 72° extension for 60 seconds. These were followed by 30 cycles with the same parameters but the annealing temperature was dropped to 50° and then there was a final 10-minute extension at 72°. Samples were run on an ABI 3730 automated DNA Analyzer and alleles were sized (to base pairs) and binned using an internal lane size standard (GS500Liz from Applied Biosystems) and GeneMapper software (Applied Biosystems).

Trout samples were also genotyped at 96 single nucleotide polymorphism loci (SNPs, see Table 2 for list) through PCR and visualized on Fluidigm EP1 integrated fluidic circuits (chips). Twenty of the SNP loci were developed to discriminate among trout species and 76 of the SNP loci have been used to identify population structure and other genetic attributes of rainbow trout in Puget Sound. Protocols followed Fluidigm's recommendations for TaqMan SNP assays as follows: assay loading mixture contains 1X Assay Loading Reagent (Fluidigm), 2.5X ROX Reference Dye (Invetrogen) and 10X custom TaqMan Assay (Applied Biosystems); sample loading mixture contains 1X TaqMan Universal PCR Master Mix (Applied Biosystems), 0.05X AmpliTaq Gold DNA polymerase (Applied Biosystems), 1X GT sampling loading reagent (Fluidigm) and 2.1 µL template DNA. Four µL assay loading mix and 5 µL sample loading mix were pipetted onto the chip and loaded by the IFC loader (Fluidigm). PCR was conducted on a Fluidigm thermal cycler using a two step profile. Initial mix thermal profile was 70°C for 30min, 25°C for 5 min, 52.3° for 10 sec, 50.1°C for 1 min 50sec, 98°C for 5 sec, 96°C for 9 min 55 sec, 96°C for 15 sec, 58.6°C for 8 sec, and 60.1°C for 43 sec. Amplification thermal profile was 40 cycles of 58.6°C for 10 sec, 96°C for 5 sec, 58.6°C for 8 sec and 60.1°C for 43 sec with a final hold at 20°C. The TaqMan assays were visualized on the Fluidigm EP1 machine using the BioMark data collection software and analyzed using Fluidigm SNP genotyping analysis software. All data were scored by two researchers.

Statistical analyses

Since the WDFW Molecular Genetics Lab is transitioning from using microsatellite loci to using SNP loci for genetic analyses, we used the program ARLEQUIN3.5 (Schneider et al. 2000) to generate several genetic statistics to assist our comparisons of the loci. We used ARLEQUIN to calculate the amount of genetic variance among collections at each locus, to estimate whether the variance was significant and to identify loci that had a lower or higher amount of genetic variance than expected (balancing or directional selection at loci, respectively) using the F_{ST} outlier test. Most of our statistics assume loci are selectively neutral: a locus under balancing selection would have less divergence among populations than expected, often due to heterozygote advantage or frequency-dependent selection and a locus under directional selection would have more divergence among populations than expected, often due to selective differences among sampling locations. We used a hierarchical analysis of molecular variance (AMOVA, Excoffier et al. 1992) to calculate the amount of genetic variance among collections, among individuals within collections and within individuals using three permutations of the dataset: just the microsatellite loci, just the SNP loci and with both locus sets combined.

Trout from the USRW were assessed to determine their species identity and their status; pure, hybrid or introgressed (hybrid beyond the first generation). In addition to species identification and genetic status, we identified whether trout were descendants of introduced out-of-basin hatchery cutthroat trout or rainbow trout or if mixture was between cutthroat trout variants or between cutthroat trout and rainbow trout or included some component of hatchery rainbow trout. We used the Bayesian analysis implemented in the program STRUCTURE2.3 (Pritchard et al. 2000) to estimate individual genetic ancestry and identify putative hybrids and introgressed individuals. STRUCTURE sorts individuals (or portions of individuals if they are hybrids) into a number of hypothetical clusters (K) or groups in order to achieve Hardy-Weinberg equilibrium and linkage equilibrium (or minimize disequilibrium) in the clusters or groups – individuals that are genetically similar to each other group together in a cluster and the clustering can be broad scale (eg. species level) or fine scale (population level). Hybrid or introgressed individuals will have ancestry in two or more genetic clusters. The program outputs a likelihood value for the number of clusters or genetic groups, given the dataset. The likelihood value reaches a maximum or asymptote when the program has detected the maximum number of genetic clusters it can identify in the dataset. We set the number of clusters or possible populations at 2–7: at $K = 2$ we hypothesized that the dataset would divide into a cutthroat trout and a rainbow trout group and at higher K values the dataset would divide into cutthroat trout and rainbow trout subspecies and populations.

We used the program GENETIX (Belkhir et al. 2004) to view differences among individual samples and collections and to view possible interspecific hybrids. GENETIX performs a factorial correspondence analysis (FCA), which generates axes that describe the maximum genetic variation among individuals and plots individuals along these axes according to their genotype. Individuals that are genetically similar plot near each other and individuals that are genetically different plot distantly from each other. Hybridization or introgression is hypothesized when individuals from one species plot within or towards the region occupied by the other species or genetic group (eg. hatchery cluster). This program also provides insights into individuals categorized phenotypically as one species that are genetically more similar to a different species since they will plot near genetically similar individuals regardless of phenotype.

Because of the long history of hatchery rainbow trout planting and a lack of detailed information on hatchery broodstocks we conducted a secondary analysis with a subset of the microsatellite data (five loci) generated for this project. In the secondary analysis we compared the genotypic subset to archived WDFW data that included four hatchery rainbow trout broodstocks (Spokane, Goldendale, Eells Springs, South Tacoma) and native Puget Sound rainbow trout (Green, Cedar, Puyallup rivers and Chester Morse Lake) and cutthroat trout (Cedar, Bear, Minter creeks) populations. The archived data had five microsatellite loci per individual in common with the contemporary data and provided insights that were unavailable using only contemporary data. We conducted the same STRUCTURE and FCA analyses with the five loci in common.

Results

Genotyping success varied among individuals and markers. Nine individuals collected in the Snoqualmie basin failed at most loci and were excluded from analyses – failures are usually a result of degraded DNA from decayed tissues or too little DNA from too small of a sample. The microsatellite loci all worked in 80% or greater of the samples. For the SNP markers, 11 loci generated no data and 9 loci produced data for less than half the samples (See Table 3). These SNPs were excluded from further consideration. Genetic variance among collections ranged from a high of 86% at species ID locus ASpI005 to -0.5% at species ID locus ASp1012 (Table 4). Negative values indicate that most of the genetic variance is among individuals and there is little to no variance among collections—the locus has little or no utility for distinguishing among populations or species. While most trout were fixed for a single allele at this locus (there are usually two alleles at a SNP locus), the alternate allele was fixed in the westslope cutthroat trout broodstock collection from Twin Lakes Hatchery (Appendix I). In most of the other species ID SNPs allele frequencies were different between cutthroat trout and rainbow trout collections (see Appendix I). Since many genetic statistics assume that loci are neutral, we tested for neutrality in these new SNP loci and the microsatellite loci. Four markers generated signals of variance that was less than (One-108) or greater than (AOmy015, ASp1004, ASp1005, and ASp1009) expected, suggesting these loci may be under balancing or directional selection, respectively (Figure 3). Selected loci are ones where heterozygous individuals may be favored and survive to reproduce (balancing selection) such that both alleles are at nearly equal frequencies. For loci under directional selection alternate alleles are favored under different selection regimes or environmental conditions such that one allele is at a high frequency in one environment and the alternate allele is at a high frequency in a different environment.

The AMOVA found high genetic variance among collections and among individuals with all combinations of the genotypic data: with microsatellite loci only, with SNP loci only and with the two marker types combined (Table 5). Genetic variance among collections was highest using only SNP loci, likely due to the high allele frequency differences at the species ID SNPs. Genetic variance among individuals was also highest using only SNP loci, possibly also driven by the species ID SNPs. Genetic variance within individuals was lower for SNPs. This was expected since SNPs have two alleles per locus as opposed to over 30 alleles at some microsatellite loci and the species ID SNPs are expected to be nearly or completely fixed in single-species collections. Examining the partitioning of genetic variance (among populations, within populations and within individuals) allows us to identify patterns of genetic variation (eg. if there is significant genetic variance between fish collected from two tributaries that tells us that there is non-random gene flow among the tributaries and that there is geographic structure to the genetic variation).

The STRUCTURE analysis identified cutthroat trout and rainbow trout in the USRW trout samples, as well as some hybrids or introgressed individuals (Figure 3a and Figure 3b). In this analysis, the user tells the program to divide the data set into a number of genetic groups. The program sorts through the data, without knowledge of the origin of the sample, and groups the data into clusters that minimize Hardy-Weinberg disequilibrium and linkage disequilibrium (Hardy-Weinberg and linkage equilibrium are genetic characteristics of unmixed groups). Thus, individuals (or portions of an individual if they are introgressed) that are collected in a single location may be classified into different genetic groups if their ancestry is from different genetic groups. For this study, we were interested in genetic identities of trout of unknown origin, so we included trout of known origin that may have been planted in the basin (hatchery cutthroat trout) or may share recent common ancestry with native Snoqualmie basin trout (Cedar River cutthroat trout) to explore which genetic group individual USRW trout were most similar to. We used the program as a hierarchical analysis that looked at genetic identity from the species level to the population level.

For this study, we first had the program divide the data into two groups and these groups corresponded to a cutthroat trout group and a rainbow trout group (Figure 3a at K = 2). In that figure, each individual fish is represented by a bar of color, blue corresponds to cutthroat trout ancestry and tan to rainbow trout ancestry. If an individual is of single ancestry, it will have a single color in its color bar. If an individual is of mixed ancestry it will have two colors in its color bar, with the proportion of each color corresponding to the percentage of ancestry in the two groups, here cutthroat trout and rainbow trout. The reader can see that samples collected as phenotypic cutthroat trout and rainbow trout in the USRW were mostly genetically cutthroat trout and rainbow trout, respectively (see Table 7 for phenotypic and genetic identification). However, some individuals identified phenotypically as one species identified genetically as the other species and several individuals appeared to have mixed ancestry. This is also seen in the cutthroat trout collection from the Cedar River where a few rainbow trout (tan color bars among the blue) were known to have been included in that collection.

At K = 3 (Figure 3a), the cutthroat trout cluster subdivided into coastal (blue) and westlope (green) cutthroat trout clusters. With this increased definition, a few of the individuals identified genetically as cutthroat trout in the Snoqualmie rainbow trout collection now identify as cutthroat trout with westslope ancestry (green individuals within the Snoqualmie rainbow trout collection). So the resolution of the analysis is at the species and subspecies level.

At K = 4 (Figure 3a), the coastal cutthroat trout cluster subdivided into the Puget Sound coastal cutthroat trout (blue) and coastal cutthroat trout from USRW (purple). We suspect that the coastal cutthroat trout cluster identified in the USRW collection (purple in Figure 3a) is a native coastal cutthroat trout population. The USRW is above a barrier falls and native trout above the falls were expected to be genetically divergent from other coastal cutthroat trout from Puget Sound since there has been no gene flow across the barrier falls. However, some of the Snoqualmie cutthroat trout had ancestry in the Puget Sound coastal cutthroat trout cluster (blue individuals) suggesting that they were descendants of hatchery cutthroat trout (Lake Whatcom broodstock) planted in the basin (see discussion below). Most of the cutthroat trout identified in the USRW rainbow trout collection shared their ancestry with the Snoqualmie cutthroat trout (purple individuals in the USRW rainbow trout collection) and a few were hatchery cutthroat trout origin (blue individuals). Now the resolution of the analysis reaches to the population level for cutthroat trout.

At K = 5 (Figure 3a), the Puget Sound coastal cutthroat trout cluster subdivided into North (Lake Whatcom -blue) and South (Cedar River - red) Puget Sound cutthroat trout and the USRW cutthroat trout (SnoqOcl in Figure 3a) remained in its own cluster (purple). Some of the Puget Sound cutthroat trout identified at K = 4 in the USRW cutthroat trout and rainbow trout collections are more similar to the south Puget Sound cutthroat trout. This may indicate that two hatchery cutthroat trout broodstocks were planted in the USRW or that there are two native cutthroat trout populations in the USRW.

At K = 6 (Figure 3a and Figure 3b), the rainbow trout cluster subdivided into two clusters that we labeled “Snoqualmie 1 and Snoqualmie 2”, tan and orange, respectively. We suspected that one of these clusters might be native rainbow trout and the other might be derived from hatchery rainbow trout planted in the basin. In Figure 3b we break down the K = 6 plot into its clusters to more easily see the distributions of ancestries in each collection. Each different color represents a different genetic group (cluster) identified by the analysis and these are named by the most common known member of the genetic group; eg. the first cluster (identified by blue color) is occupied by Lake Whatcom cutthroat trout, a known cutthroat trout broodstock stocked in the USRW, and several trout from the USRW. The USRW trout were of unknown ancestry and we hypothesized that these were derived from Lake Whatcom broodstock since the analysis grouped them in the cluster occupied by Lake Whatcom cutthroat trout and this broodstock had been planted in the basin. This breakdown into individual clusters allows the viewer to easily see whether fish are of one type—have pure ancestry (one color in color bar)—or if they are mixed ancestry (more than one color). One can also see that there are some USRW individuals in the Lake Whatcom Ocl cluster, a few more individuals in the Cedar Ocl cluster, three individuals in the Twin Lakes Ocl cluster (note: these particular fish had been field-identified as westslope cutthroat trout), but that most USRW trout cluster in their own cutthroat trout (SnoqOcl) and rainbow trout (SnoqOmy1, SnoqOmy2) clusters. This breakdown plot also shows more clearly the division among the rainbow trout collected in the USRW (SnoqOmy1 and SnoqOmy2).

We explored further the two rainbow trout groups identified in the USRW rainbow trout collection, and considered the possibility that the USRW rainbow trout had native and hatchery ancestry. We conducted a second STRUCTURE analysis in which we included archived data from hatchery rainbow trout that may have been planted in the basin as well as some native rainbow trout from Puget Sound (results not shown). This data was from several years ago with a mostly different suite of microsatellite loci. There were five loci in common with the contemporary data such that the analysis had less power to resolve genetic differences at the population level, but was still informative for the origins of the rainbow trout in the USRW. This analysis yielded insights into the identity of the two Snoqualmie rainbow trout groups: the "SnoqOmy1" rainbow trout group in Figures 4a and 4b shared ancestry with hatchery rainbow trout, in particular the broodstock from Goldendale Hatchery, suggesting that they were derived from hatchery rainbow trout. Marshall et al. (2006) similarly found that rainbow trout in the upper Cedar River from Chester Morse Lake were derived from exotic hatchery rainbow trout. The rainbow trout broodstock housed at Tokul Creek Hatchery since 1974 were "Mt. Whitney" strain that had been reared at Goldendale Hatchery during their history (Crawford 1979). The "SnoqOmy2" rainbow trout group in Figures 4a and 4b shared ancestry with native rainbow trout from the Cedar River, suggesting that they were native rainbow trout.

We used the STRUCTURE results to identify genetic origins of individual USRW trout (Table 6). Genetic identities are tabulated with field data in Table 7. Several USRW cutthroat trout and some isolated trout collected as rainbow trout clustered with the Cedar River cutthroat trout in the STRUCTURE analysis and were identified as "Cedar cutthroat" in Table 6 and Table 7. These may be cutthroat trout from a hatchery broodstock that had been planted in both Cedar and Snoqualmie rivers or another native cutthroat trout population founded from common ancestors. However, only Lake Whatcom-origin coastal cutthroat trout broodstock are recorded for Tokul Creek Hatchery (Crawford 1979), which was a main source of hatchery cutthroat trout planted in USRW. Crawford (1979) describes another coastal cutthroat trout broodstock developed for introduction in Puget Sound tributaries that had origins in the Stillaguamish and Nooksack rivers. This broodstock would likely be genetically more closely related to Lake Whatcom broodstock from North Puget Sound (rather than the Cedar River cutthroat trout if they are a native population) and there are no records of planting this other broodstock in USRW. (Note: the STRUCTURE analysis was conducted also including cutthroat trout collections from Minter and Bear creeks and Lake Washington, all from South Puget Sound. The Cedar River cutthroat trout [and some of the Snoqualmie cutthroat trout] grouped with these populations. This suggests either that the "Cedar" cutthroat trout are a native South Puget Sound cutthroat trout population or (less likely) that the same hatchery cutthroat trout were introduced in all these basins.) At this time we lack details on hatchery broodstocks planted in USRW (current information is mostly limited to numbers of hatchery fish without identifying broodstock) to examine the relationship between Cedar and Snoqualmie cutthroat trout and merely present these ideas based on the data available to this study.

The STRUCTURE analysis also suggested that several fish from USRW had mixed ancestry. The mixtures included several combinations such as a mix of hatchery and wild cutthroat trout (eg. Lake Whatcom Ocl and Snoqualmie Ocl), a mix of species with native ancestry (eg. Snoqualmie Ocl and Snoqualmie Omy2), or a mix of species and hatchery and wild ancestries (eg. Lake Whatcom Ocl and Snoqualmie Omy2).

The factorial correspondence analysis (FCA) from GENETIX supported the results from the STRUCTURE analyses. Individual fish plot in the genetic space created by axes that explain the most genetic variance in the data set. The first axis has the greatest genetic variance and cutthroat trout and rainbow trout separate along that axis (Figure 4). The separation is somewhat difficult to see since there is a continuum of distribution for the USRW trout. This continuum is due to mixing within the USRW collections in that some rainbow trout were identified as cutthroat trout or included in the collection that was predominantly cutthroat trout and *vice versa*. There was also genetic mixing within individuals since STRUCTURE suggested that several individuals from both USRW collections were hybrids or introgressed (had ancestry from both species). The cutthroat trout separate along the second axis and three individuals from the USRW rainbow trout collection plot with the westslope cutthroat trout from Twin Lakes Hatchery. STRUCTURE also identified these individuals as Twin Lakes Hatchery origin and these fish were identified in the field as westslope cutthroat trout.

We saw no evidence in the FCA for golden trout (*Oncorhynchu aguabonita*) among the USRW trout. In this type of analysis, fish with very different genetic profiles, such as golden trout or brook trout (*Salvilinus fontinalis*), would separate from all other fish in the plot. However, all fish clustered with either the rainbow trout or the cutthroat trout, suggesting that there were no golden trout or fish with partial golden trout ancestry.

We conducted the FCA with the archived WDFW data (five microsatellite loci) described above to gain more insights into genetic relationships and the ancestry of the USRW trout. Figure 5a shows the FCA with a plot of only the collection centers (the genetic information is collapsed into the center of the genetic distribution for each collection). In Figure 5a, the USRW 09IJ (mainly cutthroat trout) collection center is associated with other coastal cutthroat trout collection centers and the USRW 09IK (mainly rainbow trout but at least 30% cutthroat trout) collection center is between the coastal cutthroat trout and the rainbow trout. This placement reflects the mix of rainbow trout and cutthroat trout in the USRW 09IK trout collection suggested in the STRUCTURE analysis. Figure 5b and Figure 5c show the individual USRW 09IJ and 09IK trout, respectively, plotted in relation to the collection centers. This makes it easier to see that there was a mix of species in both USRW collections, especially in the 09IK collection.

Longitudinal and inter-basin patterns in species composition:

North Fork Snoqualmie River

In the upper North Fork a majority of the trout lineage matched pure Lake Whatcom hatchery coastal cutthroat (85%). In the Lakebed segment only three trout were sampled, but each contained different genetic backgrounds. None were pure native ancestry, but one matched native *O. mykiss* genetic ancestry. From the downstream border of the Lakebed segment downstream to the confluence with the Middle Fork a majority of samples matched hatchery-lineage rainbow trout (69%). However, the presence of pure native Snoqualmie coastal cutthroat trout (Snoq. *O. clarki*) increased in the Three Forks segment near the confluence with the Middle Fork (Figures 6 and 7).

Middle Fork Snoqualmie River

In the upper Middle Fork only four trout were sampled in the Hardscrabble reach, but all were mixed native and hatchery trout genetic ancestry (Table 7). Downstream of Hardscrabble to the confluence with the North Fork the majority of trout matched pure native coastal cutthroat trout genetic lineage (76%, Snoq. *O. clarki*; Figures 6 and 7).

South Fork Snoqualmie River

Samples from the Denny Creek segment of the upper South Fork (*n* = 4) were all pure or hybridized westslope cutthroat genetic lineage, suggesting they were derived from planted hatchery fish. No samples obtained in the upper and middle South Fork matched pure native Snoq. *O. clarki*. Conversely, most matched a pure genetic lineage of native Cedar *O. clarki* (29%), Cedar *O. mykiss* (29%) or hybridized Cedar *O. clarki* /*O. mykiss* (20%). The Asahel Curtis segment of the upper South Fork and Tinkham segment of the middle South Fork contained the highest proportions of pure Cedar *O. clarki* (62%) and hybridized Cedar *O. clarki* /*O. mykiss* (19%). No coastal cutthroat trout of native lineage were sampled in the Weeks Falls and Grouse Ridge segments, but hybrid Cedar *O. clarki* /*O. mykiss* (21%) and pure Cedar *O. mykiss* (50%) represented the majority of genetic samples in those segments. A few mixed native/hatchery rainbow and coastal cutthroat trout were also sampled in these segments (25%). In the lower South Fork downstream of Twin Falls genetically pure hatchery rainbow trout were sampled (8%) as were pure native rainbow trout (Cedar *O. mykiss*, 16%) along with hybrid rainbow and coastal cutthroat trout (Snoq. *O. clarki* and Cedar *O. clarki* /Cedar *O. mykiss*, 18%). Mixed native-lineage coastal cutthroat trout (Snoq. *O. clarki*/ Cedar *O. clarki*, 5%) were sampled in the lower South Fork as were hatchery/ native mixed coastal cutthroat (5%) and hatchery/ native mixed hybrids (13%). Between the Sallal Prairie segment and the North Bend - Three Forks segments the proportion of genetically pure native coastal cutthroat (Snoq. *O. clarki*) increased (7% v. 50%, Figures 6 and 7).

Mainstem Snoqualmie and the Three Forks segments

In the three forks segment of each fork numbers of pure native coastal cutthroat increased and this pattern continued into the mainstem Snoqualmie River. A majority of samples consisted of pure Snoq *O. clarki* (Figures 6 and 7).

Discussion

The trout collected in the USRW are a complex mix of native coastal cutthroat trout, native rainbow trout, introduced hatchery rainbow trout, introduced hatchery coastal and westslope cutthroat trout, and fish with mixed hatchery and wild ancestry of both species. Although golden trout were planted in the system, we found no evidence suggesting that the collection included golden trout. We identified native trout by comparing USRW trout genetically to local native trout populations and to hatchery rainbow and cutthroat trout that had been stocked in the region. Native Snoqualmie cutthroat trout were genetically more similar to native South Puget Sound cutthroat trout than to hatchery cutthroat trout whose original broodstock was from North Puget Sound. Further, the Snoqualmie cutthroat trout were distinct from other South Puget Sound cutthroat trout, indicating that they were restricted to the Snoqualmie River. Native Snoqualmie rainbow trout were also distinct in comparisons to hatchery and native Puget Sound rainbow trout.

North Fork Snoqualmie River

The majority of trout in the upper and middle North Fork sections were of hatchery origin, which might suggest that native trout production is inherently limited in these sections. We found weak genetic signals of native *O. clarki* and *O.mykiss* in individuals sampled from these sections, but native genetic signals were overwhelmed by hatchery genetic signals. Habitat in the Calligan and Black Canyon river segments seem to be the least diverse as off-channel habitat is more limited compared to other segments in the USRW (Thompson et al. 2011). The combination of low production and a lack of habitat diversity may have rendered native populations more vulnerable to colonization by introduced hatchery lineages. Hatchery fish introduced in multiple sequential plantings may have been relatively unchallenged if there were few native fish and little habitat complexity and thus no specialized niche for native fish. In contrast, the lower North Fork contained a greater density of complex habitat and higher trout production than other North Fork river sections (Thompson et al. 2011) and also contained the only pure native trout encountered in the North Fork during this study.

Middle Fork Snoqualmie River

Native coastal cutthroat trout dominated the species composition and distribution in the Middle Fork (Snoqualmie *O. clarki* 74% of genetic samples). Some unidentified Pacific trout were sampled in the upper and lower Middle Fork, but overall native coastal cutthroat trout were the most abundant game fish in all river sections of the Middle Fork. In contrast to the North Fork, the Middle Fork is productive and contains a highly diverse system of habitats (Thompson et al. 2011). These two factors probably helped native trout outcompete their introduced hatchery counterparts as high numbers of locally-adapted native fish already occupied the wide array of habitats when less well-adapted hatchery-strains were being stocked into the Middle Fork.

South Fork Snoqualmie River

The South Fork contained the most diverse and complex composition of trout in the USRW. Westslope cutthroat dominated most of the steepest portions of the upper South Fork, but essentially were limited to this river section. Given that there are records for stocking this variety of hatchery cutthroat trout somewhere in the South Fork, it is likely that these westslope cutthroat trout are descendants of hatchery fish stocked into the South Fork or recruited from stocked alpine lakes. Since this variety has not been stocked lately, hatchery fish may have found an unoccupied or partially occupied niche and were thus unchallenged or maybe able to exploit the resources more effectively than the sparser native trout population, especially if they were stocked multiple times.

Downstream of the steep bedrock-cascade portion of the upper South Fork the channel levels off at the Asahel Curtis segment, the area where a high proportion of sampled fish were identified as native coastal cutthroat (Cedar *O. clarki*). The external characteristics of these cutthroat trout were distinct from cutthroat trout found in all other river segments (Thompson et al. 2011). They lacked the typical narrow, elongated body, the yellow body color, and did not have the pattern of spots that cover the entire body. Instead their spots were larger in diameter and more clustered on the posterior end of the fish, much like spotting on a westslope cutthroat (see Figure 24a). Native hybrids (Cedar *O. clarki*/ Cedar *O. mykiss*) were also found in the Asahel Curtis segment and native rainbow and hybrids were found in all South Fork river segments downstream of this point except the lowermost Three Forks segment. The Grouse Ridge and Weeks Falls segments in the Mid SF were heavily populated by native Cedar strain rainbow trout (50%) and hybrids (21%).

Interestingly, Snoqualmie-type native cutthroat and rainbow trout were limited to the lower portion of the South Fork below Twin Falls and Cedar-type native cutthroat and rainbow trout were found above Twin Falls. There is a causal mechanism for the high proportion of Cedar strain trout in the South Fork upstream of Twin Falls suggested by the most recent glacial activity in the USRW (c. 14,000 ybp, see Figure 8). Before the Vashon Lobe of the Cordilleran ice sheet protruded into the region now occupied by the USRW, the upper Cedar River was the acting 'South Fork' of the Snoqualmie. After the Vashon Lobe retreated from the USRW it left a number of moraines, one of which diverted the Cedar River away from the Snoqualmie basin. However, water from the Cedar River drainage continued to flow through the moraine in the direction of the Snoqualmie basin (Figure 8, MacKin 1941, Booth 1990, Bethel 2004, Fenner 2008). That porous moraine still exists and conveys groundwater from Masonry Pool in the upper Cedar River watershed to its western slopes where the spring-fed headwaters of Boxley Creek originate, eventually flowing into the South Fork Snoqualmie. Cedar River-type trout probably migrated into the South Fork prior to the last Cordilleran encroachment, and Twin Falls, which was exposed after the last Cordilleran retreat, subsequently blocked upstream colonization by Snoqualmie-type trout. Thus, it seems the timeline of glacial activity and exposure of Twin Falls as a barrier to upstream migration were the main influences on the current distribution of native trout varieties in the South Fork, which was also heavily stocked with both rainbow and cutthroat hatchery trout.

Hatchery fish introductions also appear to influence the genetic structure of trout in the lower South Fork. For example, a private hatchery operates downstream of Twin Falls on Boxley Creek and large-bodied hatchery rainbow trout that had escaped from holding ponds in the hatchery have been captured outside of the hatchery recently (Thompson et al. 2011). Confirmed hatchery rainbow trout, identified by genetic analysis, were found in this vicinity of the main stem South Fork and may have originated from this facility if trout commonly escape. It is unknown how many trout escape from this facility or other water bodies that contain hatchery fish (e.g., private ponds) but their genetic signature is found in the trout in the basin. More intensive genetic profiling centered on these water bodies might be warranted to determine the degree of influx and introgression of trout from the hatchery into the fishery.

Conclusion

The Puget Sound region has an interesting glacial and geologic history overlain by anthropogenic activities. Pleistocene glaciers blocked drainages and formed temporary impoundment lakes that spanned present-day watershed borders, creating dynamic interconnections among waterways and providing refuge lakes for native trout. Tectonic activities further altered landscape features, forming barrier falls within basins. Europeans moving into the area added another layer of complexity by creating anthropogenic barriers (e.g., culverts) and by planting hatchery fish. Further examination of location and genetic identities of trout in relation to detailed hatchery stocking history will inform fish managers on the impact of hatchery planting on native fish and the persistence of native fish in the Upper Snoqualmie River Watershed.

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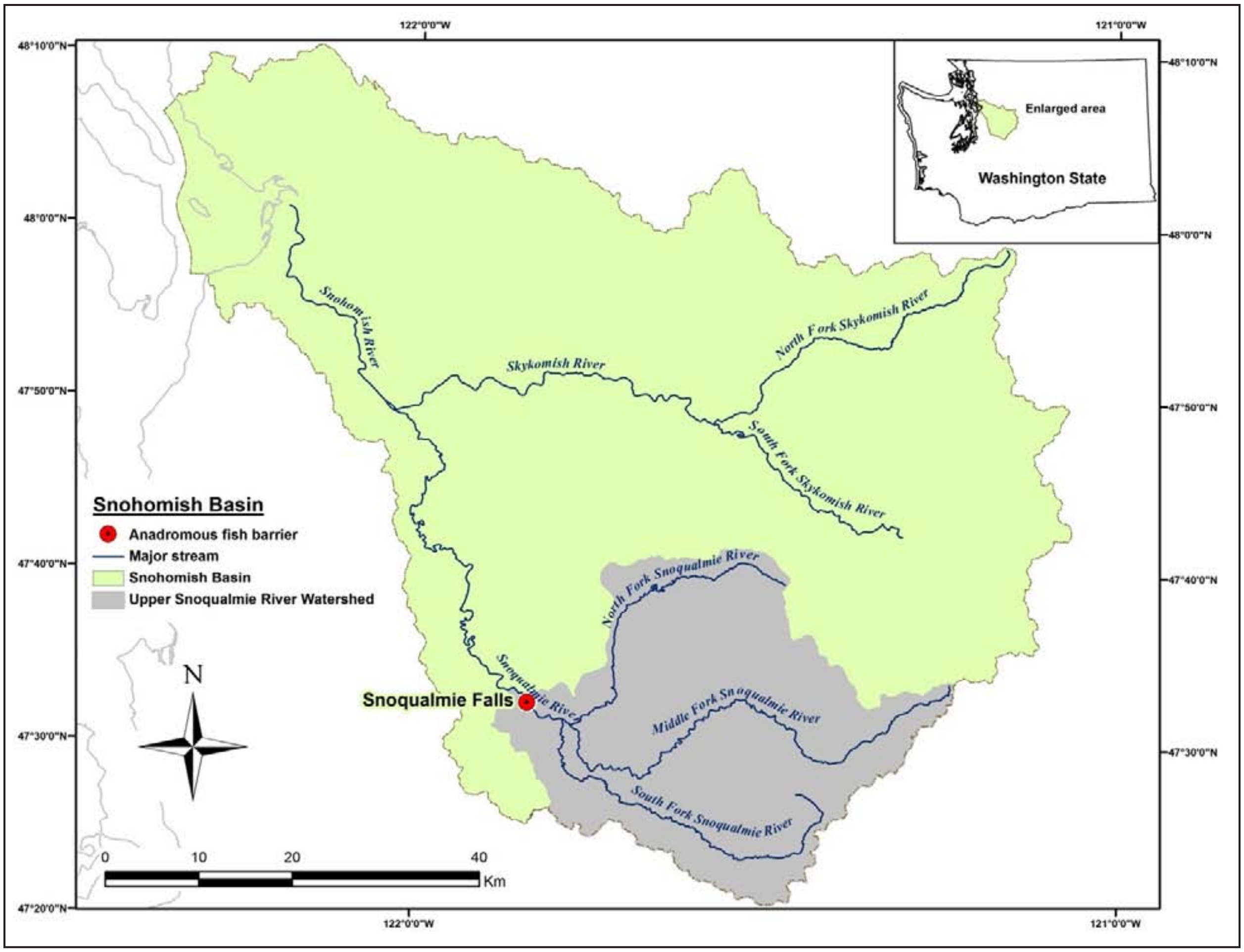

Figure 1. Map of the Snoqualmie, Skykomish and Snohomish watersheds. The upper Snoqualmie River watershed (USRW) is isolated by Snoqualmie Falls and is highlighted in grey.

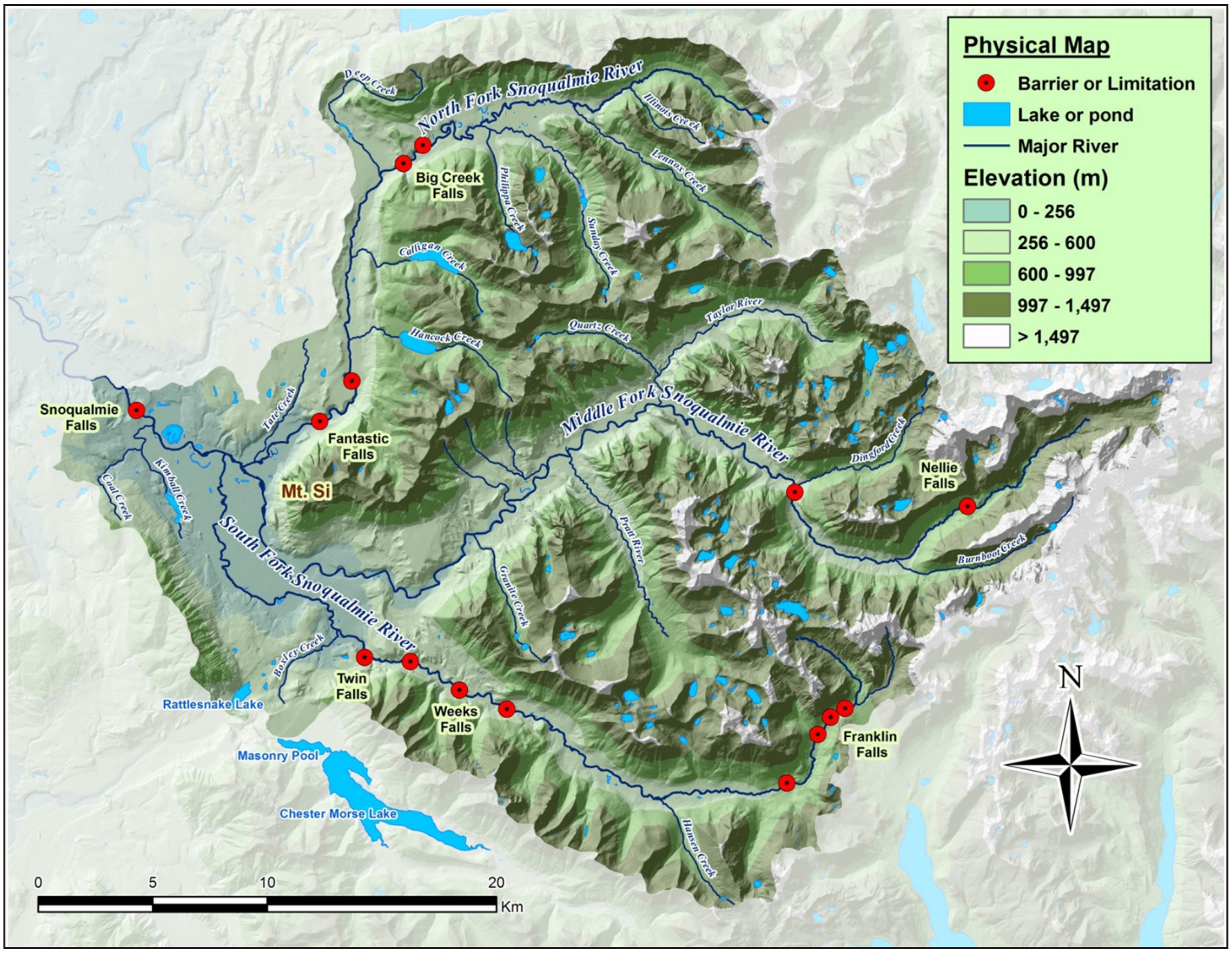

Figure 2. Physical map of the USRW showing the minimum known major barriers and limitations to fish movement. Chester Morse Lake and Masonry Pool (upper Cedar River watershed) are shown because they are linked to the South Fork Snoqualmie River through a glacial moraine near the headwaters of Boxley Creek.

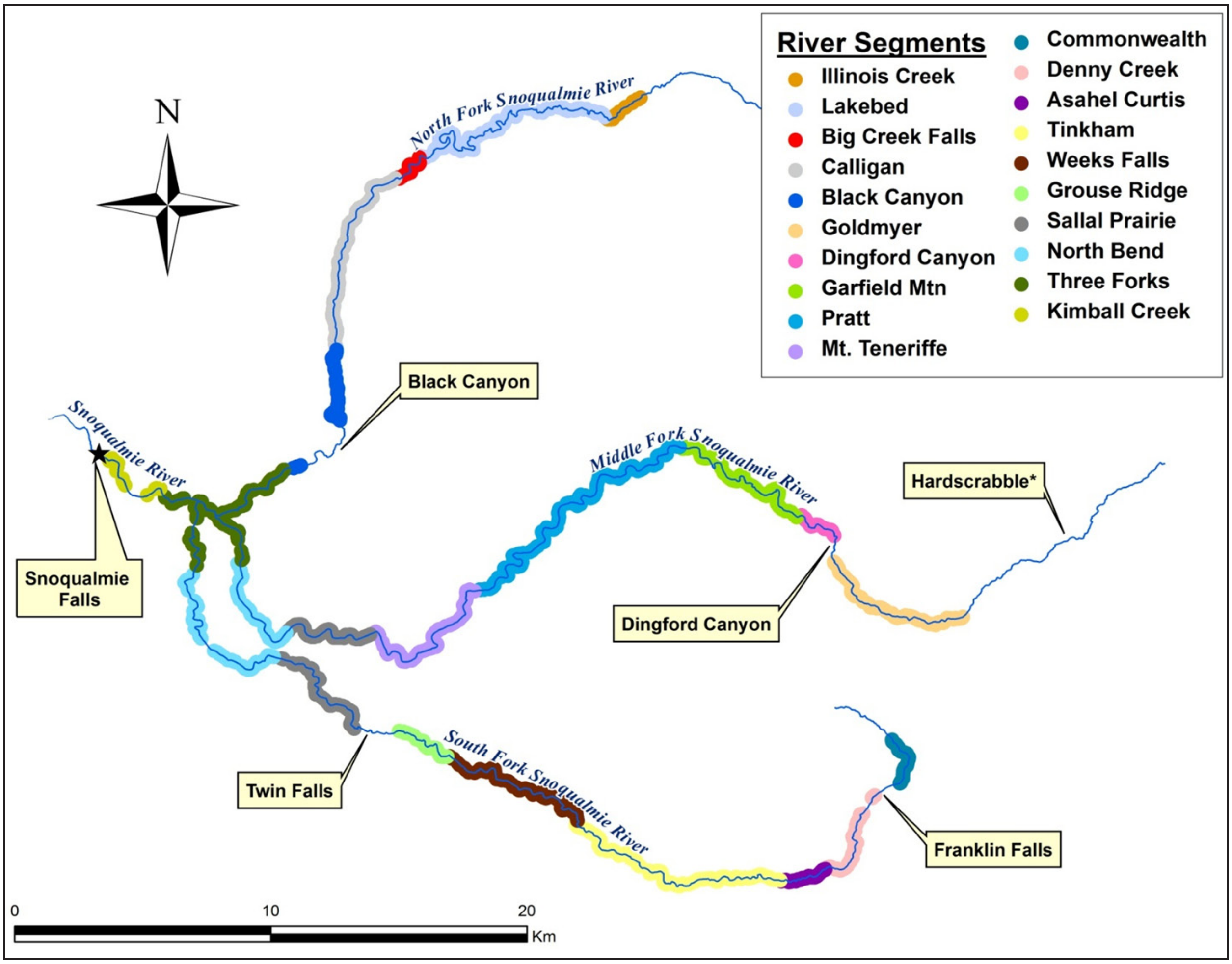

Figure 3. Color-coded river segment divisions show spatial strata for genetic sample collections. Genetic samples were obtained from each river segment and from the Hardscrabble reach in the upper Middle Fork Snoqualmie River, but were not obtained in the Commonwealth (Upper South Fork) or canyon/ falls reaches.

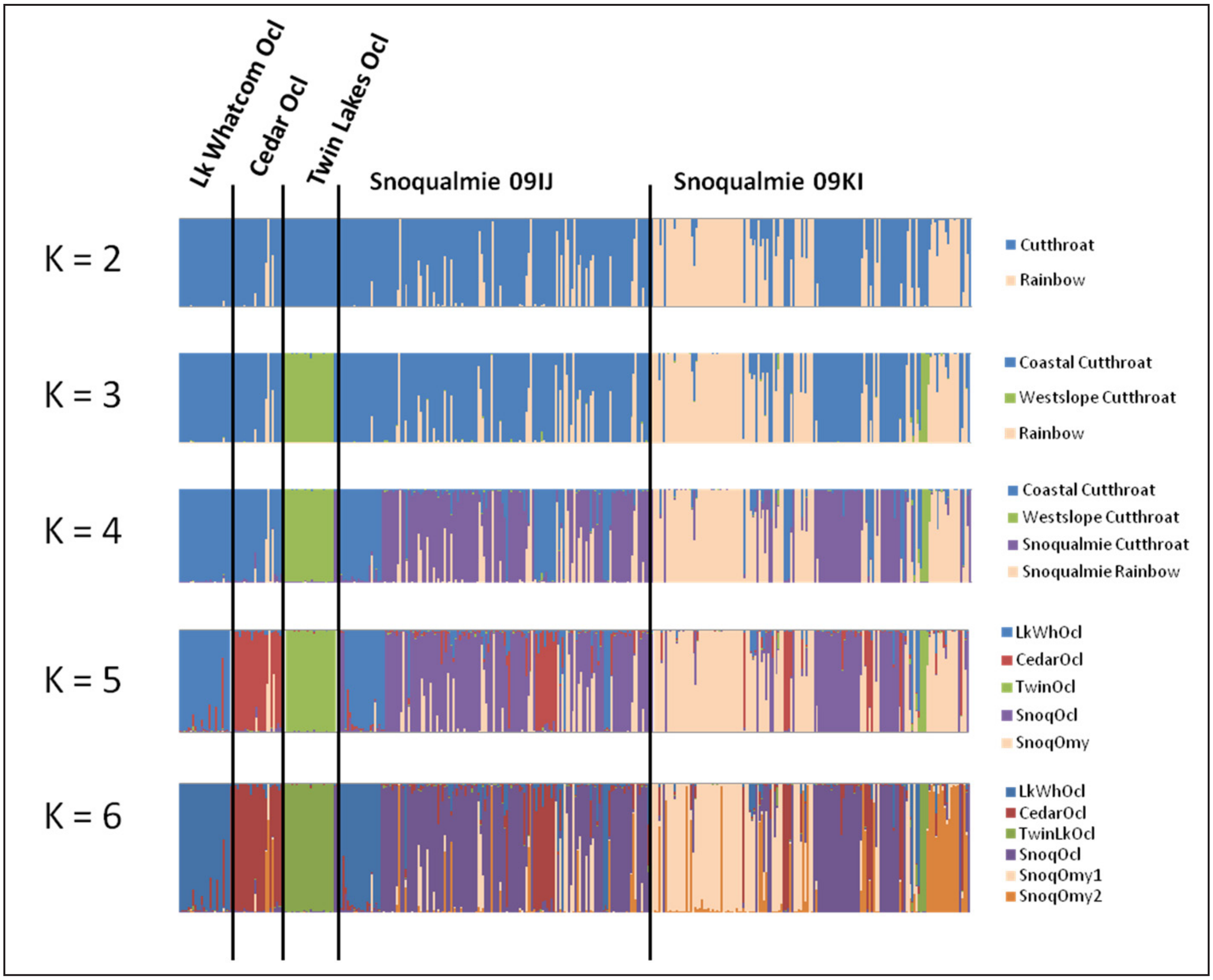

Figure 3a. STRUCTURE plot for K = 2 to K = 6. Each individual fish is represented by a bar of color, with the color corresponding to a genetic cluster or group. The genetic cluster is identified by the most common individuals in the cluster (e.g., at K = 3, one cluster is occupied by westslope cutthroat trout from Twin Lakes and the few unknown trout from the USRW that are also in that cluster are likely westslope cutthroat trout). Figure 3a shows the results of a hierarchical analysis where at increased K values, the data set partitioned according to species and then according to geographic structure and hatchery broodstocks. At K = 2, there are two genetic groups and these are occupied by cutthroat trout and rainbow trout. At K = 3, the westslope cutthroat trout break away from the coastal cutthroat trout and occupy their own cluster. At K = 4, the Snoqualmie cutthroat trout break away from the coastal cutthroat trout and occupy their own cluster. At K = 5, the Cedar cutthroat trout break away from the coastal cutthroat trout and occupy their own cluster and the Lake Whatcom cutthroat trout remain in a single cluster that includes some USRW cutthroat trout that were likely derived from Lake Whatcom broodstock. At K = 6, the Snoqualmie rainbow trout break into two clusters, 1) a putative hatchery rainbow trout cluster and 2) a putative native rainbow trout cluster. At K = 6 clusters are named as follows: Lake Whatcom coastal cutthroat trout = LkWhOcl, Cedar River coastal cutthroat trout = CedarOcl, Twin Lakes westslope cutthroat trout = TwinOcl, Snoqualmie coastal cutthroat trout = SnoqOcl, Snoqualmie rainbow trout = SnoqOmy1 (hatchery rainbow) and SnoqOmy2 (native rainbow).

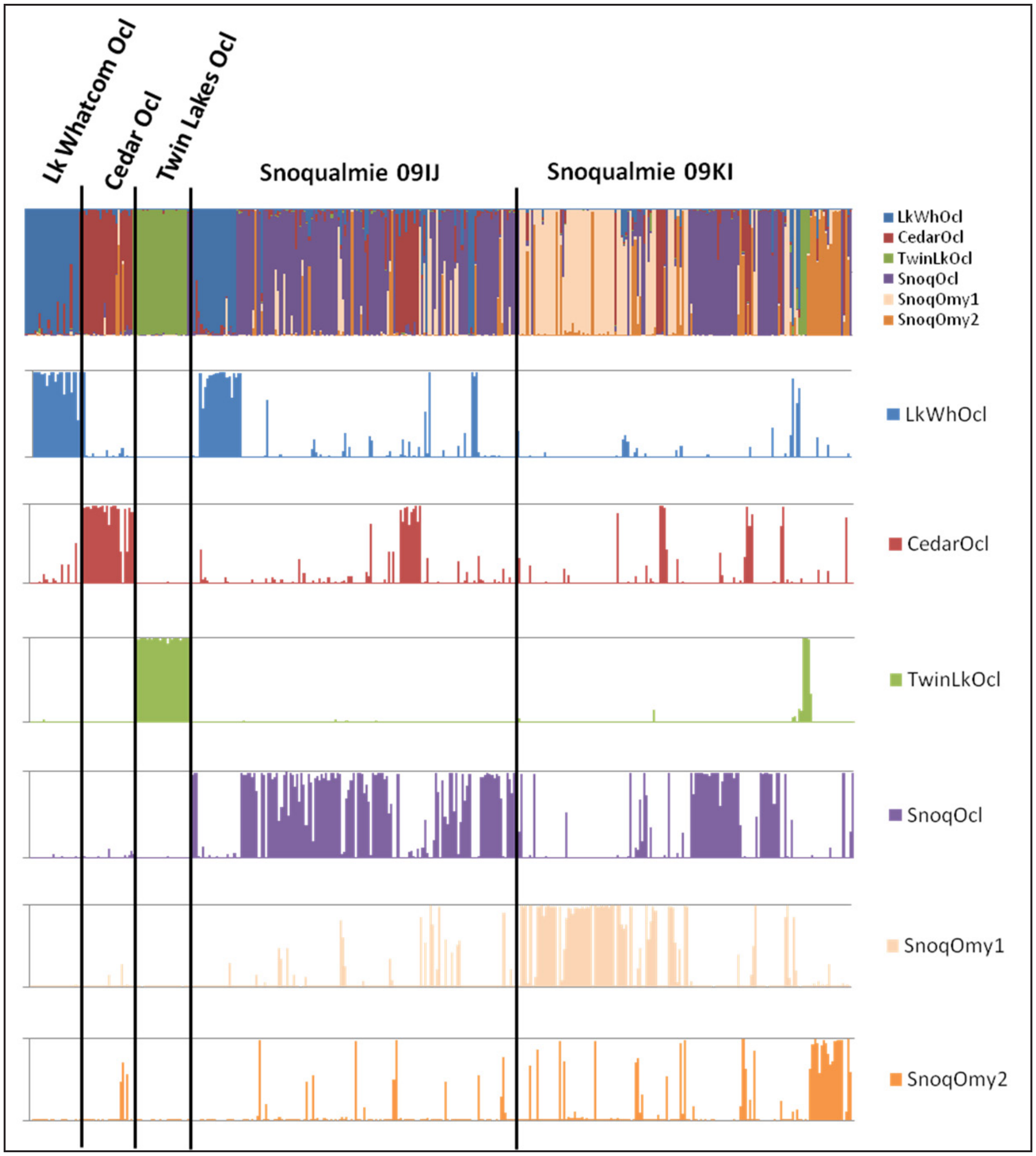

Figure 3b. This shows the breakdown of the STRUCTURE result for K = 6 from Figure 3a. The plot at the top is decomposed into its individual clusters below to enhance viewing of individual fish and membership in clusters (genetic groups). The genetic groups are labeled according to the most common member in the genetic group and nomenclature follows Figure 3a.

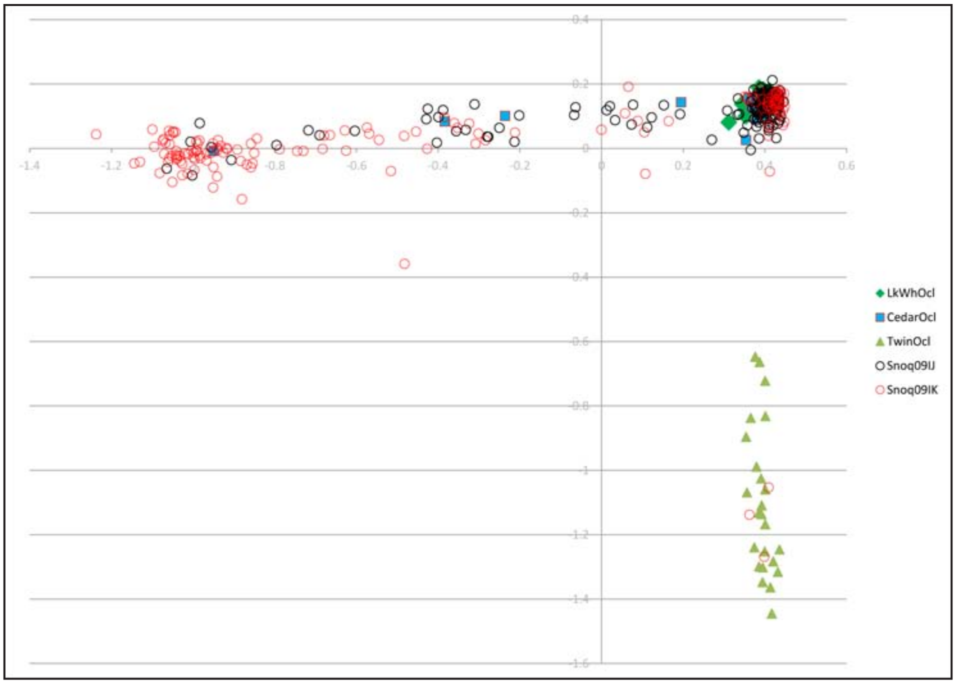

Figure 4. Factorial correspondence analysis (FCA) from GENETIX. Each individual fish is plotted in two dimensional space defined by two axes that explain the maximum amount of genetic variance in the data set. Individuals were genotyped with the full suite of loci (microsatellites and SNPs). Each collection type is indicated by a unique marker (Lake Whatcom coastal cutthroat trout = LkWhOcl, Cedar River coastal cutthroat trout = CedarOcl, Twin Lakes westslope cutthroat trout = TwinOcl, Snoqualmie 09IJ (mostly cutthroat trout) = Snoq09IJ and Snoqualmie 09IK (mostly rainbow trout) = Snoq09IK. Note: the USRW rainbow trout plotted with the Twin Lakes westslope cutthroat trout had been identified in the field as possible westslope cutthroat trout (see Table 6). Also note: many cutthroat trout plotted close to or on top of each other on the right side of the first axis. See Figure 5a for plot of collection centers rather than individuals.

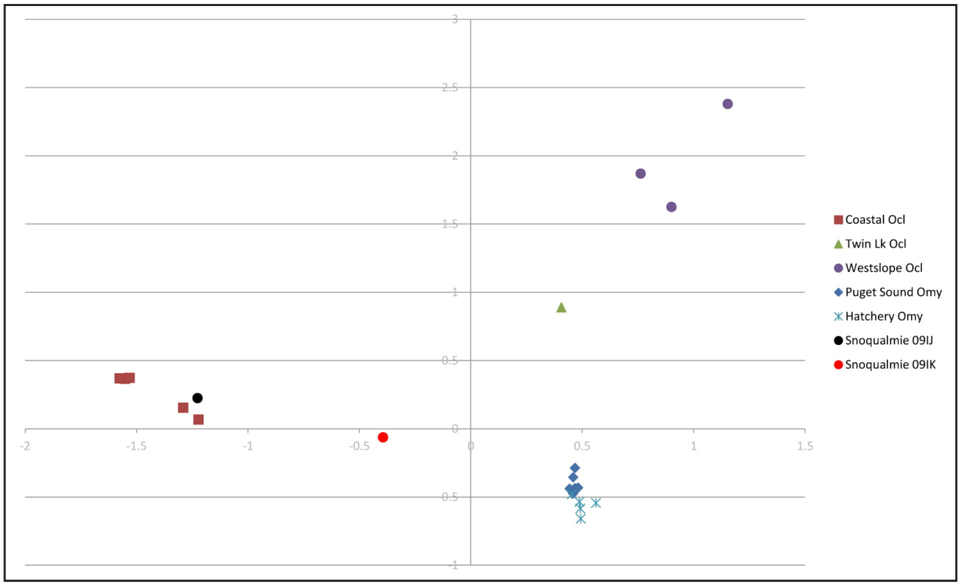

Figure 5a. FCA plot with contemporary and archived WDFW data comparison (five microsatellite loci). Only collection centers are shown in this plot; the collection center is the center of the distribution of all the individuals in the genetic space defined by the axes in the FCA. In addition to Lake Whatcom and Cedar River coastal cutthroat trout, the analysis included two other cutthroat trout collections from Puget Sound from Bear and Minter creeks (all listed as "Coastal Ocl). The Snoqualmie 09IJ (mostly cutthroat trout) cluster with the coastal cutthroat trout collections. The westslope cutthroat trout collections included Twin Lakes Hatchery broodstock (Twin Lk Ocl) and three collections from the Pend Oreille basin (westslope Ocl). The Puget Sound rainbow trout (Puget Sound Omy) included eight collections from Puget Sound tributaries (Cedar, Green and Puyallup rivers and Chester Morse Lake). Also included are four hatchery rainbow trout broodstocks (Hatchery Omy) that had been planted throughout Washington State. The Puget Sound Omy and the Hatchery Omy separated from each other on the third axis (not shown in this plot). Note that the Snoqualmie 09IK (mostly rainbow trout) plotted between the cutthroat trout and the rainbow trout collection centers since cutthroat trout were mixed in with the rainbow trout.

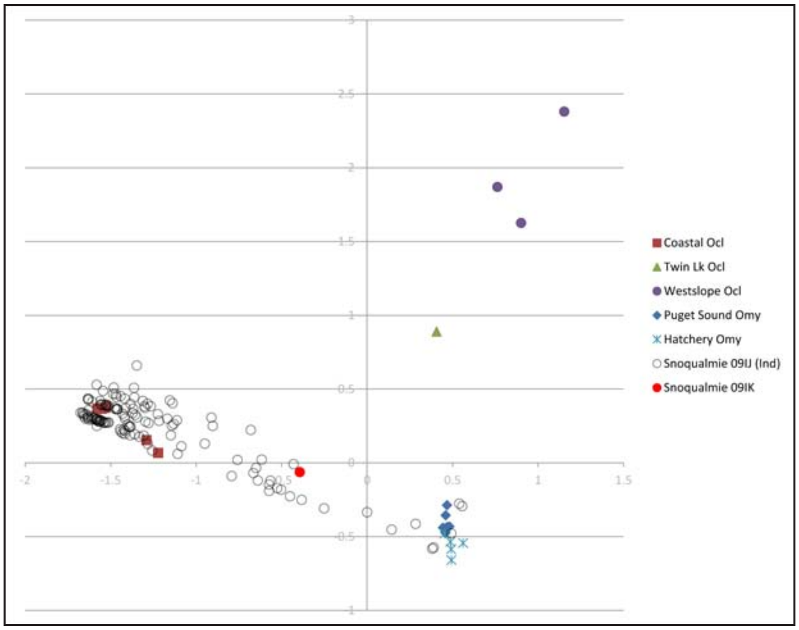

Figure 5b. The Snoqualmie 09IJ individuals (ind, mostly cutthroat trout) are plotted over the collection centers in the FCA plot from Figure 5a.

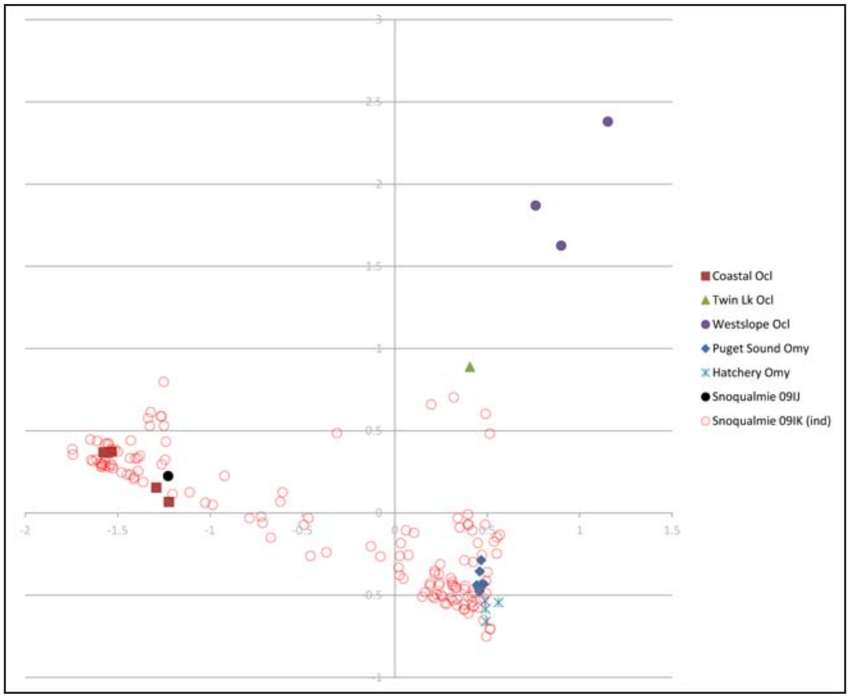

Figure 5c. The Snoqualmie 09IK individuals (ind, mostly rainbow trout) are plotted over the collection centers in the FCA plot from Figure 5a.

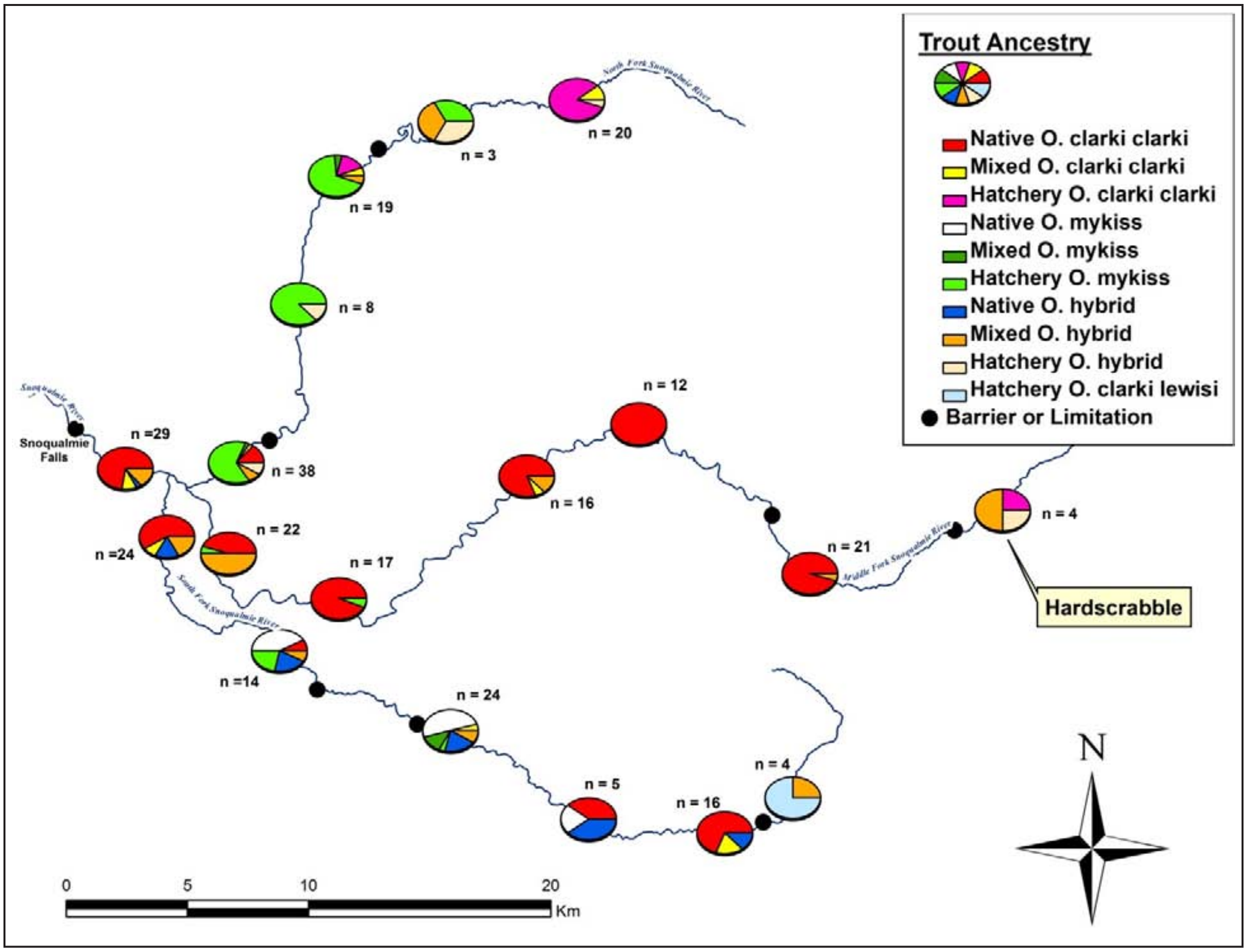

Figure 6. Inter-basin distribution of native and hatchery-origin lineages of Pacific trout in the USRW. Pie charts represent approximate sample locations. Captions next to pie charts indicate the total sample size for each pie chart. Species abbreviations: *O. clarki clarki* = coastal cutthroat, *O. mykiss* = rainbow trout, *O*. hybrid = hybrid between Pacific trout species.

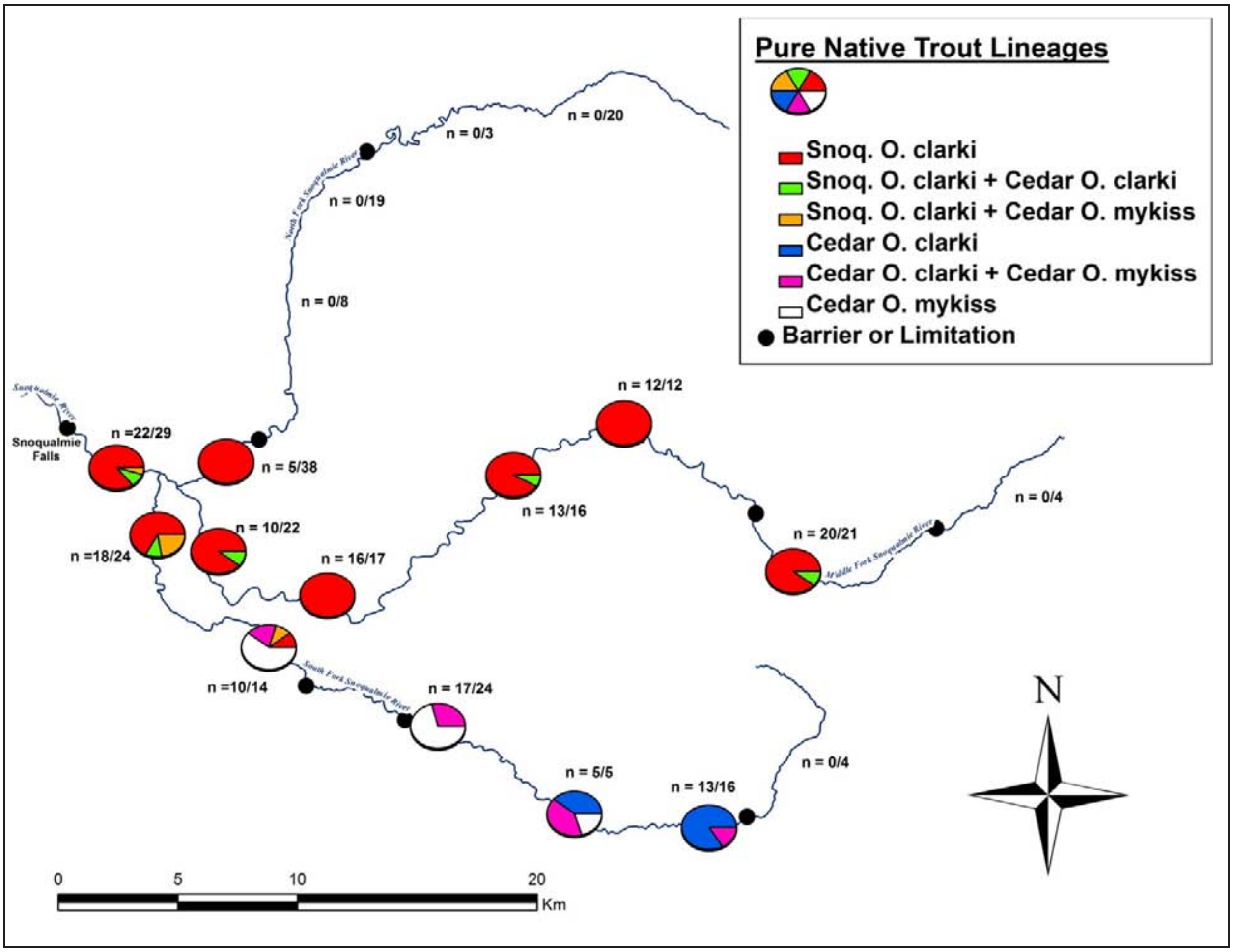

Figure 7. Inter-basin distribution of pure native lineage Pacific trout in the USRW. Pie charts represent approximate sample locations. Captions next to pie charts indicate a ratio of the total number of pure native trout per total sample size for each river segment. Abbreviations: Snoq. = upper Snoqualmie River watershed, Cedar = Cedar River watershed, *O. clarki* = coastal cutthroat, *O. mykiss* = rainbow trout.

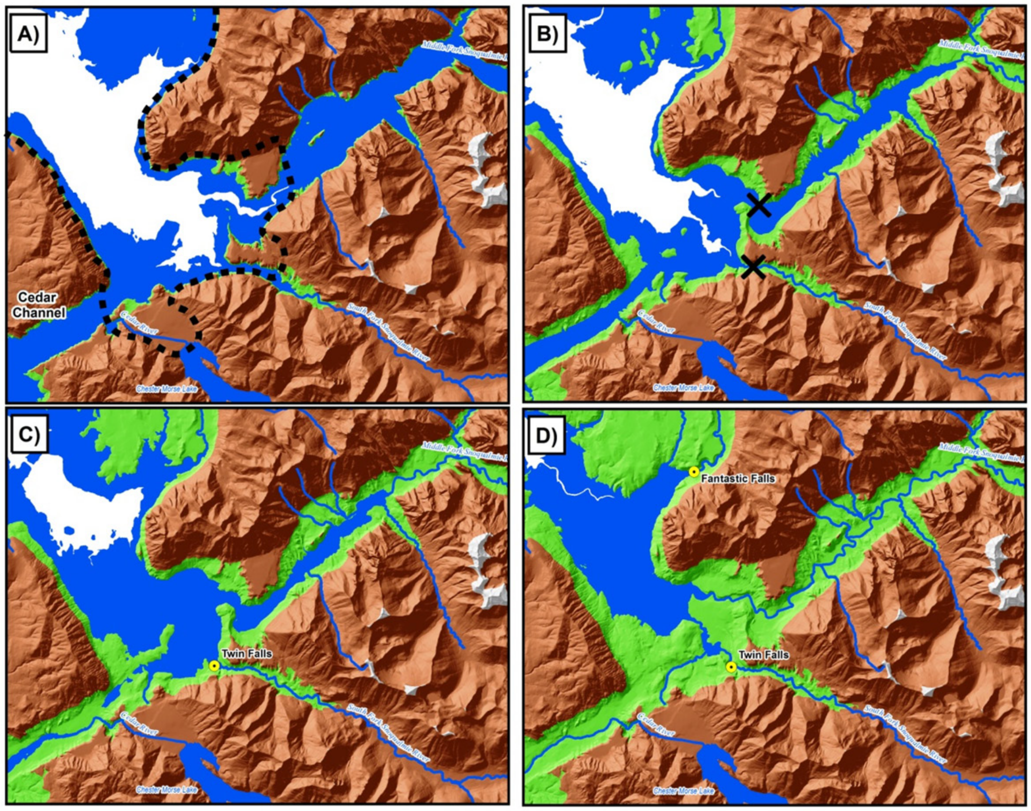

Figure 8. Conceptual illustration of the latter stages of the Vashon-Puget glacial recession (white) from the USRW (A–D: relative oldest to more recent periods). The Cedar Channel served as the original outlet of Lake Snoqualmie (blue – panel A), where native Cedar-strain coastal cutthroat and rainbow trout moved freely between the Cedar and Snoqualmie drainages. The furthest eastern extent of glacial encroachment in the USRW (black hashes – panel A) was located at the Grouse Ridge (upper X) and Cedar (lower X) moraines (panel B), which blocked the South Fork, Middle Fork, and upper Cedar River valleys until both moraines were eroded at differing rates during later periods (panels C and D). See additional conceptualizations in (MacKin 1941).

Table 1a. History of hatchery Pacific trout stockings in the North Fork, USRW (1933–1989). Stocking data were queried from 0–94Relhistoric.mdb, Stocking data were categorized by river section where release location data were available.

				1933–1989					
Fork	**River Section***	**Hatchery Facility**	**Stock**	**Coastal cutthroat**	**Cutthroat**	**Rainbow**	**Westslope cutthroat**	**Golden**	**Total**
North Fork					**422,426**	**1,345,422**			**1,767,848**
	Up				18,410	17,925			36,335
		Arlington			*2,996*				*2,996*
		Tokul Creek			*15,414*	17,925			*33,339*
	Mid				*52,170*	466,943			519,113
		Arlington				55,980			*55,980*
		Tokul Creek			*52,170*	410,963			*463,133*
	Low				23,000	134,252			157,252
		Arlington				12,537			*12,537*
		Seward Park				4,756			*4,756*
		Tokul Creek			*23,000*	116,959			*139,959*
	Unspecified				328,846	726,302			1,055,148
		Arlington				7,600			*7,600*
		Seward Park			*6,000*	177,160			*183,160*
		Tokul Creek			*322,846*	510,542			*833,388*
		Tokul Creek	*Mt. Whitney*			*31,000*			*31,000*

*All stocked bodies of water that drain into the specified River Section were pooled; includes ponds, lakes, tributaries and main stem channels.

Table 1b. History of hatchery Pacific trout stockings in the Middle Fork, USRW (1933–1989). Stocking data were queried from 0–94Relhistoric.mdb, Stocking data were categorized by river section where release location data were available.

				1933–1989					
Fork	**River Section***	**Hatchery Facility**	**Stock**	**Coastal cutthroat**	**Cutthroat**	**Rainbow**	**Westslope cutthroat**	**Golden**	**Total**
Middle Fork					**419,002**	**1,406,899**		**5,984**	**1,831,885**
	Up				20,406	6,909		5,984	33,299
		Arlington			*750*				750
		Lakewood				3,134			3,134
		Naches			*9,000*				9,000
		Tokul Creek			*10,656*	3,775		5,984	20,415
	Mid				108,344	296,363			404,707
		Arlington				12,720			12,720
		Montlake				600			600
		Montlake	*Mt. Whitney*			900			900
		Tokul Creek			*108,344*	282,143			390,487
	Low					300			300
		Tokul Creek				300			300
	Unspecified				290,252	1,103,327			1,393,579
		Arlington				5,140			5,140
		Chiwaukum			*10,500*				10,500
		Lakewood				7,099			7,099
		Naches				3,060			3,060
		Seward Park			*1,300*	115,975			117,275
		Tokul Creek			*278,452*	921,653			1,200,105
		Tokul Creek	*Mt. Whitney*			*50,400*			*50,400*

*All stocked bodies of water that drain into the specified River Section were pooled; includes ponds, lakes, tributaries and main stem channels.

Table 1c. History of hatchery Pacific trout stockings in the South Fork and Mainstem Snoqualmie, USRW (1933–1989). Stocking data were queried from 0–94Relhistoric.mdb, Stocking data were categorized by river section where release location data were available.

				1933–1989					
Fork	**River Section***	**Hatchery Facility**	**Stock**	**Coastal cutthroat**	**Cutthroat**	**Rainbow**	**Westslope cutthroat**	**Golden**	**Total**
South Fork				2,255	732,610	1,139,936	720		1,875,521
	Up				151,443	129,302			280,745
		Arlington				*900*			*900*
		NMFS				*600*			*600*
		Seward Park				*10,000*			*10,000*
		Tokul Creek			*151,443*	*117,802*			*269,245*
	Mid				66,100				66,100
		Tokul Creek			*66,100*				*66,100*
	Low				16,822	1,156			17,978
		Tokul Creek			*16,822*				*16,822*
		Tokul Creek	*Mt. Whitney*			*1,156*			*1,156*
	Unspecified			2,255	498,245	1,009,478	720		1,510,698
		Kittitas			*50,000*	*25,000*			*75,000*
		N/A			*1,488*				*1,488*
		Naches				*3,060*			*3,060*
		Puyallup Tribal				*4,000*			*4,000*
		Rattlesnake Lk			*67*				*67*
		Seward Park			*7,000*	*291,313*			*298,313*
		Tokul Creek			*439,690*	*645,072*			*1,084,762*
		Tokul Creek	*Twin Lakes*				720		*720*
		Tokul Creek	*Mt. Whitney*			*41,033*			*41,033*
		Tokul Creek	*Lk. Whatcom*	*2,255*					*2,255*
Mainstem					12,527	208,333			220,860
	Low				*12,527*	*208,333*			*220,860*
		Seward Park				*23,941*			*23,941*
		Tokul Creek			*12,527*	*184,392*			*196,919*
Total		**Grand Total**		**2,255**	**745,137**	**1,348,269**	**720**	**0**	**2,096,381**

*All stocked bodies of water that drain into the specified River Section were pooled; includes ponds, lakes, tributaries and main stem channels.

Table 1d. History of hatchery Pacific trout stockings in the USRW (1990–2007). Stocking data were queried from 0–94Relhistoric.mdb, Stocking data were categorized by river section where release location data were available.

				1990–2007					
Fork	**River Section***	**Hatchery Facility**	**Stock**	**Coastal cutthroat**	**Cutthroat**	**Rainbow**	**Westslope cutthroat**	**Golden**	**Total**
Middle Fork						**2745**			**2745**
	Up					*150*			*150*
		Tokul Creek	*Mt. Whitney*			*150*			*150*
	Mid					*2595*			*2595*
		Tokul Creek				*2070*			*2070*
			Mt. Whitney			*525*			*525*
South Fork						**2140**	**3260**		**5400**
	Unspecified					*2140*	*3260*		*5400*
		Tokul Creek	*Goldendale - McCloud*			*1260*			*1260*
		Tokul Creek	*Twin Lakes*				*3260*		*3260*
		Tokul Creek	*Mt. Whitney*			*880*			*880*
Mainstem					**600**	**2038**			**2638**
	Low				*600*	*2038*			*2638*
		Arlington	*Goldendale - McCloud*			*1296*			*1296*
		Arlington	*Spokane*			*342*			*342*
		Puyallup	*Goldendale - McCloud*			*400*			*400*
		Tokul Creek			*600*				*600*
Snoqualmie Police Ponds	n/a	*Tokul Creek*	*Goldendale - McCloud*			*744*			**744**
Unspecified High Lake	n/a	*Reiter Ponds*						*100*	**100**
Total				**0**	**600**	**7667**	**3260**	**100**	**11627**

*All stocked bodies of water that drain into the specified River Section were pooled; includes ponds, lakes, tributaries and main stem channels.

Table 2. Number of trout samples collected among river sections and segments in the upper Snoqualmie River watershed (USRW).

River Section	River Segment	Sample size (n)
Upper North Fork		**20**
	Illinois Creek	20
Middle North Fork		**30**
	Lakebed	3
	Big Creek Falls	16
	Calligan	3
	Black Canyon	8
Lower North Fork		**38**
	Black Canyon	27
	Three Forks	11
Upper Middle Fork		**25**
	Hardscrabble	4
	Goldmyer	18
	Dingford	3
Middle Middle Fork		**28**
	Garfield Mtn.	12
	Pratt	16
Lower Middle Fork		**39**
	Mt. Teneriffe	14
	Sallal Prairie	3
	North Bend	21
	Three Forks	1
Upper South Fork		**20**
	Denny Creek	4
	Asahel Curtis	16
Middle South Fork		**29**
	Tinkham	5
	Weeks Falls	11
	Grouse Ridge	13
Lower South Fork		**38**
	Sallal Prairie	14
	North Bend	22
	Three Forks	2
Upper Mainstem		**21**
	Three Forks	21
Lower Mainstem		**8**
	Three Forks	8
Total		**296**

Table 3. Microsatellite and SNP loci used in Snoqualmie River trout genetic study. To simplify nomenclature, WDFW gives SNP loci a nickname associated in the database with the original name. Both names are given in the table. Species ID SNPs are indicated by "SpI" in the WDFW nickname. Names are followed by the percentage of samples that were genotyped at each SNP locus "% genotyped".

	SNPS					
Microsatellites	**WDFW_name**	**AssayName:**	**% worked**	**WDFW_name**	**AssayName:**	**% worked**
Ogo-3	AOmy001	Omy_180	95.05%	AOmy125	Omy_u09-56.119	89.06%
Omm1138	AOmy004	Omy_ALDOA_1	84.64%	AOmy126	Omy_ADP-r3.159	31.77%
One-108	AOmy005	Omy_aspAT.123	96.09%	AOmy127	Omy_BAMBI2.312	90.10%
Ots-103	AOmy006	Omy_B1.266	95.57%	AOmy128	Omy_BAMBI4.112	95.05%
Omy-77	AOmy007	Omy_B9.164	0.00%	AOmy129	Omy_BAMBI4.238	95.57%
Ots-1	AOmy009	Omy_CRB_F_1	95.05%	AOmy131	Omy_G3PD_2.191	37.24%
Ots-3M	AOmy013	Omy_DM20_2_1	95.05%	AOmy132	Omy_G3PD_2.246	91.67%
	AOmy015	Omy_gdh.271	95.31%	AOmy133	Omy_G3PD_2.371	94.53%
	AOmy016	Omy_GH1P1_2	95.05%	AOmy134	Omy_Il-1b_.028	89.58%
	AOmy017	Omy_HOXD_1_1	95.05%	AOmy135	Omy_Il-8r1.101	95.05%
	AOmy018	Omy_ID_1	95.83%	AOmy136	Omy_MyoCL2.108	94.53%
	AOmy019	Omy_LDH	95.83%	AOmy137	Omy_u09-61.043	95.57%
	AOmy020	Omy_LDH.156	94.01%	AOmy138	Omy_u09-61.107	94.53%
	AOmy021	Omy_LDHB-2_e5	94.53%	AOmy139	Omy_u09-63.173	83.85%
	AOmy024	Omy_myo1a.264	0.00%	AOmy140	Omy_u09-64.062	91.93%
	AOmy027	Omy_nkef.241	95.57%	AOmy141	Omy_u09-64.108	0.00%
	AOmy036	Omy_sSOD	94.79%	AOmy142	Omy_u09-64.147	46.35%
	AOmy038	Omy_BAC-B4.324	0.00%	AOmy143	Omy_u09-66.139	95.57%
	AOmy039	Omy_BAC-B4.388	0.00%	AOmy144	Omy_UT16_2.173	0.00%
	AOmy040	Omy_BAC-F5.238	95.31%	AOmy145	Omy_BAC-B9.125	34.11%
	AOmy042	Omy_BAC-F5.284	94.79%	AOmy146	Omy_U11_2a.114	94.53%
	AOmy047	Omy_u07-79.166	95.57%	AOmy147	Omy_U11_2b.154	95.05%
	AOmy051	Omy_121713-115	95.57%	AOmy148	Omy_dacd1-131	95.05%
	AOmy055	Omy_127236-583	95.31%	AOmy149	Omy_gluR-79	95.05%
	AOmy062	Omy_97077-73	95.31%	AOmy150	0my_Il-1b.198	88.80%
	AOmy065	Omy_97954-618	95.83%	AOmy151	Omy_p53-262	69.27%
	AOmy067	Omy_aromat-280	33.07%	AOmy152	Omy_SECC22b-88	0.00%
	AOmy068	Omy_arp-630	31.77%	AOmy153	Omy_UT11_2.046	94.53%
	AOmy071	Omy_cd59-206	40.63%	ASpI001	Ocl_Okerca	81.25%
	AOmy073	Omy_colla1-525	95.57%	ASpI002	Ocl_Oku202	94.01%
	AOmy079	Omy_g12-82	88.80%	ASpI003	Ocl_Oku211	0.00%
	AOmy081	Omy_gh-475	95.83%	ASpI004	Ocl_Oku216	93.49%
	AOmy089	Omy_hsp-90BA-193	32.55%	ASpI005	Ocl_Oku217	95.31%
	AOmy092	Omy_IL1b-163	95.31%	ASpI006	Ocl_SsaHM5	0.00%
	AOmy100	Omy_nach-200	95.83%	ASpI007	Ocl_u800	66.67%
	AOmy103	Omy_nkef-308	92.71%	ASpI008	Ocl_u801	89.06%
	AOmy108	Omy_oxct-85	94.01%	ASpI009	Ocl_u802	95.31%
	AOmy110	Omy_star-206	95.57%	ASpI010	Ocl_u803	94.79%

Table 3. (Continued)

	SNPS					
Microsatellites	**WDFW_name**	**AssayName:**	**% worked**	**WDFW_name**	**AssayName:**	**% worked**
	AOmy111	Omy_stat3-273	94.53%	ASpI011	Ocl_u804	47.66%
	AOmy112	Omy_tgfb-207	95.31%	ASpI012	Omy_B9_228	95.05%
	AOmy113	Omy_tlr3-377	95.57%	ASpI013	Omy_CTDL1_243	96.88%
	AOmy114	Omy_tlr5-205	95.31%	ASpI014	Omy_F5_136	95.57%
	AOmy117	u09-52.284	95.83%	ASpI015	Omy_HOXD_287	0.00%
	AOmy118	Omy_u09-53.469	95.57%	ASpI016	Omy_myc-larp404-111	0.00%
	AOmy120	Omy_u09-54.311	95.57%	ASpI017	Omy_my-clgh1043-156	94.79%
	AOmy121	Omy_u09-55.112	96.09%	ASpI018	Omy_Omy-clmk436-96	92.71%
	AOmy123	Omy_u09-55.233	94.27%	ASpI019	Omy_RAG11_280	93.23%
	AOmy124	Omy_u09-56.073	94.53%	ASpI020	Omy_URO_302	94.79%

Table 4. Genetic variance per locus (% var) among populations from ARLEQUIN (invariant loci are indicated by "fixed"). Loci identified as under selection in the FST outlier test are highlighted in yellow. Variance for loci under directional selection loci are in pink.

Locus	% var	Locus	% var	Locus	% var
Ogo-3	27.31	AOmy065	21.61	AOmy137	0.27
Omm1138	24.18	AOmy073	21.81	AOmy138	-0.19
One-108	10.92	AOmy079	fixed	AOmy139	34.35
Ots-103	24.04	AOmy081	3.07	AOmy140	26.11
Omy-77	12.80	AOmy092	5.83	AOmy143	fixed
Ots-1	13.15	AOmy100	15.19	AOmy146	11.56
Ots-3M	12.20	AOmy103	10.91	AOmy147	27.61
AOmy001	21.30	AOmy108	13.28	AOmy148	0.15
AOmy004	6.64	AOmy110	10.83	AOmy149	14.77
AOmy005	0.10	AOmy111	9.06	AOmy150	5.91
AOmy006	5.56	AOmy112	18.09	AOmy151	19.36
AOmy009	21.17	AOmy113	1.77	AOmy153	fixed
AOmy013	fixed	AOmy114	6.91	ASpI001	36.95
AOmy015	0.66	AOmy117	14.79	ASpI002	34.77
AOmy016	11.22	AOmy118	10.77	ASpI004	82.47
AOmy017	68.17	AOmy120	4.44	ASpI005	86.12
AOmy018	fixed	AOmy121	1.15	ASpI007	35.98
AOmy019	2.94	AOmy123	29.76	ASpI008	34.02
AOmy020	24.81	AOmy124	4.76	ASpI009	83.27
AOmy021	16.98	AOmy125	22.00	ASpI010	36.00
AOmy027	10.60	AOmy127	32.04	ASpI012	-0.52
AOmy036	5.28	AOmy128	0.16	ASpI013	39.08
AOmy040	37.05	AOmy129	1.36	ASpI014	37.18
AOmy042	23.93	AOmy132	1.80	ASpI017	33.45
AOmy047	8.48	AOmy133	1.47	ASpI018	35.46
AOmy051	2.09	AOmy134	18.14	ASpI019	34.56
AOmy055	-0.43	AOmy135	1.33	ASpI020	32.93
AOmy062	1.31	AOmy136	18.06		

Table 5. Analysis of molecular variance (AMOVA) with microsatellites (msats), SNPs and both locus sets combined (both). Values are the percentage of the molecular variance at each level: among populations, among individuals within populations, within individuals.

	averaged over all loci in respective data sets		
	msats only	**SNPs only**	**both**
Among populations	16.74	25.97	23.69
Among individuals within populations	14.56	33.18	28.59
Within individuals	68.70	40.85	47.72

Table 6. Count of different types of trout identified in the USRW from STRUCTURE analysis (see Table 7 for details). Fish had been field-identified to species, but were inconsistently grouped according to species ID (see Table 7 for field identifications and text for explanation of categories or types). Snoqualmie *O. mykiss* population 1 (SnoqOmy1) are putative hatchery ancestry fish and Snoqualmie *O. mykiss* population 2 (SnoqOmy2) are putative native rainbow trout. Lake Whatcom cutthroat trout (LkWhOcl) and Twin Lakes cutthroat trout (TwinOcl) are hatchery ancestry cutthroat trout. Cedar and Snoqualmie cutthroat trout (CedarOcl and SnoqOcl, respectively) are putative native cutthroat trout.

Types	Snoq 09IJ	Snoq 09IK
CedarOcl	7	6
CedarOcl-SnoqOcl	5	3
CedarOcl-SnoqOmy1	1	1
CedarOcl-SnoqOmy2	3	8
LkWhOcl	20	1
LkWhOcl-CedarOcl	5	1
LkWhOcl-SnoqOcl	7	1
LkWhOcl-SnoqOmy1	2	4
LkWhOcl-SnoqOmy2	1	1
LkWhOcl-TwinOcl		1
Ocl	1	
Ocl-Omy		1
Ocl-SnoqOmy1	1	1
Ocl-SnoqOmy2	1	2
Ocl-SnoqOmy1	1	2
SnoqOcl	69	35
SnoqOcl-SnoqOmy1	14	4
SnoqOcl-SnoqOmy1,2	1	2
SnoqOcl-SnoqOmy2	3	3
SnoqOmy1	3	46
SnoqOmy1,2		4
SnoqOmy2	3	16
TwinOcl		3
TwinOcl-SnoqOmy1		1
TwinOcl-SnoqOmy2		1
Total	148	148

Table 7. Genetic identities from STRUCTURE with field collection data. Field data are in the first seven columns, followed by the genetic type indicated by the STRUCTURE analysis: pure fish had at least 90% ancestry in a single cluster (pink cells) and mixed ancestry fish had more than 10% ancestry in at least one other cluster (green cells were 10% to 50% and yellow cells were 50% to 90%). Cells are colored to aid viewing the proportion of ancestry in each cluster. The ancestry proportion values are plotted in Figure 5. Ancestry type is listed under "Genetic ID".

Date	River Section	River Segment	TL (mm)	Field ID	Type	Fish ID	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy1	SnoqOmy2
9/17/09	Upper North Fork	Illinois Creek	225	CCT	LkWhOcl	09IJ0004	0.969	0.007	0.002	0.021	0.001	0
9/17/09	Upper North Fork	Illinois Creek	194	CCT	LkWhOcl-CedarOcl	09IJ0005	0.562	0.423	0.002	0.012	0.001	0.001
9/17/09	Upper North Fork	Illinois Creek	152	CCT	LkWhOcl-SnoqOcl	09IJ0006	0.81	0.049	0.002	0.137	0.001	0.001
9/17/09	Upper North Fork	Illinois Creek	146	CCT	LkWhOcl	09IJ0007	0.906	0.078	0.002	0.012	0.002	0
9/17/09	Upper North Fork	Illinois Creek	178	CCT	LkWhOcl	09IJ0008	0.952	0.032	0.002	0.013	0.001	0.001
9/17/09	Upper North Fork	Illinois Creek	131	CCT	LkWhOcl	09IJ0009	0.947	0.015	0.002	0.035	0.001	0.001
9/17/09	Upper North Fork	Illinois Creek	107	CCT	LkWhOcl	09IJ0010	0.963	0.017	0.002	0.01	0.005	0.003
9/17/09	Upper North Fork	Illinois Creek	235	CCT	LkWhOcl	09IJ0011	0.975	0.016	0.001	0.004	0.001	0.003
9/17/09	Upper North Fork	Illinois Creek	234	CCT	LkWhOcl	09IJ0012	0.969	0.008	0.002	0.019	0.001	0
9/17/09	Upper North Fork	Illinois Creek	233	CCT	LkWhOcl	09IJ0013	0.989	0.003	0.001	0.006	0.001	0
9/17/09	Upper North Fork	Illinois Creek	205	CCT	LkWhOcl	09IJ0014	0.986	0.005	0.001	0.006	0.001	0
9/17/09	Upper North Fork	Illinois Creek	185	CCT	LkWhOcl	09IJ0015	0.989	0.003	0.001	0.005	0.001	0
9/17/09	Upper North Fork	Illinois Creek	178	CCT	LkWhOcl	09IJ0016	0.918	0.074	0.001	0.005	0.001	0
9/17/09	Upper North Fork	Illinois Creek	165	CCT	LkWhOcl	09IJ0017	0.935	0.018	0.002	0.044	0.001	0.001
9/17/09	Upper North Fork	Illinois Creek	180	CCT	LkWhOcl-SnoqOmy1	09IJ0018	0.692	0.006	0.002	0.01	0.288	0.003
9/17/09	Upper North Fork	Illinois Creek	88	CCT	LkWhOcl	09IJ0019	0.968	0.008	0.005	0.018	0.001	0.001
9/17/09	Upper North Fork	Illinois Creek	93	CCT	LkWhOcl	09IJ0020	0.928	0.009	0.002	0.061	0.001	0
6/30/10	Upper North Fork	Illinois Creek	147	CCT	LkWhOcl	09IJ0126	0.985	0.005	0.001	0.008	0.001	0
6/30/10	Upper North Fork	Illinois Creek	127	CCT	LkWhOcl	09IJ0127	0.939	0.043	0.003	0.014	0.001	0
6/30/10	Upper North Fork	Illinois Creek	93	CCT	LkWhOcl	09IJ0128	0.981	0.009	0.002	0.008	0.001	0
6/17/10	Middle North Fork	Lakebed	281	CCT	LkWhOcl-SnoqOmy2	09IJ0034	0.668	0.068	0.002	0.011	0.058	0.194
6/17/10	Middle North Fork	Lakebed	263	Onxx	SnoqOmy1	09IJ0068	0.068	0.018	0.001	0.055	0.818	0.039
6/17/10	Middle North Fork	Lakebed	300	CCT	LkWhOcl-SnoqOmy1	09IJ0069	0.284t	0.035	0.003	0.071	0.599	0.008
9/18/09	Middle North Fork	Big Creek Falls	183	CCT	LkWhOcl	09IJ0021	0.975	0.015	0.001	0.007	0.001	0
9/18/09	Middle North Fork	Big Creek Falls	169	CCT	LkWhOcl	09IJ0022	0.976	0.013	0.001	0.009	0.001	0
6/7/10	Middle North Fork	Big Creek Falls	145	CCT	LkWhOcl-SnoqOcl	09IJ0105	0.525	0.029	0.002	0.442	0.001	0.001
9/18/09	Middle North Fork	Big Creek Falls	193	RBT	SnoqOmy1	09IK0019	0.017	0.099	0.004	0.005	0.835	0.041

Table 7. (Continued)

Date	River Section	River Segment	TL (mm)	Field ID	Type	Fish ID	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy1	SnoqOmy2
9/18/09	Middle North Fork	Big Creek Falls	178	RBT	SnoqOmy1	09IK0020	0.001	0.001	0.001	0.001	0.97	0.025
9/18/09	Middle North Fork	Big Creek Falls	182	RBT	SnoqOmy1	09IK0021	0.001	0.001	0.001	0.001	0.964	0.031
9/18/09	Middle North Fork	Big Creek Falls	177	RBT	SnoqOmy1,2	09IK0022	0.001	0.001	0.001	0.001	0.895	0.102
9/18/09	Middle North Fork	Big Creek Falls	220	Onxx	SnoqOmy1	09IK0023	0.001	0.001	0.001	0.001	0.973	0.023
9/18/09	Middle North Fork	Big Creek Falls	184	RBT	SnoqOmy1	09IK0024	0.001	0.001	0.001	0.001	0.972	0.025
9/18/09	Middle North Fork	Big Creek Falls	198	RBT	SnoqOmy1	09IK0025	0.001	0.001	0.001	0.001	0.961	0.036
9/18/09	Middle North Fork	Big Creek Falls	156	RBT	SnoqOmy1	09IK0026	0.002	0.001	0.001	0.001	0.99	0.006
11/2/09	Middle North Fork	Big Creek Falls	80	RBT	SnoqOmy1	09IK0028	0.001	0.001	0.001	0.001	0.988	0.008
11/2/09	Middle North Fork	Big Creek Falls	87	RBT	SnoqOmy1	09IK0029	0.003	0.003	0.003	0.003	0.973	0.014
11/2/09	Middle North Fork	Big Creek Falls	70	Onxx	SnoqOmy1	09IK0030	0.001	0.001	0.001	0.001	0.992	0.003
11/2/09	Middle North Fork	Big Creek Falls	73	Onxx	SnoqOmy1	09IK0033	0.001	0.001	0.001	0.001	0.991	0.004
11/3/09	Middle North Fork	Big Creek Falls	252	RBT	SnoqOmy1	09IK0034	0.001	0.001	0.001	0.001	0.984	0.013
6/8/10	Middle North Fork	Calligan	352	CCT	CedarOcl-SnoqOmy1	09IJ0106	0.048	0.321	0.001	0.06	0.545	0.026
6/8/10	Middle North Fork	Calligan	146	CCT	LkWhOcl	09IJ0107	0.98	0.007	0.001	0.01	0.001	0
6/8/10	Middle North Fork	Calligan	103	RBT	SnoqOmy1	09IK0067	0.001	0.001	0.001	0.001	0.977	0.02
9/14/09	Middle North Fork	Black Canyon	401	RBT	SnoqOmy1	09IK0032	0.001	0.001	0.001	0.001	0.994	0.002
11/4/09	Middle North Fork	Black Canyon	272	RBT	SnoqOmy1	09IK0037	0.001	0.001	0.001	0.001	0.994	0.002
11/4/09	Middle North Fork	Black Canyon	128	RBT	SnoqOmy1	09IK0038	0.001	0.001	0.001	0.001	0.969	0.028
11/4/09	Middle North Fork	Black Canyon	110	RBT	SnoqOmy1	09IK0039	0.001	0.001	0.001	0.001	0.993	0.004
5/14/10	Middle North Fork	Black Canyon	401	Onxx	TwinOcl-SnoqOmy1	09IK0057	0.01	0.019	0.144	0.016	0.803	0.008
5/14/10	Middle North Fork	Black Canyon	260	RBT	SnoqOmy1	09IK0058	0.001	0.001	0.001	0.001	0.985	0.011
5/14/10	Middle North Fork	Black Canyon	269	Onxx	SnoqOmy1	09IK0059	0.001	0.001	0.001	0.001	0.931	0.065
7/1/10	Middle North Fork	Black Canyon	28	Onxx	SnoqOmy1	09IK0073	0.001	0.001	0.001	0.001	0.99	0.008
9/16/09	Lower North Fork	Black Canyon	140	CCT	SnoqOcl	09IJ0001	0.02	0.011	0.001	0.966	0.001	0
9/16/09	Lower North Fork	Black Canyon	208	CCT	SnoqOcl	09IJ0002	0.006	0.011	0.001	0.981	0.001	0
9/16/09	Lower North Fork	Black Canyon	156	CCT	SnoqOcl	09IJ0003	0.01	0.008	0.001	0.98	0.001	0
2/2/10	Lower North Fork	Black Canyon	145	CCT	LkWhOcl-SnoqOcl	09IJ0071	0.124	0.091	0.001	0.783	0.001	0
6/16/10	Lower North Fork	Black Canyon	110	RBT	SnoqOmy1	09IJ0108	0.001	0.001	0.001	0.001	0.994	0.003
6/16/10	Lower North Fork	Black Canyon	105	RBT	SnoqOcl-SnoqOmy1	09IJ0109	0.012	0.004	0.002	0.215	0.765	0.002

Table 7. (Continued)

Date	River Section	River Segment	TL (mm)	Field ID	Type	Fish ID	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy1	SnoqOmy2
6/16/10	Lower North Fork	Black Canyon	237	RBT	SnoqOmy1	09IJ0112	0.001	0.001	0.001	0.001	0.99	0.007
9/16/09	Lower North Fork	Black Canyon	214	RBT	SnoqOmy1	09IJ0149	0.001	0.001	0.001	0.001	0.994	0.002
9/16/09	Lower North Fork	Black Canyon	190	RBT	SnoqOmy1	09IJ0150	0.001	0.001	0.001	0.001	0.983	0.014
9/16/09	Lower North Fork	Black Canyon	224	RBT	SnoqOmy1	09IK0001	0.001	0.001	0.001	0.001	0.994	0.003
9/16/09	Lower North Fork	Black Canyon	251	RBT	SnoqOmy1	09IK0006	0.002	0.002	0.002	0.002	0.989	0.003
9/16/09	Lower North Fork	Black Canyon	227	RBT	SnoqOmy1	09IK0007	0.001	0.001	0.001	0.001	0.983	0.014
9/16/09	Lower North Fork	Black Canyon	205	RBT	SnoqOmy1	09IK0008	0.001	0.001	0.001	0.001	0.993	0.003
9/16/09	Lower North Fork	Black Canyon	143	RBT	SnoqOmy1	09IK0009	0.064	0.024	0.012	0.019	0.872	0.008
9/16/09	Lower North Fork	Black Canyon	192	RBT	SnoqOmy1	09IK0010	0.002	0.002	0.001	0.002	0.981	0.012
9/16/09	Lower North Fork	Black Canyon	173	RBT	SnoqOmy1	09IK0011	0.001	0.001	0.001	0.001	0.992	0.004
9/16/09	Lower North Fork	Black Canyon	228	RBT	SnoqOmy1	09IK0012	0.001	0.002	0.001	0.001	0.987	0.007
9/16/09	Lower North Fork	Black Canyon	152	RBT	SnoqOmy1	09IK0013	0.001	0.001	0.001	0.001	0.988	0.008
9/16/09	Lower North Fork	Black Canyon	212	RBT	SnoqOmy1	09IK0014	0.002	0.003	0.001	0.002	0.986	0.006
9/16/09	Lower North Fork	Black Canyon	63	RBT	SnoqOmy1	09IK0016	0.001	0.001	0.002	0.001	0.991	0.003
2/2/10	Lower North Fork	Black Canyon	134	RBT	SnoqOmy1	09IK0042	0.001	0.001	0.001	0.001	0.992	0.004
2/2/10	Lower North Fork	Black Canyon	137	RBT	SnoqOmy1	09IK0043	0.001	0.001	0.001	0.001	0.995	0.002
2/2/10	Lower North Fork	Black Canyon	98	RBT	LkWhOcl-SnoqOmy1	09IK0044	0.207	0.007	0.005	0.006	0.767	0.008
2/2/10	Lower North Fork	Black Canyon	97	RBT	LkWhOcl-SnoqOmy1	09IK0045	0.262	0.014	0.006	0.01	0.705	0.004
2/2/10	Lower North Fork	Black Canyon	91	RBT	LkWhOcl-SnoqOmy1	09IK0046	0.186	0.025	0.002	0.027	0.757	0.003
6/16/10	Lower North Fork	Black Canyon	430	CCT	CedarOcl-SnoqOmy1	09IK0068	0.084	0.303	0.003	0.061	0.535	0.014
7/1/10	Lower North Fork	Black Canyon	27	Onxx	SnoqOmy1	09IK0081	0.001	0.001	0.001	0.001	0.994	0.002
6/18/09	Lower North Fork	Three Forks	444	Onxx	SnoqOmy1	09IK0003	0.001	0.001	0.001	0.001	0.995	0.002
6/15/10	Lower North Fork	Three Forks	351	RBT	SnoqOmy1	09IK0035	0.001	0.001	0.001	0.001	0.994	0.003
6/15/10	Lower North Fork	Three Forks	278	RBT	SnoqOmy1	09IK0036	0.001	0.001	0.001	0.001	0.986	0.01
3/8/10	Lower North Fork	Three Forks	EGG	Onxx	SnoqOcl	09IK0047	0.012	0.005	0.001	0.981	0.001	0
3/8/10	Lower North Fork	Three Forks	EGG	Onxx	SnoqOmy1	09IK0048	0.004	0.004	0.001	0.003	0.986	0.002
9/8/10	Lower North Fork	Three Forks	326	Onxx	SnoqOcl-SnoqOmy1	09IK0103	0.004	0.005	0.004	0.483	0.5	0.004
9/8/10	Lower North Fork	Three Forks	259	Onxx	SnoqOmy1	09IK0104	0.001	0.001	0.001	0.001	0.994	0.003
10/7/10	Lower North Fork	Three Forks	149	CCT	SnoqOcl	09IK0116	0.01	0.004	0.007	0.977	0.001	0.001
10/7/10	Lower North Fork	Three Forks	68	Onxx	SnoqOmy1	09IK0117	0.055	0.055	0.003	0.024	0.858	0.005

Table 7. (Continued)

Date	River Section	River Segment	TL (mm)	Field ID	Type	Fish ID	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy1	SnoqOmy2
10/7/10	Lower North Fork	Three Forks	310	RBT	SnoqOmy1	09IK0118	0.001	0.001	0.001	0.001	0.995	0.001
6/15/10	Lower North Fork	Three Forks	279	RBT	SnoqOmy1,2	09IK0121	0.001	0.001	0.001	0.001	0.858	0.139
10/13/10	Upper Middle Fork	Hardscrabble	180	CCT	Ocl-Omy	09IK0119	0.257	0.024	0.06	0.442	0.108	0.11
10/13/10	Upper Middle Fork	Hardscrabble	192	CCT	LkWhOcl	09IK0120	0.915	0.008	0.07	0.006	0.001	0
10/13/10	Upper Middle Fork	Hardscrabble	191	CCT	Ocl-SnoqOmy1	09IK0122	0.623	0.007	0.164	0.004	0.199	0.003
10/13/10	Upper Middle Fork	Hardscrabble	190	CCT	LkWhOcl-TwinOcl	09IK0123	0.796	0.063	0.136	0.004	0.001	0.001
8/1/10	Upper Middle Fork	Goldmyer	135	Onxx	SnoqOcl	09IJ0085	0.005	0.006	0.002	0.986	0.001	0.001
8/1/10	Upper Middle Fork	Goldmyer	151	Onxx	SnoqOcl	09IJ0086	0.007	0.006	0.001	0.985	0.001	0
8/1/10	Upper Middle Fork	Goldmyer	250	CCT	SnoqOcl	09IK0079	0.005	0.005	0.002	0.987	0.001	0
8/1/10	Upper Middle Fork	Goldmyer	215	CCT	SnoqOcl	09IK0080	0.01	0.01	0.002	0.977	0.001	0.001
8/1/10	Upper Middle Fork	Goldmyer	208	CCT	SnoqOcl	09IK0081	0.012	0.009	0.001	0.976	0.001	0
8/1/10	Upper Middle Fork	Goldmyer	203	CCT	SnoqOcl	09IK0082	0.035	0.014	0.002	0.948	0.001	0
8/1/10	Upper Middle Fork	Goldmyer	198	CCT	SnoqOcl	09IK0083	0.005	0.012	0.002	0.981	0.001	0.001
8/1/10	Upper Middle Fork	Goldmyer	195	CCT	SnoqOcl	09IK0084	0.013	0.005	0.001	0.98	0.001	0.001
8/1/10	Upper Middle Fork	Goldmyer	185	CCT	SnoqOcl	09IK0085	0.003	0.005	0.008	0.983	0	0
8/2/10	Upper Middle Fork	Goldmyer	241	CCT	SnoqOcl	09IK0086	0.007	0.005	0.002	0.985	0.001	0
8/2/10	Upper Middle Fork	Goldmyer	133	CCT	CedarOcl-SnoqOcl	09IK0087	0.005	0.393	0.001	0.599	0.001	0
8/2/10	Upper Middle Fork	Goldmyer	136	CCT	CedarOcl-SnoqOcl	09IK0088	0.003	0.108	0.003	0.885	0.001	0
8/2/10	Upper Middle Fork	Goldmyer	134	CCT	SnoqOcl	09IK0089	0.005	0.005	0.002	0.988	0.001	0
8/2/10	Upper Middle Fork	Goldmyer	138	CCT	SnoqOcl	09IK0090	0.007	0.005	0.001	0.986	0.001	0
8/3/10	Upper Middle Fork	Goldmyer	81	Onxx	SnoqOcl	09IK0091	0.005	0.009	0.002	0.983	0.001	0
8/3/10	Upper Middle Fork	Goldmyer	30	Onxx	SnoqOcl	09IK0092	0.006	0.006	0.001	0.986	0.001	0
8/3/10	Upper Middle Fork	Goldmyer	248	CCT	SnoqOcl	09IK0093	0.003	0.072	0.004	0.919	0.001	0.001
8/6/10	Upper Middle Fork	Goldmyer	283	CCT	SnoqOcl	09IK0142	0.005	0.009	0.001	0.984	0.001	0
8/4/10	Upper Middle Fork	Dingford	245	CCT	SnoqOcl	09IK0094	0.007	0.01	0.001	0.981	0.001	0
8/4/10	Upper Middle Fork	Dingford	259	CCT	SnoqOcl	09IK0095	0.006	0.009	0.002	0.982	0.001	0
8/4/10	Upper Middle Fork	Dingford	243	Onxx	SnoqOcl-SnoqOmy1,2	09IK0096	0.013	0.04	0.002	0.387	0.39	0.168
10/21/09	Middle Middle Fork	Pratt	71	Onxx	SnoqOcl-SnoqOmy1	09IJ0070	0.005	0.005	0.021	0.686	0.248	0.035
7/9/10	Middle Middle Fork	Pratt	272	CCT	SnoqOcl	09IJ0075	0.003	0.004	0.002	0.989	0.001	0.001
7/9/10	Middle Middle Fork	Pratt	348	CCT	SnoqOcl	09IJ0083	0.004	0.01	0.025	0.96	0.001	0.001

Table 7. (Continued)

Date	River Section	River Segment	TL (mm)	Field ID	Type	Fish ID	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy1	SnoqOmy2
6/21/10	Middle Middle Fork	Pratt	298	CCT	SnoqOcl	09IJ0117	0.009	0.005	0.002	0.983	0.001	0.001
6/28/10	Middle Middle Fork	Pratt	194	CCT	SnoqOcl	09IJ0125	0.012	0.005	0.003	0.979	0.001	0.001
7/9/10	Middle Middle Fork	Pratt	222	CCT	SnoqOcl	09IJ0142	0.006	0.006	0.002	0.985	0.001	0.001
7/9/10	Middle Middle Fork	Pratt	234	CCT	SnoqOcl	09IJ0143	0.005	0.081	0.004	0.908	0.001	0.001
7/9/10	Middle Middle Fork	Pratt	193	CCT	SnoqOcl-SnoqOmy1	09IJ0144	0.004	0.011	0.013	0.747	0.216	0.008
7/9/10	Middle Middle Fork	Pratt	195	CCT	SnoqOcl	09IJ0145	0.005	0.004	0.002	0.989	0.001	0.001
7/9/10	Middle Middle Fork	Pratt	237	CCT	SnoqOcl	09IJ0146	0.009	0.009	0.012	0.969	0.001	0.001
7/9/10	Middle Middle Fork	Pratt	306	CCT	Ocl	09IJ0147	0.313	0.328	0.047	0.31	0.001	0.001
5/11/10	Middle Middle Fork	Pratt	ALEVIN	Onxx	SnoqOcl	09IK0060	0.003	0.003	0.002	0.99	0.001	0.001
5/11/10	Middle Middle Fork	Pratt	EGG	Onxx	CedarOcl-SnoqOcl	09IK0061	0.049	0.224	0.002	0.723	0.001	0.001
7/26/10	Middle Middle Fork	Pratt	139	CCT	SnoqOcl	09IK0076	0.004	0.007	0.002	0.986	0.001	0.001
7/26/10	Middle Middle Fork	Pratt	140	CCT	SnoqOcl	09IK0077	0.006	0.004	0.002	0.987	0.001	0
7/26/10	Middle Middle Fork	Pratt	134	CCT	SnoqOcl	09IK0078	0.005	0.003	0.002	0.99	0.001	0.001
10/20/09	Middle Middle Fork	Garfield Mtn.	173	CCT	SnoqOcl	09IJ0056	0.067	0.009	0.002	0.922	0.001	0.001
10/20/09	Middle Middle Fork	Garfield Mtn.	210	CCT	SnoqOcl	09IJ0057	0.004	0.003	0.001	0.954	0.01	0.028
10/20/09	Middle Middle Fork	Garfield Mtn.	126	CCT	SnoqOcl	09IJ0058	0.038	0.061	0.001	0.898	0.001	0
10/20/09	Middle Middle Fork	Garfield Mtn.	93	CCT	SnoqOcl	09IJ0059	0.007	0.013	0.001	0.978	0.001	0
10/20/09	Middle Middle Fork	Garfield Mtn.	118	CCT	SnoqOcl	09IJ0060	0.014	0.029	0.001	0.918	0.009	0.028
10/20/09	Middle Middle Fork	Garfield Mtn.	65	CCT	SnoqOcl	09IJ0061	0.003	0.004	0.003	0.989	0.001	0.001
10/20/09	Middle Middle Fork	Garfield Mtn.	167	CCT	SnoqOcl	09IJ0062	0.019	0.081	0.001	0.898	0.001	0
10/20/09	Middle Middle Fork	Garfield Mtn.	182	CCT	SnoqOcl	09IJ0063	0.007	0.006	0.002	0.983	0.001	0.001
10/20/09	Middle Middle Fork	Garfield Mtn.	123	CCT	SnoqOcl	09IJ0064	0.006	0.005	0.004	0.984	0.001	0
10/20/09	Middle Middle Fork	Garfield Mtn.	119	CCT	SnoqOcl	09IJ0065	0.013	0.022	0.034	0.928	0.001	0.001
10/20/09	Middle Middle Fork	Garfield Mtn.	119	CCT	SnoqOcl	09IJ0066	0.005	0.003	0.001	0.989	0.001	0
10/20/09	Middle Middle Fork	Garfield Mtn.	67	CCT	SnoqOcl	09IJ0067	0.003	0.017	0.002	0.969	0.005	0.004
7/24/09	Lower Middle Fork	Three Forks	232	CCT	SnoqOcl-SnoqOmy1	09IJ0030	0.007	0.014	0.002	0.778	0.145	0.054
9/25/09	Lower Middle Fork	Sallal Prairie	294	CCT	SnoqOcl	09IJ0032	0.007	0.005	0.002	0.984	0.001	0
2/4/10	Lower Middle Fork	Sallal Prairie	143	CCT	SnoqOcl	09IJ0076	0.004	0.003	0.004	0.988	0.001	0.001
6/22/10	Lower Middle Fork	Sallal Prairie	103	CCT	SnoqOcl	09IJ0119	0.004	0.003	0.002	0.989	0.001	0.001
10/9/09	Lower Middle Fork	North Bend	298	CCT	SnoqOcl	09IJ0033	0.025	0.01	0.002	0.962	0.001	0.001

Table 7. (Continued)

Date	River Section	River Segment	TL (mm)	Field ID	Type	Fish ID	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy1	SnoqOmy2
9/30/09	Lower Middle Fork	North Bend	419	CCT	SnoqOcl-SnoqOmy1	09IJ0040	0.038	0.011	0.004	0.427	0.473	0.048
9/30/09	Lower Middle Fork	North Bend	293	CCT	SnoqOcl-SnoqOmy1	09IJ0041	0.01	0.048	0.002	0.587	0.349	0.004
9/30/09	Lower Middle Fork	North Bend	305	CCT	SnoqOcl	09IJ0042	0.018	0.016	0.001	0.963	0.001	0
10/1/09	Lower Middle Fork	North Bend	276	CCT	SnoqOcl	09IJ0043	0.003	0.002	0.002	0.992	0.001	0.001
10/1/09	Lower Middle Fork	North Bend	266	CCT	SnoqOcl-SnoqOmy1	09IJ0044	0.006	0.006	0.005	0.498	0.472	0.013
10/1/09	Lower Middle Fork	North Bend	142	CCT	SnoqOcl	09IJ0045	0.004	0.004	0.003	0.989	0.001	0.001
10/1/09	Lower Middle Fork	North Bend	166	CCT	SnoqOcl	09IJ0046	0.005	0.025	0.003	0.966	0.001	0.001
10/1/09	Lower Middle Fork	North Bend	174	CCT	SnoqOcl-SnoqOmy1	09IJ0047	0.007	0.009	0.002	0.821	0.149	0.012
10/1/09	Lower Middle Fork	North Bend	154	CCT	SnoqOcl	09IJ0048	0.01	0.005	0.008	0.976	0.001	0.001
10/1/09	Lower Middle Fork	North Bend	142	CCT	CedarOcl-SnoqOcl	09IJ0049	0.004	0.311	0.005	0.658	0.011	0.01
10/1/09	Lower Middle Fork	North Bend	93	CCT	SnoqOcl	09IJ0050	0.004	0.004	0.001	0.99	0	0
10/9/09	Lower Middle Fork	North Bend	302	CCT	Ocl-Omy2	09IJ0055	0.213	0.034	0.001	0.202	0.003	0.547
9/11/10	Lower Middle Fork	North Bend	301	Onxx	SnoqOcl-SnoqOmy1	09IJ0104	0.004	0.005	0.003	0.129	0.854	0.004
9/14/10	Lower Middle Fork	North Bend	314	CCT	SnoqOcl	09IJ0110	0.006	0.01	0.002	0.982	0.001	0.001
10/18/10	Lower Middle Fork	North Bend	370	CCT	SnoqOcl-SnoqOmy1	09IJ0111	0.004	0.025	0.002	0.759	0.208	0.002
6/22/10	Lower Middle Fork	North Bend	321	CCT	SnoqOcl-SnoqOmy1	09IJ0118	0.015	0.005	0.002	0.54	0.423	0.016
6/24/10	Lower Middle Fork	North Bend	111	CCT	SnoqOcl	09IJ0122	0.013	0.011	0.002	0.973	0.001	0.001
5/13/10	Lower Middle Fork	North Bend	202	Onxx	SnoqOcl-SnoqOmy1	09IK0018	0.006	0.008	0.002	0.524	0.458	0.002
5/13/10	Lower Middle Fork	North Bend	319	RBT	SnoqOmy1	09IK0063	0.001	0.001	0.001	0.001	0.994	0.003
5/13/10	Lower Middle Fork	North Bend	229	Onxx	SnoqOcl-SnoqOmy1	09IK0056	0.005	0.059	0.002	0.356	0.573	0.005
9/21/09	Lower Middle Fork	Mt. Teneriffe	188	CCT	SnoqOcl	09IJ0023	0.005	0.004	0.001	0.989	0.001	0
9/21/09	Lower Middle Fork	Mt. Teneriffe	219	CCT	SnoqOcl	09IJ0024	0.006	0.009	0.026	0.955	0.003	0.001
9/21/09	Lower Middle Fork	Mt. Teneriffe	207	CCT	SnoqOcl	09IJ0025	0.005	0.015	0.012	0.966	0.001	0.001
9/21/09	Lower Middle Fork	Mt. Teneriffe	183	CCT	SnoqOcl	09IJ0026	0.005	0.005	0.002	0.986	0.001	0.001
9/21/09	Lower Middle Fork	Mt. Teneriffe	184	CCT	SnoqOcl	09IJ0027	0.009	0.006	0.002	0.982	0.001	0
9/21/09	Lower Middle Fork	Mt. Teneriffe	239	CCT	SnoqOcl	09IJ0028	0.005	0.052	0.001	0.937	0.003	0.001
9/21/09	Lower Middle Fork	Mt. Teneriffe	241	CCT	SnoqOcl	09IJ0029	0.008	0.004	0.001	0.985	0.001	0
9/23/09	Lower Middle Fork	Mt. Teneriffe	175	CCT	SnoqOcl	09IJ0035	0.003	0.003	0.002	0.991	0.001	0.001
9/23/09	Lower Middle Fork	Mt. Teneriffe	94	CCT	SnoqOcl	09IJ0036	0.007	0.008	0.002	0.982	0.001	0
9/23/09	Lower Middle Fork	Mt. Teneriffe	201	CCT	SnoqOcl	09IJ0037	0.005	0.076	0.002	0.913	0.004	0

Table 7. (Continued)

Date	River Section	River Segment	TL (mm)	Field ID	Type	Fish ID	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy1	SnoqOmy2
9/23/09	Lower Middle Fork	Mt. Teneriffe	145	CCT	SnoqOcl	09IJ0038	0.006	0.045	0.007	0.94	0.001	0.001
9/23/09	Lower Middle Fork	Mt. Teneriffe	122	CCT	SnoqOcl	09IJ0039	0.003	0.003	0.002	0.991	0.001	0.001
9/24/09	Lower Middle Fork	Mt. Teneriffe	249	CCT	SnoqOcl	09IK0004	0.012	0.008	0.002	0.977	0.001	0.001
9/23/09	Lower Middle Fork	Mt. Teneriffe	212	RBT	SnoqOmy1	09IK0027	0.003	0.004	0.003	0.003	0.961	0.025
10/19/10	Upper South Fork	Denny Creek	239	WCT	TwinOcl	09IK0124	0.001	0.001	0.995	0.001	0	0
10/19/10	Upper South Fork	Denny Creek	208	WCT	TwinOcl	09IK0125	0.001	0.001	0.995	0.001	0.001	0.001
10/19/10	Upper South Fork	Denny Creek	229	WCT	TwinOcl	09IK0126	0.001	0.001	0.991	0.005	0.001	0
10/19/10	Upper South Fork	Denny Creek	155	Onxx	TwinOcl-SnoqOmy2	09IK0127	0.003	0.003	0.343	0.002	0.021	0.629
5/24/10	Upper South Fork	Asahel Curtis	239	CCT	CedarOcl	09IJ0094	0.04	0.925	0.002	0.008	0.003	0.022
5/24/10	Upper South Fork	Asahel Curtis	200	CCT	LkWhOcl-CedarOcl	09IJ0095	0.215	0.777	0.001	0.006	0.001	0
5/24/10	Upper South Fork	Asahel Curtis	205	CCT	CedarOcl	09IJ0096	0.028	0.954	0.001	0.016	0.001	0.001
5/24/10	Upper South Fork	Asahel Curtis	154	CCT	CedarOcl	09IJ0097	0.004	0.973	0.013	0.005	0.001	0.003
5/24/10	Upper South Fork	Asahel Curtis	136	CCT	LkWhOcl-CedarOcl	09IJ0098	0.18	0.737	0.002	0.069	0.008	0.004
5/24/10	Upper South Fork	Asahel Curtis	139	CCT	CedarOcl	09IJ0099	0.005	0.901	0.001	0.091	0.001	0.001
5/24/10	Upper South Fork	Asahel Curtis	121	CCT	CedarOcl	09IJ0100	0.024	0.947	0.001	0.027	0.001	0.001
5/24/10	Upper South Fork	Asahel Curtis	77	CCT	CedarOcl	09IJ0101	0.012	0.981	0.001	0.005	0.001	0
5/24/10	Upper South Fork	Asahel Curtis	79	CCT	LkWhOcl-CedarOcl	09IJ0102	0.117	0.776	0.001	0.105	0.001	0
5/24/10	Upper South Fork	Asahel Curtis	73	CCT	CedarOcl	09IJ0103	0.008	0.987	0.001	0.003	0.001	0.001
5/24/10	Upper South Fork	Asahel Curtis	244	WCT	CedarOcl	09IK0060	0.005	0.98	0.002	0.012	0.001	0.001
5/24/10	Upper South Fork	Asahel Curtis	135	Onxx	CedarOcl	09IK0069	0.004	0.986	0.001	0.008	0.001	0.001
5/24/10	Upper South Fork	Asahel Curtis	141	Onxx	CedarOcl	09IK0062	0.009	0.957	0.001	0.032	0.001	0.001
5/24/10	Upper South Fork	Asahel Curtis	89	Onxx	CedarOcl-SnoqOmy2	09IK0063	0.006	0.427	0.007	0.014	0.011	0.534
9/28/10	Upper South Fork	Asahel Curtis	155	CCT	CedarOcl-SnoqOmy2	09IK0114	0.008	0.731	0.002	0.007	0.019	0.234
9/28/10	Upper South Fork	Asahel Curtis	191	CCT	CedarOcl	09IK0115	0.018	0.97	0.001	0.01	0.001	0.001
9/2/10	Middle South Fork	Tinkham	217	CCT	CedarOcl	09IK0041	0.029	0.894	0.002	0.041	0.001	0.034
9/2/10	Middle South Fork	Tinkham	189	Onxx	SnoqOmy2	09IK0097	0.001	0.001	0.001	0.001	0.004	0.992
9/2/10	Middle South Fork	Tinkham	226	Onxx	CedarOcl-SnoqOmy2	09IK0098	0.006	0.332	0.002	0.022	0.007	0.632
9/2/10	Middle South Fork	Tinkham	242	CCT	CedarOcl	09IK0099	0.003	0.975	0.002	0.018	0.001	0.001
9/2/10	Middle South Fork	Tinkham	248	CCT	CedarOcl-SnoqOmy2	09IK0100	0.009	0.727	0.002	0.014	0.002	0.246
9/2/10	Middle South Fork	Weeks Falls	248	CCT	LkWhOcl-CedarOcl	09IK0101	0.121	0.874	0.001	0.003	0.001	0.001

Table 7. (Continued)

Date	River Section	River Segment	TL (mm)	Field ID	Type	Fish ID	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy1	SnoqOmy2
9/2/10	Middle South Fork	Weeks Falls	247	RBT	SnoqOmy1,2	09IK0102	0.001	0.001	0.001	0.001	0.143	0.854
10/19/10	Middle South Fork	Weeks Falls	177	Onxx	SnoqOmy2	09IK0128	0.012	0.01	0.003	0.032	0.005	0.938
10/19/10	Middle South Fork	Weeks Falls	154	RBT	SnoqOmy2	09IK0129	0.001	0.001	0.001	0.001	0.005	0.993
10/19/10	Middle South Fork	Weeks Falls	185	RBT	SnoqOmy2	09IK0130	0.004	0.009	0.004	0.003	0.039	0.941
10/19/10	Middle South Fork	Weeks Falls	168	CCT	Ocl-Omy2	09IK0131	0.233	0.17	0.002	0.009	0.003	0.583
10/19/10	Middle South Fork	Weeks Falls	148	Onxx	SnoqOmy2	09IK0132	0.001	0.005	0.001	0.002	0.07	0.922
10/19/10	Middle South Fork	Weeks Falls	138	Onxx	SnoqOmy2	09IK0133	0.001	0.001	0.011	0.001	0.002	0.984
10/19/10	Middle South Fork	Weeks Falls	144	Onxx	SnoqOmy2	09IK0134	0.005	0.008	0.003	0.006	0.033	0.944
10/19/10	Middle South Fork	Weeks Falls	142	Onxx	CedarOcl-SnoqOmy2	09IK0135	0.003	0.161	0.001	0.01	0.014	0.811
10/19/10	Middle South Fork	Weeks Falls	99	Onxx	Ocl-Omy2	09IK0136	0.144	0.014	0.002	0.125	0.034	0.681
8/7/09	Middle South Fork	Grouse Ridge	100	CCT	SnoqOmy2	09IJ0031	0.001	0.001	0.001	0.001	0.01	0.986
10/19/10	Middle South Fork	Grouse Ridge	81	CCT	CedarOcl-SnoqOmy2	09IJ0129	0.057	0.354	0.002	0.025	0.003	0.558
10/19/10	Middle South Fork	Grouse Ridge	111	Onxx	CedarOcl-SnoqOmy2	09IJ0140	0.007	0.192	0.002	0.025	0.005	0.77
10/19/10	Middle South Fork	Grouse Ridge	112	RBT	SnoqOmy1	09IJ0141	0.001	0.001	0.001	0.001	0.9	0.096
8/7/09	Middle South Fork	Grouse Ridge	41	Onxx	CedarOcl-SnoqOmy2	09IK0002	0.028	0.223	0.002	0.036	0.045	0.666
8/7/09	Middle South Fork	Grouse Ridge	97	Onxx	SnoqOmy1,2	09IK0005	0.001	0.001	0.001	0.002	0.122	0.873
8/7/09	Middle South Fork	Grouse Ridge	98	RBT	SnoqOmy2	09IK0015	0.001	0.001	0.001	0.001	0.019	0.978
5/6/10	Middle South Fork	Grouse Ridge	255	Onxx	CedarOcl-SnoqOmy2	09IK0017	0.009	0.186	0.004	0.007	0.076	0.717
10/19/10	Middle South Fork	Grouse Ridge	222	RBT	SnoqOmy1,2	09IK0137	0.001	0.001	0.001	0.001	0.274	0.723
10/19/10	Middle South Fork	Grouse Ridge	222	RBT	SnoqOmy2	09IK0138	0.001	0.001	0.001	0.001	0.021	0.974
10/19/10	Middle South Fork	Grouse Ridge	206	RBT	SnoqOmy2	09IK0139	0.001	0.002	0.001	0.001	0.005	0.99
10/19/10	Middle South Fork	Grouse Ridge	187	Onxx	SnoqOmy2	09IK0140	0.003	0.002	0.001	0.002	0.014	0.979
10/19/10	Middle South Fork	Grouse Ridge	170	Onxx	SnoqOmy2	09IK0141	0.001	0.001	0.001	0.001	0.008	0.99
9/8/10	Lower South Fork	Three Forks	312	CCT	SnoqOcl	09IJ0087	0.016	0.047	0.002	0.906	0.015	0.014
9/8/10	Lower South Fork	Three Forks	332	CCT	SnoqOcl	09IK0105	0.004	0.005	0.003	0.987	0.001	0
6/29/10	Lower South Fork	Sallal Prairie	259	Onxx	SnoqOmy2	09IJ0074	0.002	0.002	0.003	0.002	0.014	0.976
4/30/10	Lower South Fork	Sallal Prairie	170	CCT	CedarOcl-SnoqOmy2	09IJ0091	0.004	0.402	0.001	0.006	0.085	0.503
4/30/10	Lower South Fork	Sallal Prairie	206	RBT	SnoqOmy2	09IJ0092	0.001	0.001	0.001	0.001	0.008	0.99
9/9/09	Lower South Fork	Sallal Prairie	311	RBT	SnoqOmy2	09IK0031	0.001	0.001	0.001	0.001	0.019	0.978
1/13/10	Lower South Fork	Sallal Prairie	274	RBT	SnoqOmy1	09IK0040	0.001	0.001	0.001	0.001	0.994	0.003

Table 7. (Continued)

Date	River Section	River Segment	TL (mm)	Field ID	Type	Fish ID	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy1	SnoqOmy2
6/3/10	Lower South Fork	Sallal Prairie	552	Onxx	SnoqOmy1	09IK0065	0.001	0.001	0.002	0.001	0.991	0.005
6/3/10	Lower South Fork	Sallal Prairie	416	RBT	SnoqOmy1	09IK0066	0.001	0.001	0.001	0.001	0.991	0.005
6/29/10	Lower South Fork	Sallal Prairie	241	Onxx	SnoqOmy2	09IK0069	0.001	0.001	0.001	0.001	0.049	0.946
6/29/10	Lower South Fork	Sallal Prairie	237	Onxx	Ocl-Omy1	09IK0070	0.137	0.018	0.005	0.299	0.457	0.085
6/29/10	Lower South Fork	Sallal Prairie	233	RBT	SnoqOmy2	09IK0071	0.001	0.001	0.001	0.001	0.012	0.985
6/29/10	Lower South Fork	Sallal Prairie	272	CCT	CedarOcl-SnoqOmy2	09IK0143	0.005	0.829	0.004	0.006	0.045	0.111
4/30/10	Lower South Fork	Sallal Prairie	179	RBT	SnoqOmy2	09IK0144	0.001	0.001	0.001	0.001	0.005	0.992
4/30/10	Lower South Fork	Sallal Prairie	159	RBT	SnoqOcl-SnoqOmy2	09IK0145	0.048	0.014	0.006	0.309	0.027	0.597
4/30/10	Lower South Fork	Sallal Prairie	172	CCT	SnoqOcl	09IK0146	0.009	0.009	0.002	0.98	0.001	0
3/31/10	Lower South Fork	North Bend	ALEVIN	Onxx	SnoqOcl	09IJ0077	0.018	0.007	0.001	0.973	0.001	0
4/29/10	Lower South Fork	North Bend	189	CCT	SnoqOcl-SnoqOmy2	09IJ0078	0.005	0.005	0.009	0.749	0.069	0.163
4/29/10	Lower South Fork	North Bend	199	CCT	CedarOcl-SnoqOcl	09IJ0079	0.007	0.144	0.002	0.846	0.001	0
4/29/10	Lower South Fork	North Bend	155	CCT	LkWhOcl-SnoqOcl	09IJ0080	0.251	0.095	0.001	0.651	0.001	0.001
4/29/10	Lower South Fork	North Bend	135	CCT	LkWhOcl-CedarOcl	09IJ0081	0.203	0.756	0.001	0.037	0.001	0.002
4/29/10	Lower South Fork	North Bend	125	CCT	SnoqOcl	09IJ0082	0.007	0.003	0.001	0.987	0.001	0
7/13/10	Lower South Fork	North Bend	334	CCT	SnoqOcl	09IJ0084	0.01	0.007	0.001	0.98	0.001	0
4/29/10	Lower South Fork	North Bend	95	CCT	SnoqOcl	09IJ0088	0.029	0.014	0.001	0.944	0.011	0.001
4/29/10	Lower South Fork	North Bend	96	CCT	CedarOcl-SnoqOcl	09IJ0089	0.068	0.408	0.007	0.514	0.001	0.001
4/29/10	Lower South Fork	North Bend	280	CCT	SnoqOcl-SnoqOmy1	09IJ0090	0.006	0.007	0.002	0.633	0.347	0.005
5/5/10	Lower South Fork	North Bend	363	CCT	SnoqOcl	09IJ0093	0.005	0.005	0.001	0.979	0.005	0.005
7/8/10	Lower South Fork	North Bend	279	CCT	SnoqOcl	09IJ0136	0.024	0.053	0.002	0.92	0.001	0
7/8/10	Lower South Fork	North Bend	263	CCT	SnoqOcl	09IJ0137	0.005	0.005	0.002	0.978	0.005	0.005
7/8/10	Lower South Fork	North Bend	214	CCT	SnoqOcl	09IJ0138	0.024	0.024	0.002	0.949	0.001	0
7/8/10	Lower South Fork	North Bend	211	CCT	SnoqOcl-SnoqOmy2	09IJ0139	0.005	0.004	0.001	0.692	0.004	0.295
7/13/10	Lower South Fork	North Bend	343	CCT	SnoqOcl	09IJ0148	0.016	0.008	0.002	0.973	0.001	0.001
4/29/10	Lower South Fork	North Bend	128	Onxx	SnoqOcl-SnoqOmy2	09IK0049	0.066	0.098	0.009	0.119	0.004	0.704
4/29/10	Lower South Fork	North Bend	120	RBT	LkWhOcl-SnoqOmy2	09IK0057	0.11	0.008	0.001	0.098	0.021	0.762
4/29/10	Lower South Fork	North Bend	109	Onxx	SnoqOcl-SnoqOmy1	09IK0051	0.005	0.005	0.006	0.676	0.22	0.088
4/29/10	Lower South Fork	North Bend	223	RBT	SnoqOcl-SnoqOmy1,2	09IK0059	0.006	0.016	0.002	0.194	0.471	0.311
6/3/10	Lower South Fork	North Bend	ALEVIN	Onxx	SnoqOcl	09IK0064	0.003	0.005	0.001	0.989	0.001	0

Table 7. (Continued)

Date	River Section	River Segment	TL (mm)	Field ID	Type	Fish ID	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy1	SnoqOmy2
7/13/10	Lower South Fork	North Bend	28	Onxx	SnoqOcl-SnoqOmy2	09IK0075	0.005	0.003	0.001	0.743	0.07	0.177
10/6/09	Upper Mainstem	Three Forks	294	CCT	CedarOcl-SnoqOcl	09IJ0051	0.005	0.13	0.002	0.854	0.004	0.005
10/6/09	Upper Mainstem	Three Forks	317	CCT	SnoqOcl-SnoqOmy1,2	09IJ0052	0.007	0.017	0.002	0.379	0.124	0.472
10/6/09	Upper Mainstem	Three Forks	322	CCT	SnoqOcl	09IJ0053	0.01	0.004	0.009	0.976	0.001	0
10/8/09	Upper Mainstem	Three Forks	336	CCT	LkWhOcl-SnoqOcl	09IJ0054	0.1	0.008	0.005	0.879	0.004	0.004
6/18/10	Upper Mainstem	Three Forks	320	CCT	SnoqOcl	09IJ0113	0.09	0.011	0.001	0.897	0.001	0
6/18/10	Upper Mainstem	Three Forks	300	CCT	SnoqOcl-SnoqOmy2	09IJ0114	0.014	0.013	0.006	0.481	0.007	0.48
6/18/10	Upper Mainstem	Three Forks	259	CCT	SnoqOcl-SnoqOmy1	09IJ0115	0.013	0.004	0.001	0.393	0.585	0.004
6/18/10	Upper Mainstem	Three Forks	210	CCT	SnoqOcl	09IJ0116	0.005	0.008	0.001	0.984	0.001	0
6/25/10	Upper Mainstem	Three Forks	95	CCT	LkWhOcl-SnoqOcl	09IJ0123	0.288	0.04	0.003	0.669	0.001	0.001
6/25/10	Upper Mainstem	Three Forks	95	CCT	CedarOcl-SnoqOcl	09IJ0124	0.003	0.151	0.006	0.839	0.001	0.001
7/7/10	Upper Mainstem	Three Forks	113	CCT	SnoqOcl	09IJ0130	0.014	0.049	0.001	0.935	0.001	0.001
7/7/10	Upper Mainstem	Three Forks	132	CCT	SnoqOcl	09IJ0131	0.016	0.04	0.001	0.939	0.004	0.001
7/7/10	Upper Mainstem	Three Forks	133	CCT	SnoqOcl	09IJ0132	0.024	0.008	0.002	0.966	0.001	0
7/7/10	Upper Mainstem	Three Forks	169	CCT	SnoqOcl	09IJ0133	0.004	0.006	0.001	0.988	0.001	0.001
7/7/10	Upper Mainstem	Three Forks	182	CCT	SnoqOcl	09IJ0134	0.017	0.011	0.001	0.969	0.001	0.001
7/7/10	Upper Mainstem	Three Forks	227	CCT	SnoqOcl	09IJ0135	0.026	0.007	0.001	0.966	0.001	0
7/7/10	Upper Mainstem	Three Forks	161	Onxx	SnoqOcl	09IK0074	0.009	0.004	0.001	0.985	0.001	0
9/13/10	Upper Mainstem	Three Forks	300	CCT	SnoqOcl	09IK0106	0.013	0.005	0.002	0.979	0.001	0
9/13/10	Upper Mainstem	Three Forks	254	CCT	SnoqOcl	09IK0107	0.005	0.006	0.001	0.987	0.001	0
9/13/10	Upper Mainstem	Three Forks	225	CCT	SnoqOcl	09IK0108	0.007	0.006	0.001	0.985	0.001	0
9/13/10	Upper Mainstem	Three Forks	290	CCT	SnoqOcl	09IK0109	0.016	0.005	0.002	0.976	0	0
2/2/10	Lower Mainstem	Three Forks	198	CCT	SnoqOcl	09IJ0072	0.009	0.088	0.002	0.9	0.001	0.001
2/2/10	Lower Mainstem	Three Forks	145	CCT	SnoqOcl	09IJ0073	0.004	0.003	0.002	0.99	0.001	0
6/23/10	Lower Mainstem	Three Forks	421	CCT	Ocl-Omy1	09IJ0120	0.132	0.284	0.004	0.054	0.51	0.017
6/23/10	Lower Mainstem	Three Forks	246	Onxx	SnoqOcl-SnoqOmy1	09IJ0121	0.006	0.005	0.001	0.413	0.565	0.009
9/13/10	Lower Mainstem	Three Forks	282	CCT	SnoqOcl	09IK0110	0.009	0.011	0.001	0.979	0.001	0
9/13/10	Lower Mainstem	Three Forks	292	CCT	LkWhOcl-SnoqOcl	09IK0111	0.345	0.024	0.001	0.628	0.001	0.001
9/13/10	Lower Mainstem	Three Forks	226	CCT	SnoqOcl	09IK0112	0.004	0.005	0.002	0.987	0.001	0
9/13/10	Lower Mainstem	Three Forks	195	CCT	SnoqOcl	09IK0113	0.006	0.005	0.001	0.987	0.001	0

Appendix I. Allele frequencies: values over 0.5 are in pink cells and values between 0.1 and 0.5 are in green cells. The column "Private?" lists alleles found in a single collection in this study (private alleles).

Locus	Allele	Size	LkWh Ocl	Cedar Ocl	Twin Ocl	Snoq Ocl	Snoq Omy	Overall	Private?
Ogo-3	1	182	1	0.8947	0	0.874	0.4563	0.6603	
Ogo-3	2	186	0	0	0	0.0076	0.0278	0.0144	
Ogo-3	3	191	0	0.0263	0	0.0229	0.0317	0.024	
Ogo-3	4	194	0	0	0	0	0.004	0.0016	SnoqOmy
Ogo-3	5	195	0	0.0789	0	0.0458	0.1944	0.1026	
Ogo-3	6	197	0	0	0	0.0115	0.0516	0.0256	
Ogo-3	7	199	0	0	0	0.0115	0.1349	0.0593	
Ogo-3	8	200	0	0	0	0.0038	0.004	0.0032	
Ogo-3	9	201	0	0	0	0.0038	0.0198	0.0096	
Ogo-3	10	203	0	0	0	0.0038	0.0278	0.0128	
Ogo-3	11	218	0	0	0.0263	0	0	0.0016	TwinOcl
Ogo-3	12	226	0	0	0	0.0153	0.0159	0.0128	
Ogo-3	13	228	0	0	0	0	0.0079	0.0032	SnoqOmy
Ogo-3	14	230	0	0	0.6579	0	0.0198	0.0481	
Ogo-3	15	242	0	0	0.0263	0	0	0.0016	TwinOcl
Ogo-3	16	251	0	0	0.2105	0	0	0.0128	TwinOcl
Ogo-3	17	253	0	0	0.0263	0	0.004	0.0032	
Ogo-3	18	261	0	0	0.0526	0	0	0.0032	TwinOcl
Ogo-3		# samples	17	19	19	131	126	312	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
Omm1138+a	1	150	0	0	0	0.0038	0.018	0.0091	
Omm1138+a	2	152	0	0	0	0.0114	0.0468	0.0244	
Omm1138+a	3	154	0	0	0	0.0152	0.0755	0.0381	
Omm1138+a	4	156	0	0.0667	0.125	0.0568	0.3273	0.1723	
Omm1138+a	5	158	0	0	0	0.0379	0.0935	0.0549	
Omm1138+a	6	160	0	0	0.825	0.0985	0.054	0.1128	
Omm1138+a	7	162	0.6136	0.0333	0	0.0758	0.0216	0.0823	
Omm1138+a	8	166	0.3864	0.9	0.025	0.7008	0.3633	0.5046	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Omm1138+a	9	170	0	0	0.025	0	0	0.0015	TwinOcl
Omm1138+a		# samples	22	15	20	132	139	328	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
One-108	1	134	0	0	0	0.0036	0.0071	0.0045	
One-108	2	148	0	0.25	0	0.0362	0.0143	0.0344	
One-108	3	152	0.0263	0.4167	0	0.3659	0.1536	0.2395	
One-108	4	156	0.2105	0.0833	0	0.3116	0.1857	0.2231	
One-108	5	161	0.1053	0.0278	0	0.0326	0.0071	0.024	
One-108	6	164	0	0.0556	0	0.0217	0.0929	0.0509	
One-108	7	169	0	0	0	0.0254	0.0429	0.0284	
One-108	8	173	0.0263	0	0	0.0145	0.0214	0.0165	
One-108	9	177	0	0	0	0.0036	0.025	0.012	
One-108	10	181	0	0	0	0.0109	0.0143	0.0105	
One-108	11	185	0	0	0	0.0109	0.0321	0.018	
One-108	12	189	0	0	0	0.0036	0.0179	0.009	
One-108	13	193	0	0	0	0.0145	0.0607	0.0314	
One-108	14	197	0	0	0	0.0181	0.0214	0.0165	
One-108	15	201	0.4211	0.0833	0	0.0072	0.0393	0.0479	
One-108	16	205	0.1579	0.0278	0	0.0435	0.0929	0.0674	
One-108	17	209	0	0.0556	0	0.0072	0.0321	0.0195	
One-108	18	213	0	0	0	0	0.0107	0.0045	SnoqOmy
One-108	19	217	0	0	0	0	0.0036	0.0015	SnoqOmy
One-108	20	225	0	0	0	0.0036	0.0107	0.006	
One-108	21	233	0	0	0.6842	0	0	0.0389	TwinOcl
One-108	22	237	0	0	0.1842	0.0072	0.0393	0.0299	
One-108	23	241	0	0	0	0.0072	0.0179	0.0105	
One-108	24	244	0	0	0	0	0.0107	0.0045	SnoqOmy
One-108	25	249	0	0	0.0526	0.0109	0.0143	0.0135	
One-108	26	253	0	0	0	0.0036	0.0071	0.0045	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
One-108	27	257	0	0	0.0263	0.0036	0	0.003	
One-108	28	261	0	0	0.0526	0.029	0.0036	0.0165	
One-108	29	267	0	0	0	0.0036	0	0.0015	SnoqOcl
One-108	30	317	0.0526	0	0	0	0.0214	0.012	
One-108		# samples	19	18	19	138	140	334	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
Ots-103	1	50	0	0	0	0.2555	0.1187	0.1537	
Ots-103	2	56	0	0	0	0.0073	0.0971	0.0433	
Ots-103	3	60	0.95	0.9211	0	0.6168	0.2914	0.4821	
Ots-103	4	64	0	0	0.075	0	0	0.0045	TwinOcl
Ots-103	5	72	0	0	0.45	0.0073	0.0072	0.0328	
Ots-103	6	74	0	0	0.1	0	0.0036	0.0075	
Ots-103	7	76	0	0	0.25	0	0.0072	0.0179	
Ots-103	8	78	0	0.0526	0	0.0036	0.0036	0.006	
Ots-103	9	82	0.05	0.0263	0.075	0.1095	0.4568	0.2433	
Ots-103	10	86	0	0	0.05	0	0.0144	0.009	
Ots-103		# samples	20	19	20	137	139	335	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
Omy-77	1	83	0	0	0	0	0.0219	0.0091	SnoqOmy
Omy-77	2	97	0	0	0	0.0074	0.0401	0.0197	
Omy-77	3	99	0	0	0.0938	0.0185	0.1241	0.0636	
Omy-77	4	103	0	0	0.8438	0.0111	0.0365	0.0606	
Omy-77	5	105	0	0	0	0.0037	0.0401	0.0182	
Omy-77	6	107	0	0	0.0312	0	0.0365	0.0167	
Omy-77	7	108	0	0.2955	0.0312	0.1852	0.0876	0.1333	
Omy-77	8	110	0	0	0	0.0148	0.0219	0.0152	
Omy-77	9	112	0	0	0	0.0111	0	0.0045	SnoqOcl
Omy-77	10	114	0	0	0	0.0444	0.1095	0.0636	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Omy-77	11	116	0.025	0.1136	0	0.0074	0.0146	0.0182	
Omy-77	12	118	0.025	0	0	0.0074	0.0365	0.0197	
Omy-77	13	120	0	0.0455	0	0	0.0036	0.0045	
Omy-77	14	122	0	0.0227	0	0.0111	0.0036	0.0076	
Omy-77	15	124	0	0.0227	0	0.0037	0.0182	0.0106	
Omy-77	16	126	0.025	0.1364	0	0.037	0.0657	0.053	
Omy-77	17	128	0	0.0227	0	0.0481	0.0766	0.053	
Omy-77	18	130	0.625	0.0909	0	0.0444	0.0255	0.0727	
Omy-77	19	132	0.225	0.2045	0	0.4111	0.1861	0.2727	
Omy-77	20	134	0.025	0	0	0.0148	0.0219	0.0167	
Omy-77	21	136	0	0.0455	0	0.0889	0.0219	0.0485	
Omy-77	22	140	0.05	0	0	0.0296	0.0073	0.0182	
Omy-77		# samples	20	22	16	135	137	330	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
Ots-1	1	158	0	0	0	0	0.0407	0.0171	SnoqOmy
Ots-1	2	160	0	0	0	0	0.0185	0.0078	SnoqOmy
Ots-1	3	164	0	0	0	0.0038	0.0185	0.0093	
Ots-1	4	166	0	0.0227	0	0.0573	0.1593	0.0916	
Ots-1	5	168	0	0.0227	0	0.0267	0.063	0.0388	
Ots-1	6	170	0	0	0	0.0038	0.1	0.0435	
Ots-1	7	172	0	0	0	0	0.0037	0.0016	SnoqOmy
Ots-1	8	177	0	0	0	0	0.0037	0.0016	SnoqOmy
Ots-1	9	179	0	0	0	0.0115	0.0407	0.0217	
Ots-1	10	181	0	0	0	0	0.0037	0.0016	SnoqOmy
Ots-1	11	237	0	0.0227	0	0.0038	0.0037	0.0047	
Ots-1	12	241	0	0	0	0.0229	0.0519	0.0311	
Ots-1	13	243	0	0	0.0357	0	0.0074	0.0047	
Ots-1	14	245	0	0	0	0	0.0259	0.0109	SnoqOmy
Ots-1	15	247	0	0	0	0	0.0037	0.0016	SnoqOmy

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Ots-1	16	258	0	0	0.7857	0.0802	0.0259	0.0776	
Ots-1	17	260	0.05	0.4091	0	0.0763	0.063	0.0885	
Ots-1	18	262	0.875	0.1364	0	0.2557	0.1111	0.2143	
Ots-1	19	264	0	0	0	0	0.0037	0.0016	SnoqOmy
Ots-1	20	266	0	0.0227	0	0.0038	0.0037	0.0047	
Ots-1	21	268	0	0.0227	0	0	0	0.0016	CedarOcl
Ots-1	22	270	0.075	0	0	0.1718	0.0593	0.0994	
Ots-1	23	272	0	0.0227	0	0.0458	0.0148	0.0264	
Ots-1	24	276	0	0.3182	0	0.0267	0.0481	0.0528	
Ots-1	25	280	0	0	0	0.0802	0.037	0.0481	
Ots-1	26	282	0	0	0	0.0802	0.0741	0.0637	
Ots-1	27	288	0	0	0	0.0267	0	0.0109	SnoqOcl
Ots-1	28	292	0	0	0	0.0191	0.0111	0.0124	
Ots-1	29	297	0	0	0	0.0038	0	0.0016	SnoqOcl
Ots-1	30	315	0	0	0.0357	0	0	0.0016	TwinOcl
Ots-1	31	319	0	0	0.0357	0	0.0037	0.0031	
Ots-1	32	323	0	0	0.1071	0	0	0.0047	TwinOcl
Ots-1		# samples	20	22	14	131	135	322	

Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
Ots-3M	1	128	0.1	0.0909	0	0.015	0.0109	0.0228	
Ots-3M	2	132	0	0	0.125	0	0.029	0.0182	
Ots-3M	3	134	0	0	0	0.0038	0.0399	0.0182	
Ots-3M	4	136	0.025	0.0455	0	0.0752	0.2464	0.1383	
Ots-3M	5	138	0	0.0455	0	0.0639	0.2065	0.1155	
Ots-3M	6	140	0	0	0.125	0.0075	0.0616	0.035	
Ots-3M	7	145	0	0	0.75	0	0.0181	0.0441	
Ots-3M	8	152	0	0	0	0.0075	0	0.003	SnoqOcl
Ots-3M	9	158	0	0	0	0.0038	0.0036	0.003	
Ots-3M	10	160	0	0.1591	0	0.0038	0	0.0122	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Ots-3M	11	162	0.025	0	0	0.0075	0.0072	0.0076	
Ots-3M	12	164	0	0.0682	0	0.0338	0.0072	0.0213	
Ots-3M	13	166	0.1	0	0	0.0038	0.0036	0.0091	
Ots-3M	14	168	0	0.0227	0	0	0.0036	0.003	
Ots-3M	15	170	0	0	0	0.0451	0.0217	0.0274	
Ots-3M	16	172	0	0.1818	0	0.203	0.1486	0.1565	
Ots-3M	17	174	0	0.0455	0	0.2632	0.0725	0.1398	
Ots-3M	18	176	0	0.1818	0	0.0451	0.0217	0.0395	
Ots-3M	19	178	0	0.0227	0	0.0038	0.0072	0.0061	
Ots-3M	20	180	0	0.0227	0	0.0865	0.0181	0.0441	
Ots-3M	21	182	0	0.0227	0	0.0827	0.0399	0.0517	
Ots-3M	22	184	0	0	0	0	0.0036	0.0015	SnoqOmy
Ots-3M	23	186	0	0	0	0	0.0036	0.0015	SnoqOmy
Ots-3M	24	188	0	0	0	0	0.0036	0.0015	SnoqOmy
Ots-3M	25	190	0	0.0682	0	0.0113	0.0036	0.0106	
Ots-3M	26	192	0.425	0	0	0.0226	0.0036	0.0365	
Ots-3M	27	194	0	0.0227	0	0	0	0.0015	CedarOcl
Ots-3M	28	196	0	0	0	0.0038	0	0.0015	SnoqOcl
Ots-3M	29	198	0.325	0	0	0.0075	0.0145	0.0289	
Ots-3M		# samples	20	22	16	133	138	329	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy001	1	3	0	0.0833	0	0.0845	0.3793	0.1904	
AOmy001	2	4	1	0.9167	1	0.9155	0.6207	0.8096	
AOmy001		# samples	24	24	24	148	145	365	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy004	1	2	0.1458	0.1739	0	0.36	0.3192	0.2892	
AOmy004	2	3	0.8542	0.8261	1	0.64	0.6808	0.7108	
AOmy004		# samples	24	23	23	125	130	325	

Appendix I. (Continued)

Locus	Allele	Size	LkWh Ocl	Cedar Ocl	Twin Ocl	Snoq Ocl	Snoq Omy	Overall	Private?
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy005	1	3	0	0	0	0.0068	0.0203	0.0109	
AOmy005	2	5	1	1	1	0.9932	0.9797	0.9891	
AOmy005		# samples	24	24	24	148	148	368	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy006	1	4	1	0.9792	1	0.9493	0.8537	0.9196	
AOmy006	2	5	0	0.0208	0	0.0507	0.1463	0.0804	
AOmy006		# samples	24	24	24	148	147	367	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy009	1	3	1	0.9583	1	0.9592	0.6849	0.8548	
AOmy009	2	5	0	0.0417	0	0.0408	0.3151	0.1452	
AOmy009		# samples	24	24	24	147	146	365	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy013	1	3	1	1	1	1	1	1	
AOmy013		# samples	24	24	24	146	146	364	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy015	1	3	1	0.9792	1	0.9932	0.969	0.9836	
AOmy015	2	5	0	0.0208	0	0.0068	0.031	0.0164	
AOmy015		# samples	24	24	24	148	145	365	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy016	1	3	1	0.9783	1	0.9558	0.7925	0.8973	
AOmy016	2	5	0	0.0217	0	0.0442	0.2075	0.1027	
AOmy016		# samples	24	23	24	147	147	365	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy017	1	2	0	0	1	0.0101	0.0972	0.1061	
AOmy017	2	4	1	1	0	0.9899	0.9028	0.8939	
AOmy017		# samples	24	24	23	148	144	363	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy018	1	3	1	1	1	1	1	1	
AOmy018		# samples	24	24	24	148	147	367	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy019	1	2	0	0	0	0	0.0411	0.0164	SnoqOmy
AOmy019	2	4	1	1	1	1	0.9589	0.9836	
AOmy019		# samples	24	24	24	148	146	366	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy020	1	3	0	0.3043	1	0.2483	0.3147	0.3116	
AOmy020	2	5	1	0.6957	0	0.7517	0.6853	0.6884	
AOmy020		# samples	24	23	24	147	143	361	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy021	1	3	1	0.9583	1	0.9097	0.6701	0.8278	
AOmy021	2	5	0	0.0417	0	0.0903	0.3299	0.1722	
AOmy021		# samples	24	24	24	144	147	363	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy027	1	2	0	0.0625	0	0.0236	0.1803	0.0858	
AOmy027	2	3	1	0.9375	1	0.9764	0.8197	0.9142	
AOmy027		# samples	24	24	24	148	147	367	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy036	1	4	0	0.0208	0.2292	0.1724	0.2568	0.1887	
AOmy036	2	5	1	0.9792	0.7708	0.8276	0.7432	0.8113	
AOmy036		# samples	24	24	24	145	146	363	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy040	1	3	0	0.0833	0	0.1027	0.5578	0.2712	
AOmy040	2	4	1	0.9167	1	0.8973	0.4422	0.7288	
AOmy040		# samples	24	24	24	146	147	365	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy042	1	1	1	1	1	0.9626	0.6724	0.8544	
AOmy042	2	5	0	0	0	0.0374	0.3276	0.1456	
AOmy042		# samples	24	24	24	147	145	364	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy047	1	4	1	0.9583	1	0.9865	0.863	0.9372	
AOmy047	2	5	0	0.0417	0	0.0135	0.137	0.0628	
AOmy047		# samples	24	24	24	148	146	366	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy051	1	2	0	0.0208	0	0.0236	0.0714	0.0395	
AOmy051	2	5	1	0.9792	1	0.9764	0.9286	0.9605	
AOmy051		# samples	24	24	24	148	147	367	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy055	1	3	1	1	1	0.9899	0.9863	0.9904	
AOmy055	2	4	0	0	0	0.0101	0.0137	0.0096	
AOmy055		# samples	24	24	24	148	146	366	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy062	1	2	1	0.9583	1	0.983	0.9456	0.9686	
AOmy062	2	5	0	0.0417	0	0.017	0.0544	0.0314	
AOmy062		# samples	24	24	24	147	147	366	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy065	1	3	0	0.0208	0	0.0608	0.3412	0.163	
AOmy065	2	5	1	0.9792	1	0.9392	0.6588	0.837	
AOmy065		# samples	24	24	24	148	148	368	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy073	1	3	0	0.1042	0	0.102	0.4075	0.211	
AOmy073	2	5	1	0.8958	1	0.898	0.5925	0.789	
AOmy073		# samples	24	24	24	147	146	365	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy079	1	3	0.0208	0.0833	------	0.0608	0.2222	0.1279	
AOmy079	2	5	0.9792	0.9167	------	0.9392	0.7778	0.8721	
AOmy079		# samples	24	24	------	148	144	340	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy081	1	3	1	0.9792	1	0.9864	0.9286	0.9645	
AOmy081	2	5	0	0.0208	0	0.0136	0.0714	0.0355	
AOmy081		# samples	24	24	24	147	147	366	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy092	1	4	0	0	0	0.0169	0.1027	0.0478	
AOmy092	2	5	1	1	1	0.9831	0.8973	0.9522	
AOmy092		# samples	24	24	24	148	146	366	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy100	1	2	0	0.0208	0	0.0608	0.2721	0.1349	
AOmy100	2	5	1	0.9792	1	0.9392	0.7279	0.8651	
AOmy100		# samples	24	24	24	148	147	367	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy103	1	4	1	0.9167	1	0.9724	0.808	0.9085	
AOmy103	2	5	0	0.0833	0	0.0276	0.192	0.0915	
AOmy103		# samples	24	24	24	145	138	355	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy108	1	2	1	1	1	0.9493	0.7676	0.8878	
AOmy108	2	5	0	0	0	0.0507	0.2324	0.1122	
AOmy108		# samples	24	24	23	148	142	361	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy110	1	2	1	0.9583	1	0.9358	0.7687	0.8787	
AOmy110	2	4	0	0.0417	0	0.0642	0.2313	0.1213	
AOmy110		# samples	24	24	24	148	147	367	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy111	1	1	1	0.9375	1	0.9479	0.7993	0.8939	
AOmy111	2	4	0	0.0625	0	0.0521	0.2007	0.1061	
AOmy111		# samples	24	24	24	144	147	363	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy112	1	3	1	0.875	1	0.9048	0.637	0.8082	
AOmy112	2	5	0	0.125	0	0.0952	0.363	0.1918	
AOmy112		# samples	24	24	24	147	146	365	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy113	1	3	1	1	1	0.9797	0.9422	0.9687	
AOmy113	2	5	0	0	0	0.0203	0.0578	0.0313	
AOmy113		# samples	24	24	24	148	147	367	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy114	1	2	1	0.913	1	0.973	0.8562	0.926	
AOmy114	2	5	0	0.087	0	0.027	0.1438	0.074	
AOmy114		# samples	24	23	24	148	146	365	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy117	1	4	0	0	0	0.0709	0.2736	0.1386	
AOmy117	2	5	1	1	1	0.9291	0.7264	0.8614	
AOmy117		# samples	24	24	24	148	148	368	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy118	1	3	1	0.9792	1	0.9831	0.8367	0.9264	
AOmy118	2	5	0	0.0208	0	0.0169	0.1633	0.0736	
AOmy118		# samples	24	24	24	148	147	367	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy120	1	3	0.9583	0.9583	1	0.9595	0.8639	0.9237	
AOmy120	2	5	0.0417	0.0417	0	0.0405	0.1361	0.0763	
AOmy120		# samples	24	24	24	148	147	367	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy121	1	2	1	0.9792	1	0.9831	0.9493	0.9715	
AOmy121	2	4	0	0.0208	0	0.0169	0.0507	0.0285	
AOmy121		# samples	24	24	24	148	148	368	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy123	1	2	1	0.9375	1	0.869	0.4896	0.7396	
AOmy123	2	4	0	0.0625	0	0.131	0.5104	0.2604	
AOmy123		# samples	24	24	24	145	144	361	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy124	1	2	1	0.9583	1	0.9824	0.8986	0.9489	
AOmy124	2	3	0	0.0417	0	0.0176	0.1014	0.0511	
AOmy124		# samples	24	24	24	142	148	362	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy125	1	3	0	0.0625	0	0.0882	0.3893	0.1988	
AOmy125	2	5	1	0.9375	1	0.9118	0.6107	0.8012	
AOmy125		# samples	24	24	18	136	140	342	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy127	1	4	0.0208	0.1042	0.1875	0.1223	0.5746	0.2942	
AOmy127	2	5	0.9792	0.8958	0.8125	0.8777	0.4254	0.7058	
AOmy127		# samples	24	24	24	139	134	345	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy128	1	2	0	0	0	0.0034	0.017	0.0082	
AOmy128	2	4	1	1	1	0.9966	0.983	0.9918	
AOmy128		# samples	24	24	24	146	147	365	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy129	1	3	1	1	1	0.9966	0.9694	0.9864	
AOmy129	2	5	0	0	0	0.0034	0.0306	0.0136	
AOmy129		# samples	24	24	24	148	147	367	

Appendix I. (Continued)

Locus	Allele	Size	LkWh Ocl	Cedar Ocl	Twin Ocl	Snoq Ocl	Snoq Omy	Overall	Private?
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy132	1	3	1	1	1	0.9577	0.9239	0.9531	
AOmy132	2	5	0	0	0	0.0423	0.0761	0.0469	
AOmy132		# samples	24	24	24	142	138	352	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy133	1	2	1	1	1	0.9931	0.9623	0.9821	
AOmy133	2	3	0	0	0	0.0069	0.0377	0.0179	
AOmy133		# samples	24	24	24	145	146	363	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy134	1	3	1	0.8846	1	0.8921	0.6301	0.7951	
AOmy134	2	5	0	0.1154	0	0.1079	0.3699	0.2049	
AOmy134		# samples	22	13	24	139	146	344	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy135	1	3	1	1	1	0.9662	0.9375	0.9615	
AOmy135	2	5	0	0	0	0.0338	0.0625	0.0385	
AOmy135		# samples	24	24	24	148	144	364	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy136	1	3	1	0.9583	1	0.9218	0.6713	0.8356	
AOmy136	2	5	0	0.0417	0	0.0782	0.3287	0.1644	
AOmy136		# samples	24	24	24	147	143	362	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy137	1	2	1	1	1	0.9797	0.966	0.9782	
AOmy137	2	5	0	0	0	0.0203	0.034	0.0218	
AOmy137		# samples	24	24	24	148	147	367	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy138	1	4	1	1	1	1	0.993	0.9972	
AOmy138	2	5	0	0	0	0	0.007	0.0028	SnoqOmy
AOmy138		# samples	24	24	24	148	143	363	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy139	1	2	0.9286	0.1087	0	0.725	0.3546	0.4736	
AOmy139	2	5	0.0714	0.8913	1	0.275	0.6454	0.5264	
AOmy139		# samples	14	23	24	120	141	322	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy140	1	3	1	0.8636	1	0.8322	0.4792	0.711	
AOmy140	2	5	0	0.1364	0	0.1678	0.5208	0.289	
AOmy140		# samples	24	22	20	143	144	353	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy143	1	5	1	1	1	1	1	1	
AOmy143		# samples	24	24	24	148	147	367	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy146	1	3	0.6042	0.5	0.9375	0.465	0.3537	0.4627	
AOmy146	2	5	0.3958	0.5	0.0625	0.535	0.6463	0.5373	
AOmy146		# samples	24	24	24	143	147	362	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy147	1	3	0	0.0208	0	0.0845	0.431	0.2068	
AOmy147	2	5	1	0.9792	1	0.9155	0.569	0.7932	
AOmy147		# samples	24	24	24	148	145	365	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy148	1	2	1	0.9792	1	0.9932	0.9762	0.9863	
AOmy148	2	5	0	0.0208	0	0.0068	0.0238	0.0137	
AOmy148		# samples	24	24	24	146	147	365	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy149	1	3	0	0.0208	0	0.0479	0.2517	0.1219	
AOmy149	2	5	1	0.9792	1	0.9521	0.7483	0.8781	
AOmy149		# samples	24	24	24	146	147	365	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy150	1	2	1	0.9792	1	0.975	0.8759	0.9355	
AOmy150	2	5	0	0.0208	0	0.025	0.1241	0.0645	
AOmy150		# samples	24	24	8	140	145	341	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy151	1	2	0	0.0526	0	0.2209	0.4391	0.266	
AOmy151	2	5	1	0.9474	1	0.7791	0.5609	0.734	
AOmy151		# samples	21	19	24	86	115	265	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
AOmy153	1	2	1	1	1	1	1	1	
AOmy153		# samples	24	21	24	147	147	363	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI001	1	3	1	0.8077	1	0.7958	0.3511	0.641	
ASpI001	2	5	0	0.1923	0	0.2042	0.6489	0.359	
ASpI001		# samples	24	13	24	120	131	312	

Appendix I. (Continued)

Locus	Allele	Size	LkWh Ocl	Cedar Ocl	Twin Ocl	Snoq Ocl	Snoq Omy	Overall	Private?
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI002	1	2	0	0.0625	0	0.1259	0.5548	0.2784	
ASpI002	2	3	1	0.9375	1	0.8741	0.4452	0.7216	
ASpI002		# samples	24	24	24	143	146	361	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI004	1	2	0	0	1	0.0142	0.0342	0.0864	
ASpI004	2	3	1	1	0	0.9858	0.9658	0.9136	
ASpI004		# samples	24	24	24	141	146	359	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI005	1	2	0	0	0.9583	0	0.0274	0.0738	
ASpI005	2	3	1	1	0.0417	1	0.9726	0.9262	
ASpI005		# samples	24	24	24	148	146	366	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI007	1	3	1	0.625	1	0.7473	0.3092	0.5449	
ASpI007	2	5	0	0.375	0	0.2527	0.6908	0.4551	
ASpI007		# samples	2	8	24	91	131	256	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI008	1	2	0	0.087	0	0.1602	0.5804	0.3085	
ASpI008	2	5	1	0.913	1	0.8398	0.4196	0.6915	
ASpI008		# samples	24	23	24	128	143	342	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI009	1	3	1	1	0.0625	1	0.9692	0.9262	
ASpI009	2	5	0	0	0.9375	0	0.0308	0.0738	
ASpI009		# samples	24	24	24	148	146	366	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI010	1	3	0	0.1042	0	0.113	0.5621	0.2769	
ASpI010	2	5	1	0.8958	1	0.887	0.4379	0.7231	
ASpI010		# samples	24	24	24	146	145	363	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI012	1	2	1	1	1	1	0.9966	0.9986	
ASpI012	2	3	0	0	0	0	0.0034	0.0014	SnoqOmy
ASpI012		# samples	24	24	24	146	146	364	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI013	1	2	1	0.9583	0	0.726	0.3367	0.5548	
ASpI013	2	3	0	0.0417	1	0.274	0.6633	0.4452	
ASpI013		# samples	24	24	24	146	147	365	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI014	1	3	0	0.0833	0	0.1081	0.5646	0.2752	
ASpI014	2	4	1	0.9167	1	0.8919	0.4354	0.7248	
ASpI014		# samples	24	24	24	148	147	367	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI017	1	3	0	0.1087	0	0.1336	0.5578	0.2857	
ASpI017	2	5	1	0.8913	1	0.8664	0.4422	0.7143	
ASpI017		# samples	24	23	24	146	147	364	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI018	1	2	0	0.0833	0	0.1187	0.5586	0.2795	
ASpI018	2	3	1	0.9167	1	0.8813	0.4414	0.7205	
ASpI018		# samples	24	24	24	139	145	356	

Appendix I. (Continued)

Locus	**Allele**	**Size**	**LkWh Ocl**	**Cedar Ocl**	**Twin Ocl**	**Snoq Ocl**	**Snoq Omy**	**Overall**	**Private?**
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI019	1	2	1	0.9167	1	0.8759	0.4448	0.7207	
ASpI019	2	5	0	0.0833	0	0.1241	0.5552	0.2793	
ASpI019		# samples	24	24	24	141	145	358	
Locus	Allele	Size	LkWhOcl	CedarOcl	TwinOcl	SnoqOcl	SnoqOmy	Overall	Private?
ASpI020	1	3	0.9583	0.9167	1	0.8664	0.4414	0.7149	
ASpI020	2	5	0.0417	0.0833	0	0.1336	0.5586	0.2851	
ASpI020		# samples	24	24	24	146	145	363	