Project Title: Population structure and genetic characteristics of summer steelhead (*Oncorhynchus mykiss*) in the Deschutes River Sub-basin, Oregon

Project Progress Report FY2007

Submitted: March 2008

Andrew P. Matala[1]
(Andrew_Matala@fws.gov)

William R. Ardren[1]
(William_Ardren@fws.gov)

and

David Hand[2]
(david_hand@fws.gov)

Doug Olson[2]
(doug_olson@fws.gov)

Howard Schaller[2]
Howard_Schaller@fws.gov

[1]U.S. Fish & Wildlife Service
Abernathy Fish Technology Center
Conservation Genetics Program
1440 Abernathy Creek Road
Longview, WA 98632
TEL: 360-425-6072
FAX: 360-636-1855

[2]U.S. Fish & Wildlife Service
Columbia River Fisheries Program Office
1211 SE Cardinal Ct., Suite 100
Vancouver, WA 98683
TEL: 360-604-2518
FAX: 360-604-2500

Cooperators: Oregon Department of Fish and Wildlife, Confederated Tribes of the Warm Springs Reservation of Oregon, NOAA Fisheries-Northwest Fisheries Science Center, and the Columbia River Inter-Tribal Fish Commission

BACKGROUND

Summer steelhead trout (anadromous form of *Oncorhynchus mykiss*) in the Deschutes River subbasin, are part of the Mid-Columbia Steelhead Evolutionarily Significant Unit (ESU) that has been listed as threatened by NOAA-Fisheries since 1999. In order to evaluate recovery needs and implement a recovery plan for steelhead in the Deschutes River, the Interior Columbia River Technical Recovery Team (2003) attempted to characterize population structure and identify discrete populations throughout the subbasin. The Deschutes River Basin represents a region of substantial diversity among *O. mykiss spp* (Kostow 1995), likely indicative of multiple colonization events (Currens *et al.* 1990), and the influence of geologic and hydrologic barriers (Currens *et al.* 1990; Zimmerman and Ratliff 2003, Stuart *et al.* 2007). The current distribution and genetic origins of populations throughout the Deschutes River Basin have not been clearly delineated. Similarly the relationship between life history types (i.e. resident and anadromous) through much of the region is poorly understood.

With a limited amount of genetic data and information available, the recovery team relied on life-history information and differences in topographic and habitat conditions to describe populations. Two potentially independent (distinct) populations were identified: 1) Deschutes River eastside tributaries, encompassing all of the eastside tributaries below Pelton Dam including the main-stem from its mouth to the confluence of Trout Creek, and 2) Deschutes River westside tributaries, encompassing all of the westside tributaries below Pelton Dam including the main-stem above the confluence of Trout Creek. The recovery team also identified that the areas above Pelton and Round Butte dams likely supported 1 or more populations historically. However, the team updated the population delineations in 2005, and clarified that areas historically used (or likely used) by anadromous O. mykiss would be included in the two existing population delineations (NMFS 2005). Therefore, the Deschutes-Eastside population now includes Willow Creek and its tributaries; the Deschutes-Westside population now includes Whychus Creek and any historically used portions of the Metolius River. The recovery team noted that the lack of comprehensive genetic information limited their ability to infer the relationship among putative populations, particularly between mainstem and tributary spawners. This lack of information was also recognized as a constraint on fishery managers and on the planning process for reintroductions in the upper subbasin (Northwest Power and Conservation Council 2004, Pelton-

Round Butte Hydroelectric Project Anadromous Fish Reintroduction Plan.). An analysis of genetic diversity will likely aid managers and recovery planners by improving our understanding of factors influencing the pattern and level of population structure of Deschutes River summer steelhead.

Another concern for fishery managers is the impact of stray hatchery steelhead on the wild steelhead populations. An average 47.1% of Round Butte Hatchery (RBH) marked steelhead passing Sherars Falls are not captured but remain in the Basin (ODFW 2004). The fate of these fish has implications for management, particularly in regard to their presence on spawning grounds, and reproductive success. Genetic structure analysis may provide evidence of measurable introgression between RBH steelhead and potential independent populations of wild steelhead in the lower Deschutes River or its tributaries. The large number of out-of-basin stray hatchery steelhead entering the Deschutes River presents an even greater potential for measurable introgression. Hatchery strays have accounted for an average of over 60% of the steelhead migrating past Sherars Falls since 1995 (Hand and Olson 2004). A paucity of information currently exists on the impact of straying on local populations; however, Chilcote (2003) used data from the Deschutes River steelhead population as part of an analysis of mixed spawning populations of wild and hatchery steelhead, and estimated a reduced level of productivity in populations that had a higher proportion of hatchery fish on the spawning grounds. It will be difficult to assess the impact of hatchery strays on the wild steelhead populations in the Deschutes River without first collecting a baseline of genetic information to characterize both stray populations and wild populations.

The Warm Springs River system is considered a valuable spawning area for wild summer steelhead native to the Deschutes River subbasin. Only wild summer steelhead are provided access to spawning grounds above the barrier at the Warm Springs National Fish Hatchery (WSNFH). Stray wild fish have no identifying marks, are indistinguishable from Warm Springs wild steelhead, and comprise an unknown proportion of the total return. Although the number of stray wild steelhead in the Deschutes is unknown, hatchery-marked stray steelhead comprised an average of 51% of total returns to the Warm Springs River between 1980 and 2003 (Hand and Olson 2004). Most of the hatchery strays that could be accounted for in the Warm Springs came from the Snake River basin. However there is a potential for unmarked juvenile hatchery origin steelhead to stray into the Warm Springs River. In 2003 approximately two million hatchery steelhead juveniles were released in the Columbia River basin without adipose fin clips. Genetically characterizing wild fish returning to the Warm Springs River provides both a genetic profile of Warm Springs River wild summer steelhead and a benchmark to assist in identifying wild strays or unmarked hatchery origin fish entering the system.

In 2004 the Columbia River Fisheries Program Office (CRFPO) secured funding for population monitoring and evaluation projects, as well as to help answer questions concerning hatchery operations and impacts to native fish communities. Representatives of state, federal and tribal agencies[1] met in The Dalles (December 2004) to develop a preliminary study plan addressing the Interior Columbia River Technical Recovery Team (2003) conclusion, which stated that insufficient information was available to describe the genetic relationship between steelhead in the mainstem Deschutes River, and east and west side tributaries of the Deschutes River below the Pelton Dam complex. At this meeting the representatives agreed that the study objectives would be implemented in a three-phase approach: 1) develop an understanding of the population structure and genetic variability among steelhead occupying tributaries and the mainstem Deschutes River downstream of the Pelton Round Butte Project with a three year genetic sampling protocol 2) evaluate the effect of out-of-basin strays on the Deschutes River populations (rate of strays and reproductive contribution of strays), and 3) provide information pertinent to brood stock selection that would assist with efforts to reintroduce steelhead to currently inaccessible portions of the middle and upper basin.

The results from the first two years of phase 1 (populations structure among east, west, and mainstem collections) will be provided in this progress report that begins to examine spatial, temporal and life history influences on population structure. The preliminary evaluation among Deschutes River summer steelhead integrates the TRT population attributes with a genetic characterization of *O. mykiss* from five tributaries and two mainstem locations downstream of the Pelton Round Butte Project.

METHODS

The CRFPO was responsible for coordinating field collections between agencies, and

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[1] CRFPO, Abernathy Fish Technology Center (AFTC), NOAA-Fisheries, Confederated Tribes of the Warm Springs Reservation of Oregon (CTWSRO), Oregon Department of Fish and Wildlife (ODFW) The Dalles and Bend District Offices, and La Grande Research Office.

sampling protocols were collaboratively developed. Target locations for tributary collections are identified in this report by region: westside, eastside, and Deschutes River mainstem. The ODFW led efforts to collect biological/genetic samples from three eastside tributaries (BuckHollow, BakeOven, and Trout Creeks) and the mainstem Deschutes River, while the CTWSRO collected samples from two westside tributaries (Warm Springs River and Shitike Creek; Figures 1&2). Juvenile steelhead were also collected from the mainstem Deschutes River above the confluence of Trout Creek (upper mainstem) and from the mainstem Deschutes River between Sherars Falls and the confluence of Trout Creek (lower mainstem). Genotypic data for a sample of juvenile fish (n=61) identified as resident *O. mykiss* through assignment tests (Hatch *et al.*), was provided by the Columbia River Inter-Tribal Fish Commission (CRITFC).

We set a target sample size of 50 juvenile steelhead from each population collected in both 2005 and 2006. Some areas within the basin are difficult to sample and typically support fewer fish with an anticipated lower yield from sampling. A standard target sample size of 50 individuals improves the likelihood uniform sampling (equal size) among sites, while meeting cost considerations associated with sample collection and processing. To help avoid non-random sampling (family groups) no more than 10 fin-clips were collected from each 100m of stream. For each population, field biologists identified sample sites for collection of progeny of anadromous steelhead. Sites and samples were identified based on a combination of factors including: 1) known steelhead spawning areas, 2) streamflow (time of year), 3) size and physical appearance of juveniles, and 4) stream access. Scale samples, fork lengths, and geo-reference information were recorded (when possible) for each sample collected. Based on the factors above, juvenile samples were classified as either a) anadromous steelhead (STH) if field crews were reasonably confident of anadromous parentage, b) resident (Omy) if field crews were reasonably confident of resident parentage, or c) unknown (Unk) if the parentage was indeterminate (Figures 1 and 2). In both 2005 and 2006, the target of 50 juvenile steelhead was not reached at all locations (Table 1) due to sampling limitations. A detailed description of sample collection for each population follows.

Eastside tributary sampling

In BakeOven and BuckHollow creeks, electrofishing was used to collect samples in the fall of both 2005 and 2006. The BakeOven creek samples in 2005 (n=50, STH) and 2006 (n=50, STH) were collected from sample sites approximately 12 rkm upstream from the confluence of the Deschutes River in a stretch of stream that ODFW biologists considered to be predominately inhabited by anadromous steelhead. In 2005, sample sites in BuckHollow Creek were limited to the lower 200 meters of the creek due to landowner access issues. The 2005 samples (n=50, UNK) were of unknown origin and could potentially contain a mix of resident and anadromous samples. In 2006, samples (n=50, STH) were collected from sites approximately 19 rkm upstream from the confluence of the Deschutes River in a known steelhead spawning area. In Trout Creek, samples were collected at a rotary screw trap, operated by ODFW, located near the mouth of the creek. Scale samples and gentic samples have been collected at the trap for several years as part of a long-term monitoring and evaluation program. Genetic samples from 2006 anadromous smolts (n=57, STH) were transferred to the genetics lab in September of 2007 and will be included in a future report.

Westside tributary sampling

Due to concerns from NOAA-Fisheries and the CTWSRO, in-stream sample collection from Shitike Creek and the Warm Springs River was attempted using a combination of seining and dip-netting. In 2005, samples (n=30, Unk) were collected at rkm 7 of Shitike Creek in an area with both anadromous and resident forms. Samples (n=40, STH) were also collected at rkm 14 in a predominately anadromous spawning area. These 40 samples are classified as “smolts” in Table 1 but may be either smolts or pre-smolt steelhead. In the Warm Springs River, samples were collected from rkm 10 of Mill Creek (n=4, STH), a tributary to the Warm Springs River, and from the mainstem Warm Springs River at rkm 43 (n=5, STH) for a total of 9 STH samples in 2005. The low sample size was due to the lack of available juveniles in locations where only anadromous steelhead were located.

Due to difficulty in in-stream sampling of juvenile steelhead during 2005, in-stream sample efforts in both the Warm Springs River and Shitike Creek during 2006 were abandoned in favor of collecting smolts at rotary screw traps. In Shitike Creek, genetic samples were collected as part of a CRITFC kelt reconditioning project. The AFTC coordinated with the CRITFC project in an attempt to obtain samples from steelhead smolts from Shitike Creek in both 2005 and 2006, however no steelhead samples (only resident forms) were collected at the rotary trap.

In the Warm Springs River, steelhead smolt samples (n=46, STH) were collected in 2006 from a trap located near the mouth of the river. Smolts were identified based on out-migration timing, appearance (smolt characteristics), and size. However, a large number of stray hatchery steelhead migrate up the Warm Springs River. To ensure greater accuracy in our genetic evaluation of Warm Springs river fish, juvenile samples collected in 2005 (n=9, STH) were grouped together with 2006 samples (n=46, STH), and for comparison our analyses included samples of adult natural-origin and stray hatchery-origin steelhead sampled at Warm Springs hatchery from 2005 and 2006.

Mainstem and Round Butte sampling

In 2005, electrofishing was used to collect samples (n=40, Unk) from the lower mainstem Deschutes River below Trout creek between rkm 117 and rkm 139, at the confluence of Trout Creek. Samples (n=10, Unk) also were collected from the upper mainstem above Trout Creek at rkm 158. Both the lower and upper collections occurred during the fall and may have contained resident, anadromous, or a mix of both life history forms. Electrofishing was used again in the fall of 2006 to collect samples (n=100, Unk) from the mainstem Deschutes River below Trout Creek, between rkm 98 and rkm139. These samples likewise contained resident, anadromous, or a mix of life history forms. The Round Butte hatchery collection contains samples (n=50, STH) from brood year 2005 steelhead collected from raceways.

In the mainstem Deschutes River (above Trout Creek) 2006 sampling effort, locations were targeted in which predominately anadromous forms were present. A drift boat was used to observe active spawning by adult anadromous steelhead during the springtime and GPS locations were recorded for steelhead redd locations. In early June, field crews returned to the steelhead redd locations and use dip-netting techniques to capture newly emergent fry. Based on the location, timing, and size of the fish collected, field crews were reasonably confident that these samples (n=36, STH) were made up of primarily anadromous origin juveniles.

Table 1. Phase-1 target collection locations, target sample sizes and actual number collected. Samples are denoted as resident (Omy), unknown (Unk) and anadromous (STH).

	Juvenile (in-stream)		Juvenile (in-stream)		smolts (rotary trap or in-stream)		Smolts (rotary trap)	
	2005	2005	2006	2006	2005	2005	2006	2006
Location (collection)	Target	Actual	Target	Actual	Target	Actual	Target	Actual
Warm Springs River	*50*	9,STH	*50*	13,STH	*50*	0	*50*	46
Shitike Cr.	*50*	30,Unk	*50*	62,Omy	*50*	40	*50*	0
Trout Cr.	*50*	0	*50*	0	*50*	0	*50*	*57
BakeOven	*50*	50,STH	*50*	50,STH	---	---	---	---
BuckHollow	*50*	50,Unk	*50*	42,STH	---	---	---	---
Mainstem-Upper	*50*	0	*50*	36,STH	---	---	---	---
Mainstem-Lower	*50*	50,Unk	*50*	100,Unk	---	---	---	---

(*) not evaluated in this report.

Microsatellite Amplification

DNA was extracted from all samples in a Chelex 100 (Sigma Chemical Co.) resin solution as described by Miller and Kapuscinski (1996). Samples were PCR amplified and genotyped following the methods of Ardren *et al.* (1999). We evaluated a suite of 17 microsatellite loci. Included among this suite are 12 loci being evaluated in the Steven Phelps Allele Nomenclature (SPAN) standardization effort for steelhead trout; five additional loci were added to provide increased resolution in these analyses (appendix 1).

QA/QC: ground-truthing and error rate analysis

Laboratory error rate was determined through a quality-assurance/quality-control (QAQC) procedure involving random re-sampling and duplicate genotypic analyses. Original data and replicate data were collected by different laboratory personnel, and data concordance was determined by the lead researcher. Samples were chosen at random (every 10th sample) from among the complete data set, DNA was re-extracted from tissue, re-amplified at 17 loci using PCR, and re-genotyped. The original sample scores were then aligned with the scores generated from the duplicate analysis and an error rate was calculated as the proportion of mismatches (i.e. differing allelic scores).

Analysis

Allele frequencies were generated with the program CONVERT (Glaubitz 2004;

appendix 2), and numbers of alleles, private alleles, observed and expected heterozygosities, and index of inbreeding (F_{is}) were generated using the software GDA version 1.0 (Lewis and Zaykin 2001). Tests for departures from Hardy-Weinberg equilibrium (HWE) expectations (i.e. random mating), were conducted using GENEPOP version 3.4 (Raymond and Rousset 1995). Statistical significance (α) was adjusted for the number of simultaneous tests k (α/k for $\alpha = 0.05$) by the sequential Bonferroni correction (Rice 1989). The program FSTAT version 2.9.3.2 (Goudet 1995) was used to calculate allelic richness, and F_{st} values (θ of Weir and Cockerham 1984), which indicate the proportion of total variation attributed to differences among collections. Genepop (Raymond and Rousset 1995) was used to generate Pairwise F_{st} values among populations, and significance was tested using ARLEQUIN version 3.1 (Excoffier *et al.* 2005)

A pairwise matrix of Cavalli-Sforza and Edwards (1967) genetic chord distances (CSE) and an un-rooted neighbor-joining (NJ) phylogram were generated using PHYLIP version 3.5C (Felsenstein 1992). The SEQBOOT option was implemented to generate 1000 simulated data sets, and a consensus topology with bootstrap support was generated using the CONSENSE option in PHYLIP. Likelihood based procedures implemented by the program WHICHRUN version 4.1 (Banks and Eichert 1999) were used to assign population-of-origin of each sample using a jackknife resampling method. This procedure involved removing an individual fish from the baseline, recalculating the baseline allele frequencies (omitting the individual), and assigning the omitted fish (now treated as an unknown) back to a baseline source. Individual fish in the baseline were evaluated sequentially, and the proportion that assigned correctly to their true baseline source, based on multilocus genotype frequencies, represents the assignment accuracy of the analysis. We used the program STRUCTURE version 2 (Pritchard and Donnelly 2000) to estimate the membership coefficients ($\hat{Q}$), or fractional membership in K inferred populations for each individual sample in each of 15 given populations using the program default settings (population admixture and allele correlation). The burn-in and run lengths for the Monte Carlo Markov Chain (MCMC) procedure were set at 500,000 and 1,000,000 respectively, and we evaluated K ranging from 2-7 populations.

RESULTS

Data quality assurance/control

We conducted a quality QAQC test during each collection year. The total number of samples evaluated was 126, and the actual number of allelic comparisons made across 17 loci was 3912 (excluded comparisons with a missing score). We observed a total of 12 scoring discrepancies, usually associated with weakly amplified samples, for a total error rate of 0.31%. Error rates <1% are typically considered acceptable for populations structure analyses.

Descriptive Statistics

There were high levels of polymorphism or allelic variability across loci evaluated in the 2005-2006 phase-1 analysis. Numbers of alleles ranged from 3 at *µOts3* and *µOne14* in the Deschutes River lower mainstem 2005 and Round Butte Hatchery collections respectively, to 20 at *µOmy1001* in the BuckHollow Creek 2006 and Warm Springs River smolt 2006 collections (mean = 11 over loci and collections). Observed heterozygosity ranged from 0.17 at *µSsa289* in the Deschutes River lower mainstem 2006 collection, to 1.00 at *µOmy1001* in the BuckHollow Creek 2005 collection, with a mean of 0.76 over loci and collections (Table 2). We observed five departures from expected genotypic proportions among 255 total HWE tests. Of these, four departures occurred at locus *µOts1*, which was subsequently removed from further analysis. A heterozygote deficit was observed at *µOmy7i* within the Warm Springs River 2006 smolt collection. The number of private alleles among collections ranged from 0 (in 1/3 of collections) to 4 in the BakeOven Creek 2005 collection (Table 2).

Population Genetic Structure Analysis

We observed an estimated overall F_{st} of 0.027, indicating significant variability among the 15 collections of *O. mykiss* (steelhead and resident trout) evaluated in the 2005-2006 Deschutes River study (95% C.I. = 0.023-0.033). When pairs of collections were evaluated, all but 5 pairwise F_{st} comparisons were highly significant (appendix 3). When collections were pooled by region (i.e. eastside, westside, and mainstem), the largest among-region variability was observed between eastside tributaries and the mainstem collections (Figure 3a). The eastside vs. westside, and westside vs. mainstem comparisons have F_{st} values far below global

F_{ST} (95% C.I.). Furthermore, comparisons made between the Shitike Creek 2006 juveniles and each eastside tributary appear to be responsible for most of the among-region variability between east- and westside tributaries (Figure 3a).

For within-region comparisons, the relative genetic variability between the upper and lower Deschutes River mainstem is substantial (>global F_{ST}) compared to the variability among the temporally stratified collections from the lower mainstem (Figure 3b). For westside tributaries, variability between the Shitike Creek 2006 (Unk) collection and all remaining collections is high relative to replicate Shitike Creek collections and comparisons between Warm Springs River (STH) and Shitike Creek 2005 collections (Figure 3b). In nearly all cases, pairwise comparisons that do not include the Deschutes River lower mainstem (Unk) or Shitike Creek 2006 (Omy) collections exhibit relatively lower variability, well below the global F_{ST} value (Figure 3b).

The genetic distance relationship among the 15 sample collections is demonstrated in the topology of an unrooted NJ phylogram (Figure 4). The confidence or concordance of the topology is indicated with bootstrap values at some of the nodes, and reveals greatest similarities on three branches: 1) temporal replicate collections from BuckHollow Creek, 2) temporal replicate collections of stray hatchery fish from the Warm Springs River, and 3) Shitike Creek 2006 (Omy) and Deschutes River mainstem collections. The greatest genetic distance occurs between two clusters; the major node separates the Deschutes River mainstem and the Shitike Creek 2006 collections from all remaining collections.

Results of assignment tests were largely variable among collections and regions (e.g. E vs. W). Assignment success (assignment to correct collection-of-origin) ranged from 18% in the Warm Springs River (Strays) 2006 collection to 70% in the Round Butte Hatchery Juveniles 2005 collection, with a mean of 38% (Figures 5). Assignment success to correct tributary- or region-of-origin among replicates was only slightly improved except in the Deschutes River lower mainstem collections (Unk), for which Shitike Creek 2006 (Omy) assignments were also highly represented. Moreover, 99% of the Shitike Creek 2006 collection (Omy) either assigned to collection-of-origin or to one of three Deschutes River mainstem collections (Figure 5).
The proportion of Deschutes River mainstem assignments observed among the 12 tributary collections ranged from 0% (BakeOven Creek 2005) to 50% (Shitike Creek 2006), with a mean of 10%.

Proportional membership in K=6 inferred population clusters where Pr(K) = 1 (Table 3) is displayed graphically in a bar plot, and indicates high geneflow or mixed membership among most collections. The highest (>50%) membership fidelity per cluster and individual is observed among the Warm Springs River (Stray) 2005 collection (Figure 6; #1), among Deschutes River upper mainstem fish (Figure 6; #15), and among Shitike Creek 2006 and two Deschutes River lower mainstem collections (Figure 6; #'s 8, 13, 14), which also appear to be members (proportionally) of the same inferred population cluster.

DISCUSSION

Overall, the Deschutes River Basin is a hot spot of diversity for *O. mykiss*. The paucity of genetic information that has been available for a genetic characterization of populations within the basin has been an impediment to understanding population structure and implementing informed conservation efforts. Similarly the relationship between life history types (i.e. resident and anadromous) and delineation of regional populations through much of the basin is poorly understood. The distribution or level of genetic divergence among the tributaries throughout the Deschutes River Basin will ultimately affect summer-run steelhead restoration and conservation issues. This progress report summarizes the preliminary analyses and results for 2005-2006 phase-1 objectives described in the study plan for evaluating summer-run steelhead in the Deschutes River of Oregon. Completion of phase-1 objectives will require another full year to obtain a minimum of three sample years.

In our preliminary analyses to evaluate putative populations identified by the Columbia River TRT we observed very little genetic divergence among or within collections (STH) from the eastside tributaries and the Warm Springs River (a westside tributary). The BuckHollow Creek 2005 collection was identified as origin "unknown"; however, we observed no evidence of genetic differentiation between the BuckHollow temporal replicate collections and those from other tributaries (with the exception of Shitike Creek in 2006). The "unknown" collection is likely to represents an anadromous group similar to the others. Based on these preliminary results that include only a single known resident collection (Shitike Creek 2006 from the westside) it is difficult to speculate about geneflow restrictions or panmixia among sympatric life history types (i.e. resident vs. anadromous) where they may co-occur.

Several tests including evaluation of genetic distance and population clustering revealed the greatest genetic similarity between the lower mainstem temporal replicate collections (Unk) and the Shitike Creek 2006 collection (Omy). For example, among these three collections the greatest mean population membership is given to inferred population #2, ranging from 69-87% (Table 3; designated green in figure 6). On an individual sample basis we observed 70%, 79% and 92% of individuals with greater than 70% proportional membership in inferred population #2 among the Deschutes Lower Mainstem 2005 (DLM5), Deschutes Lower Mainstem 2006 (DLM6), and Shitike Creek 2006 (SC6) collections respectively (Figure 6). Conversely, we observed evidence of restricted geneflow between the lower mainstem collections and SC6 in comparison to all remaining collections, including the upper mainstem collection (STH). The pairwise F_{st} comparisons indicate that observed genetic variation between any of those three collections and the remaining 12 collections exceeds the variation observed due to temporal or regional differences among the remaining 12 collections (Figures 3a and 3b).

We found evidence of significant genetic differentiation among both Shitike Creek 2006 fish (known resident) and fish of “unknown” origin from the Deschutes River lower mainstem, compared with all remaining collections (including the STH collection from the upper mainstem). Assuming that the identified life history type (i.e. anadromous or resident) is accurate among collections, differential spawning times and differential habitat utilization (i.e. assortative mating) would help explain observed geneflow restrictions. If migratory behavior is prevalent among resident fish in this region, then samples collected from the Deschutes River lower mainstem and Shitike Creek in 2006 may represent the same resident *O. mykiss* origin, and may have been sampled from a single reproductive group (i.e. population). Further (temporal) sampling and subsequent analyses will be necessary to substantiate or clarify these conclusions. Notably, there was greater genetic similarity among 2005 (STH) and 2005 (Unk) Shitike Creek collections, than is observed among either of the two and the Shitike Creek 2006 collection (Omy) which suggests the putative 2005 (Unk) fish are likely to have been collected from among an anadromous population component.

Round Butte hatchery fish assigned to collection-of-origin with the highest accuracy, however, there is little evidence of genetic differentiation between those hatchery fish and anadromous collections from the eastside tributaries and the Warm Springs River. The population membership analysis (bar plots) revealed that the stray hatchery collections from the

Warm Springs River appear to be of mixed or multiple origins and may include some Round Butte Hatchery fish. Determining or examining the sources of stray hatchery fish (e.g. Snake River Basin) and their genetic influence on native Deschutes River populations is not feasible until a SPAN genotypic baseline[2] is available, or until more information is provided from phase-2 analyses of the collaborative study plan. Interestingly, the upper mainstem collection (STH) is genetically distant from both in-basin and out-of-basin hatchery samples evaluated in this report.

Subsequent phases: progress and direction

During the collection periods for 2005 and 2006, the collaborative agencies were also engaged in collecting samples for subsequent phases (2-4) of this study plan. The Conservation Genetics Program at AFTC has catalogued and entered the following samples in its repository: out-of-basin hatchery origin steelhead, and natural origin steelhead collected at Sherars Falls, temporal replicate steelhead samples from Trout Creek, resident redband trout collections from Ochoco Creek, McKay Creek, Crooked River, Tumalo Creek, Whychus Creek, and Crane Prairie Reservoir. Additional steelhead sampling may need to occur in order to cover areas where we were unable to meet our target of 50 samples per collection; in particular, larger collections of steelhead are needed from the Warm Springs River above the hatchery, Shitike Creek, and from the upper Deschutes Mainstem.

ACKNOWLEDGEMENTS

We extend our appreciation and gratitude to the inter-agency field crew and personnel for their efforts in collecting genetic tissue samples used in these analyses. We also thank Jeff Olsen of USFWS Anchorage Conservation Genetics Laboratory for technical support and editing during the drafting of this report. The findings and conclusions in this report are those of the authors and do not necessarily represent the views of the United States Fish and Wildlife Service.

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[2] The SPAN baseline is a collective of genotypic data contributed by a consortium of multiple state and federal agencies and Tribes. The data are standardized among laboratories and available for sharing among all collaborative parties for the benefit of steelhead trout management, conservation, and research.

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Table 2. Descriptive statistics for 15 genetic sample collections. Column headings are defined as follows: **n** is the number of individuals, **A** is the number of alleles, **AP** is the number of private alleles, **AR** is the allelic richness, **H_E** is Nei's (1978) unbiased estimate of expected heterozygosity, **H_O** is the observed heterozygosity, and **F_{is}** is the index of inbreeding. Bold values with the symbol (*****) indicate statistical significance (Rice 1989; α = 0.05 adjusted by α/k).

	BakeOven Creek 2005 (STH)							BakeOven Creek 2006 (STH)						
Locus	n	A	AP	AR	H_E	H_O	F_{is}	n	A	AP	AR	H_E	H_O	F_{is}
μOcl1	50	10	0	9.6	0.8267	0.8400	-0.0163	49	10	0	8.5	0.7589	0.7755	-0.0221
μOgo4	50	9	0	8.3	0.8105	0.7800	0.0380	50	7	0	6.5	0.7857	0.6800	0.1357
μOmy7i	50	12	1	11.0	0.8731	0.9000	-0.0311	50	10	0	9.6	0.8495	0.7800	0.0826
μOts100	50	14	0	12.3	0.8838	0.9000	-0.0185	50	13	0	12.2	0.9022	0.8600	0.0473
μOts3	50	6	0	5.3	0.6990	0.6600	0.0563	50	5	0	4.4	0.6182	0.6200	-0.0030
μOts4	50	7	0	6.5	0.7814	0.7400	0.0535	50	7	0	6.5	0.8051	0.8600	-0.0690
μOgo3	50	7	0	6.3	0.7422	0.6000	0.1932	50	7	0	5.9	0.7281	0.7400	-0.0165
μOki23	50	14	0	11.7	0.7194	0.6800	0.0553	50	12	0	10.2	0.7428	0.7600	-0.0234
μOmy1011	50	17	0	14.3	0.8871	0.9000	-0.0147	50	14	0	12.6	0.8891	0.8400	0.0557
μOmy77	50	14	1	12.4	0.8954	0.9000	-0.0052	50	12	0	11.6	0.9083	0.8600	0.0537
μSsa289	50	4	0	3.4	0.3368	0.3200	0.0503	50	6	0	4.6	0.2556	0.2800	-0.0967
μSsa407	50	13	0	11.8	0.8990	0.9600	-0.0686	50	15	0	12.8	0.8897	0.8400	0.0564
μSsa408	50	12	0	10.6	0.8707	0.9400	-0.0805	50	17	0	14.9	0.9234	0.9400	-0.0181
μOke4	50	9	0	8.3	0.8053	0.8800	-0.0939	50	11	0	9.3	0.8541	0.8400	0.0167
μOmy1001	50	19	1	16.0	0.9107	0.8000	0.1227	50	16	0	14.3	0.9242	0.8800	0.0483
μOne14	50	6	1	5.3	0.6640	0.6800	-0.0243	50	6	0	5.3	0.5814	0.6000	-0.0323

	BuckHollow Creek 2005 (Unk)							BuckHollow Creek 2006 (STH)						
Locus	n	A	AP	AR	H_E	H_O	F_{is}	n	A	AP	AR	H_E	H_O	F_{is}
μOcl1	45	11	0	9.2	0.7973	0.8889	-0.1164	42	11	0	9.8	0.7375	0.7619	-0.0335
μOgo4	45	11	0	9.6	0.8362	0.8889	-0.0638	42	9	0	8.6	0.8445	0.8095	0.0419
μOmy7i	45	11	0	10.6	0.8669	0.8444	0.0262	42	10	0	8.7	0.8081	0.8810	-0.0914
μOts100	45	13	0	11.8	0.8784	0.8222	0.0646	42	15	0	12.7	0.8807	0.8095	0.0817
μOts3	45	5	0	4.5	0.6310	0.6000	0.0496	42	6	0	5.5	0.7131	0.7857	-0.1031
μOts4	45	6	0	5.6	0.6522	0.6000	0.0809	42	6	0	5.6	0.7361	0.7143	0.0300
μOgo3	45	5	0	4.5	0.6742	0.7333	-0.0889	42	7	0	6.4	0.7269	0.7381	-0.0156

μOki23	45	15	0	12.9	0.8619	0.9111	-0.0578	42	12	0	10.5	0.7567	0.8095	-0.0707
μOmy1011	45	15	0	13.4	0.9096	0.9111	-0.0017	42	13	0	11.8	0.8543	0.8571	-0.0034
μOmy77	45	14	0	13.4	0.9104	0.9111	-0.0008	40	16	0	14.0	0.9063	0.7000	0.2299
μSsa289	45	6	0	5.0	0.4225	0.4667	-0.1059	42	7	0	5.8	0.5075	0.4286	0.1571
μSsa407	45	15	0	12.9	0.8859	0.9111	-0.0288	42	15	0	12.9	0.8867	0.9048	-0.0206
μSsa408	45	18	0	15.3	0.9206	0.9333	-0.0140	42	18	0	16.0	0.9197	0.9286	-0.0098
μOke4	45	12	0	10.4	0.8522	0.8000	0.0619	42	9	1	8.2	0.8425	0.8095	0.0396
μOmy1001	45	19	0	17.3	0.9348	1.0000	-0.0706	42	20	0	17.6	0.9203	0.9762	-0.0616
μOne14	45	8	0	6.5	0.5665	0.6000	-0.0598	42	7	0	6.2	0.6741	0.7143	-0.0603

	Deschutes River lower mainstem 2005 (Unk)							Deschutes River lower mainstem 2006 (Unk)						
Locus	n	A	AP	AR	H_E	H_O	F_{is}	n	A	AP	AR	H_E	H_O	F_{is}
μOcl1	50	8	0	6.8	0.7226	0.8400	-0.1644	95	11	0	8.4	0.7716	0.7684	0.0041
μOgo4	50	7	0	5.8	0.6925	0.6400	0.0766	95	8	0	5.9	0.6532	0.6526	0.0009
μOmy7i	50	9	0	8.5	0.8341	0.8800	-0.0556	96	11	0	9.5	0.8571	0.8333	0.0279
μOts100	50	15	0	11.7	0.8022	0.7000	0.1286	96	11	0	8.8	0.8081	0.7708	0.0464
μOts3	50	3	0	2.5	0.4216	0.3000	0.2905	95	5	0	4.3	0.5532	0.5053	0.0870
μOts4	50	6	0	5.7	0.4685	0.4800	-0.0248	95	7	0	5.6	0.4563	0.4526	0.0080
μOgo3	50	8	0	6.6	0.7749	0.7800	-0.0066	96	7	0	5.7	0.7153	0.7500	-0.0488
μOki23	50	12	0	10.2	0.8398	0.8000	0.0479	96	14	0	9.9	0.8147	0.8333	-0.0230
μOmy1011	50	15	0	12.5	0.8618	0.9000	-0.0448	95	15	0	11.8	0.8760	0.9368	-0.0699
μOmy77	50	14	0	11.8	0.8776	0.8600	0.0202	95	12	0	10.4	0.8687	0.8632	0.0064
μSsa289	50	6	0	5.2	0.2586	0.2000	0.2283	96	7	0	4.2	0.1683	0.1771	-0.0525
μSsa407	50	15	0	12.1	0.8539	0.8400	0.0165	96	15	0	11.3	0.8428	0.8646	-0.0260
μSsa408	50	15	0	12.0	0.8697	0.8800	-0.0120	96	15	0	11.8	0.8796	0.8542	0.0290
μOke4	50	8	0	6.8	0.7459	0.7200	0.0350	96	12	0	8.0	0.7483	0.6875	0.0817
μOmy1001	50	16	0	14.2	0.8986	0.8400	0.0658	96	18	1	12.8	0.8331	0.7604	0.0876
μOne14	50	6	0	4.6	0.2396	0.2600	-0.0861	96	6	0	4.7	0.3360	0.3333	0.0078

	Deschutes River upper mainstem 2006 (STH)							Round Butte Hatchery 2005 (STH)						
Locus	n	A	AP	AR	H_E	H_O	F_{is}	n	A	AP	AR	H_E	H_O	F_{is}
μOcl1	38	9	0	8.2	0.8018	0.7632	0.0488	50	11	0	9.7	0.7923	0.7400	0.0667
μOgo4	38	8	0	7.3	0.7575	0.8684	-0.1486	49	8	0	7.8	0.8399	0.7959	0.0529
μOmy7i	38	9	0	8.7	0.8702	0.8421	0.0327	50	11	0	9.9	0.8493	0.9400	-0.1080

μOts100	37	14	0	13.2	0.8849	0.8378	0.0538	50	10	0	9.7	0.8618	0.7400	0.1426
μOts3	38	4	0	4.0	0.6018	0.5526	0.0826	50	5	0	4.9	0.6697	0.7800	-0.1667
μOts4	38	7	0	6.4	0.7333	0.7105	0.0315	49	7	0	6.4	0.7671	0.6939	0.0963
μOgo3	38	8	1	7.3	0.7411	0.7368	0.0058	50	6	0	5.3	0.7071	0.6800	0.0387
μOki23	37	13	0	12.1	0.8290	0.8649	-0.0440	49	11	0	9.9	0.7151	0.7143	0.0012
μOmy1011	38	14	0	12.9	0.9042	0.9211	-0.0189	50	14	0	12.9	0.8945	0.7800	0.1292
μOmy77	38	12	0	11.3	0.8779	0.7632	0.1322	48	14	0	11.8	0.8875	0.7708	0.1327
μSsa289	38	6	0	5.6	0.4919	0.4737	0.0376	50	6	0	5.4	0.4251	0.4400	-0.0355
μSsa407	38	13	0	12.3	0.8674	0.8947	-0.0320	50	14	0	12.8	0.8873	0.9600	-0.0829
μSsa408	38	15	0	14.0	0.9133	0.9474	-0.0378	47	14	0	12.7	0.8954	0.9149	-0.0220
μOke4	37	10	0	9.4	0.8164	0.8649	-0.0603	49	8	0	7.5	0.8435	0.8367	0.0081
μOmy1001	38	14	0	13.7	0.9214	0.8158	0.1160	49	16	0	14.7	0.9137	0.9388	-0.0277
μOne14	38	5	0	4.7	0.3867	0.3421	0.1166	50	3	0	2.9	0.5279	0.4200	0.2060

	Warm Springs River strays 2005 (STH)							Warm Springs River strays 2006 (STH)						
Locus	n	A	AP	AR	H_E	H_O	F_{is}	n	A	AP	AR	H_E	H_O	F_{is}
μOcl1	56	11	0	9.9	0.8024	0.8036	-0.0014	94	13	0	10.3	0.7765	0.7660	0.0137
μOgo4	57	11	0	9.8	0.8387	0.9123	-0.0886	94	11	0	8.9	0.8454	0.8191	0.0313
μOmy7i	57	11	0	10.4	0.8752	0.9298	-0.0630	94	14	0	11.5	0.8751	0.8617	0.0154
μOts100	55	12	0	9.5	0.7993	0.8727	-0.0927	94	14	0	11.1	0.8533	0.7766	0.0904
μOts3	57	6	0	5.7	0.7168	0.7544	-0.0529	94	6	0	5.3	0.7153	0.7447	-0.0413
μOts4	57	7	0	5.9	0.7757	0.6842	0.1188	94	7	0	6.1	0.7437	0.6702	0.0992
μOgo3	57	6	0	4.6	0.6827	0.7193	-0.0542	94	9	0	6.3	0.7204	0.7660	-0.0636
μOki23	57	12	1	10.3	0.7833	0.8772	-0.1211	94	18	1	13.4	0.8432	0.7872	0.0667
μOmy1011	56	14	0	12.1	0.8843	0.9464	-0.0709	94	15	0	13.1	0.8942	0.9255	-0.0353
μOmy77	55	16	0	13.3	0.8789	0.7455	0.1530	94	15	0	12.4	0.8946	0.7872	0.1206
μSsa289	56	5	0	4.4	0.5944	0.6429	-0.0823	94	6	0	4.8	0.4547	0.4894	-0.0768
μSsa407	56	16	0	12.3	0.8792	0.9107	-0.0362	94	16	0	11.4	0.8674	0.8404	0.0313
μSsa408	57	14	0	12.1	0.8933	0.8947	-0.0016	94	18	0	15.4	0.9198	0.9255	-0.0062
μOke4	57	10	0	9.1	0.8551	0.9123	-0.0674	91	11	0	9.0	0.8334	0.7473	0.1039
μOmy1001	57	19	0	15.5	0.9180	0.8596	0.0641	91	19	0	16.3	0.9299	0.9121	0.0193
μOne14	57	6	0	4.9	0.6928	0.7018	-0.0131	91	8	1	5.5	0.6389	0.6703	-0.0494

	Warm Springs River (NOR) 2006 (STH)							Warm Springs River smolts 2006 (STH)						
Locus	n	A	AP	AR	H_E	H_O	F_{is}	n	A	AP	AR	H_E	H_O	F_{is}
μOcl1	27	11	0	10.9	0.7952	0.7407	0.0698	67	13	0	10.4	0.7942	0.8507	-0.0718
μOgo4	26	8	0	8.0	0.8431	0.8077	0.0428	67	12	0	9.5	0.8149	0.7313	0.1033
μOmy7i	26	10	0	10.0	0.8627	0.6538	0.2458	67	15	0	11.9	0.8706	0.7463	*0.1437
μOts100	26	11	0	11.0	0.8778	0.8077	0.0814	67	15	0	12.8	0.8951	0.9104	-0.0173
μOts3	27	6	0	5.9	0.6723	0.5185	0.2321	66	7	0	5.6	0.6557	0.7273	-0.1101
μOts4	26	7	0	7.0	0.6727	0.6538	0.0286	67	7	0	6.4	0.7233	0.6716	0.0719
μOgo3	27	7	0	6.9	0.7533	0.6667	0.1170	67	7	0	6.3	0.7219	0.7164	0.0077
μOki23	27	12	0	11.9	0.8428	0.8148	0.0338	67	15	0	12.6	0.8684	0.8806	-0.0142
μOmy1011	27	15	0	14.9	0.8910	0.9259	-0.0400	67	17	0	13.9	0.8942	0.9104	-0.0183
μOmy77	27	13	0	12.9	0.9036	0.8519	0.0583	66	15	0	12.4	0.9057	0.8182	0.0973
μSsa289	27	4	0	4.0	0.4780	0.5556	-0.1659	67	7	0	5.2	0.3202	0.3134	0.0212
μSsa407	27	13	0	12.8	0.8882	0.9630	-0.0859	67	15	0	12.6	0.8631	0.8657	-0.0030
μSsa408	27	14	0	14.0	0.9308	0.9259	0.0054	67	17	0	15.5	0.9302	0.9851	-0.0595
μOke4	27	8	0	8.0	0.8288	0.9259	-0.1197	67	11	0	9.3	0.8256	0.8209	0.0058
μOmy1001	26	16	0	16.0	0.9125	0.8846	0.0312	67	20	0	17.0	0.9295	0.9403	-0.0117
μOne14	27	5	0	5.0	0.6212	0.6667	-0.0746	67	7	0	5.8	0.6509	0.6567	-0.0090

	Shitike Creek Juveniles 2005 (Unk)							Shitike Creek Juveniles 2006 (Omy)						
Locus	n	A	AP	AR	H_E	H_O	F_{is}	n	A	AP	AR	H_E	H_O	F_{is}
μOcl1	30	10	0	9.7	0.8249	0.8667	-0.0516	61	9	0	7.8	0.7483	0.7705	-0.0299
μOgo4	30	8	0	7.7	0.8073	0.8333	-0.0328	59	8	0	6.4	0.6496	0.5932	0.0874
μOmy7i	30	10	0	10.0	0.8638	0.9000	-0.0426	59	10	0	9.4	0.8524	0.7966	0.0660
μOts100	30	9	0	8.8	0.8548	0.8667	-0.0141	61	12	0	9.7	0.7763	0.8197	-0.0563
μOts3	30	5	1	4.9	0.6136	0.5667	0.0776	61	5	1	3.5	0.5198	0.5246	-0.0092
μOts4	29	5	0	5.0	0.7217	0.7586	-0.0521	60	6	0	5.4	0.5305	0.5333	-0.0053
μOgo3	30	6	0	5.8	0.7006	0.6667	0.0492	61	6	0	6.0	0.7739	0.7705	0.0044
μOki23	30	8	0	7.9	0.7588	0.6333	0.1677	61	13	1	9.6	0.8202	0.8197	0.0007
μOmy1011	30	14	0	13.5	0.9017	0.9000	0.0019	61	13	0	11.3	0.8717	0.9180	-0.0536
μOmy77	30	12	0	11.6	0.8887	0.8333	0.0633	61	11	0	9.7	0.8625	0.8689	-0.0074
μSsa289	30	7	1	6.8	0.5514	0.6000	-0.0898	61	5	0	4.2	0.2418	0.2623	-0.0854
μSsa407	30	12	1	11.6	0.8864	0.9000	-0.0156	60	14	0	11.2	0.8216	0.8667	-0.0554
μSsa408	30	15	0	14.2	0.8887	0.9333	-0.0511	60	16	0	13.5	0.8818	0.8833	-0.0018

μOke4	30	10	0	9.7	0.8627	0.8667	-0.0047	61	8	0	6.3	0.6575	0.7541	-0.1483
μOmy1001	30	14	0	13.6	0.9113	0.7000	0.2349	61	15	0	11.6	0.7862	0.8525	-0.0850
μOne14	30	6	0	5.7	0.6215	0.6000	0.0351	61	6	0	4.9	0.2693	0.2295	0.1489

	Shitike Creek 2005 (STH)							Mean						
Locus	n	A	AP	AR	H_E	H_O	F_{is}	n	A	AP	AR	H_E	H_O	F_{is}
μOcl1	39	12	0	10.2	0.8139	0.7692	0.0555	53	11	0	9.3	0.7843	0.7964	-0.0156
μOgo4	39	12	0	10.2	0.7766	0.7179	0.0764	53	9	0	8.0	0.7864	0.7687	0.0228
μOmy7i	39	12	0	11.2	0.8611	0.8974	-0.0427	53	11	0	10.1	0.8580	0.8458	0.0143
μOts100	38	13	1	11.2	0.8533	0.7368	0.1381	53	13	0	11.1	0.8541	0.8154	0.0458
μOts3	39	5	0	4.5	0.5877	0.6410	-0.0920	53	5	0	4.7	0.6259	0.6187	0.0114
μOts4	39	7	0	6.5	0.6047	0.5385	0.1109	53	7	0	6.0	0.6781	0.6508	0.0409
μOgo3	39	7	0	6.5	0.7552	0.8205	-0.0877	53	7	0	6.0	0.7278	0.7256	0.0030
μOki23	39	14	0	12.2	0.8305	0.8462	-0.0191	53	13	0	11.0	0.8018	0.8021	-0.0005
μOmy1011	39	15	0	13.6	0.9028	0.8718	0.0347	53	15	0	13.0	0.8878	0.8963	-0.0097
μOmy77	39	13	0	12.2	0.8931	0.8462	0.0532	53	14	0	12.1	0.8906	0.8253	0.0741
μSsa289	39	6	0	5.4	0.3227	0.3590	-0.1141	53	6	0	4.9	0.3886	0.4006	-0.0310
μSsa407	38	13	0	11.9	0.8712	0.8947	-0.0274	53	14	0	12.2	0.8727	0.8944	-0.0252
μSsa408	39	16	0	14.7	0.9251	0.8974	0.0303	53	16	0	13.8	0.9042	0.9189	-0.0165
μOke4	39	11	0	9.8	0.8352	0.8205	0.0178	53	10	0	8.6	0.8138	0.8191	-0.0065
μOmy1001	38	17	0	15.0	0.9105	0.8684	0.0468	53	17	0	15.0	0.9037	0.8686	0.0391
μOne14	39	5	0	4.9	0.5804	0.4872	0.1624	53	6	0	5.1	0.5368	0.5308	0.0112

Table 3. Estimating number of populations (*K*) using likelihood based procedures in the program "Structure". The value Pr(*K*) estimates how well *K* models the data, where (*) indicates inferred number of populations. Proportion of population membership for each of 15 given genetic sample collections is shown with highest proportion in bold text. Collections are identified as follows: 1-Warm Springs River (Strays) 2005, 2-Warm Springs River (Strays) 2006, 3-Warm Springs River (NOR adults) 2006, 4-Warm Springs River Smolts 2006, 5-Round Butte Hatchery juveniles 2005, 6-Shitike Creek steelhead 2005 (STH), 7-Shitike Creek 2005 (Unk), 8-Shitike Creek 2006 (Omy), 9-BuckHollow Creek 2005 (STH), 10- BuckHollow Creek 2006 (STH), 11-BakeOven Creek 2005 (STH), 12-BakeOven Creek 2006 (STH), 13-Deschutes River lower mainstem 2005 (Unk), 14-Deschutes River lower mainstem 2006 (Unk), 15-Deschutes River upper mainstem 2006 (STH).

K	ln Pr(X|*K*)	Pr(X|*K*)	Pr(*K*)
2	-645.80	3.41E-281	0.00
3	-390.60	2.32E-170	0.00
4	-288.90	3.41E-126	0.00
5	-56.60	2.624E-25	0.00
***6**	**0.00**	**1**	**1.00**
7	-12.40	4.119E-06	0.00

Given populations	Inferred Clusters (populations)						
	1	2	3	4	5	6	# individuals
1. WSS5	0.0210	0.0120	**0.6410**	0.1260	0.1000	0.1000	57
2. WSS6	0.0270	0.0270	**0.4210**	0.1490	0.1870	0.1880	94
3. WSN6	0.0380	0.1530	**0.2800**	0.1280	0.1980	0.2040	27
4. WSsm6	0.0510	0.0740	0.1160	0.1170	0.3180	**0.3250**	67
5. RBH5	0.0360	0.0570	0.0950	0.1480	0.3380	**0.3270**	50
6. SCst5	0.0760	**0.2430**	0.1950	0.1260	0.1790	0.1810	39
7. SC5	0.0260	0.1950	**0.2180**	0.1670	0.1970	0.1980	30
8. SC6	0.0250	**0.8750**	0.0170	0.0220	0.0310	0.0310	61
9. BH5	0.0460	0.0900	0.1430	**0.3730**	0.1740	0.1740	45
10. BH6	0.0540	0.0330	0.2040	**0.3030**	0.2040	0.2020	42
11. BO5	0.0330	0.0170	0.1320	**0.3780**	0.2200	0.2200	50
12. BO6	0.0470	0.0570	0.1550	**0.2980**	0.2230	0.2190	50
13. DLM5	0.2080	**0.6940**	0.0150	0.0220	0.0300	0.0300	50
14. DLM6	0.0850	**0.7810**	0.0240	0.0230	0.0440	0.0430	96
15. DUM6	**0.6750**	0.1010	0.0210	0.1160	0.0430	0.0440	38

Figure 1. Genetic sample locations for 2005.

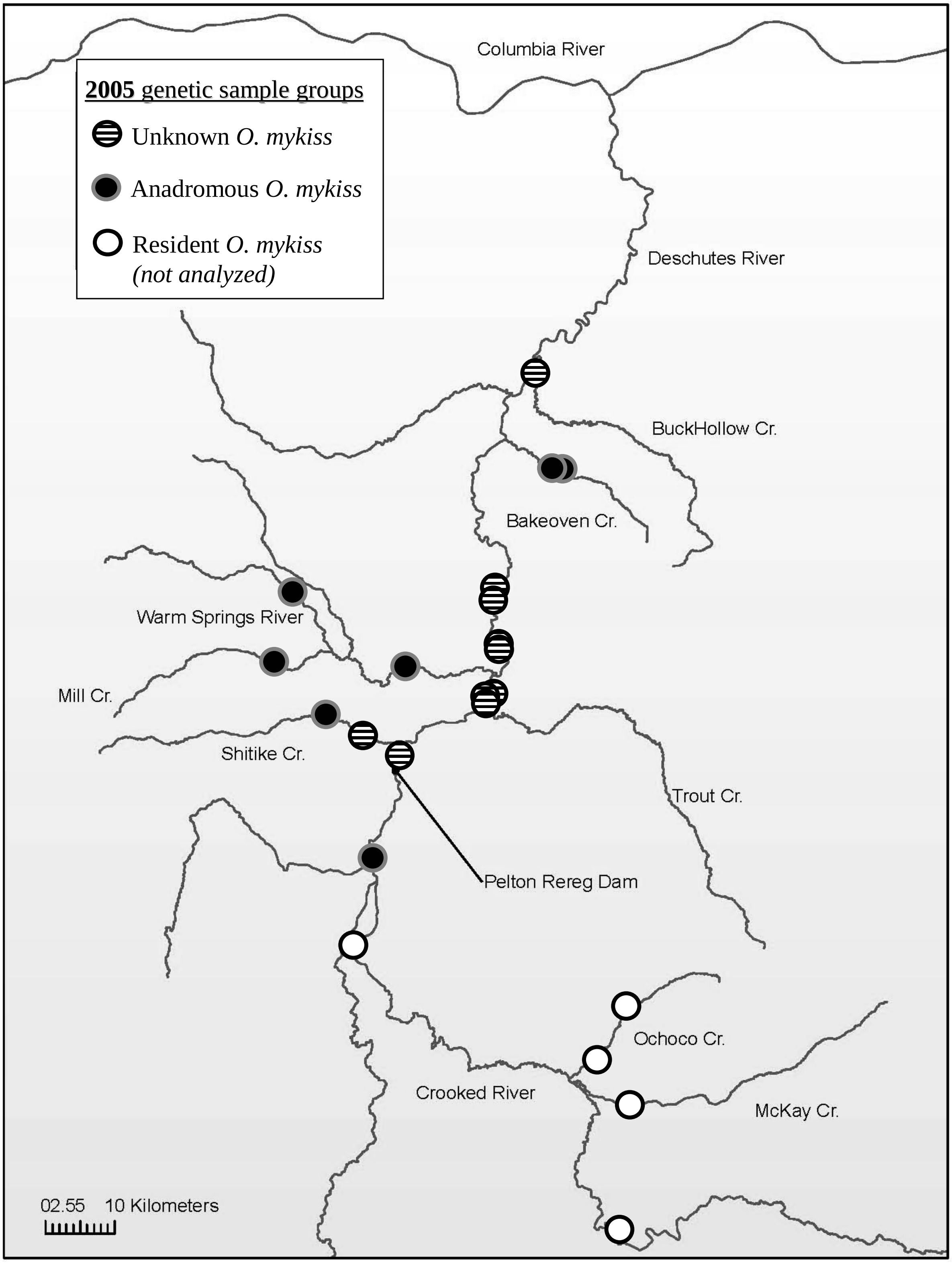


Figure 2. Genetic sample locations for 2006.

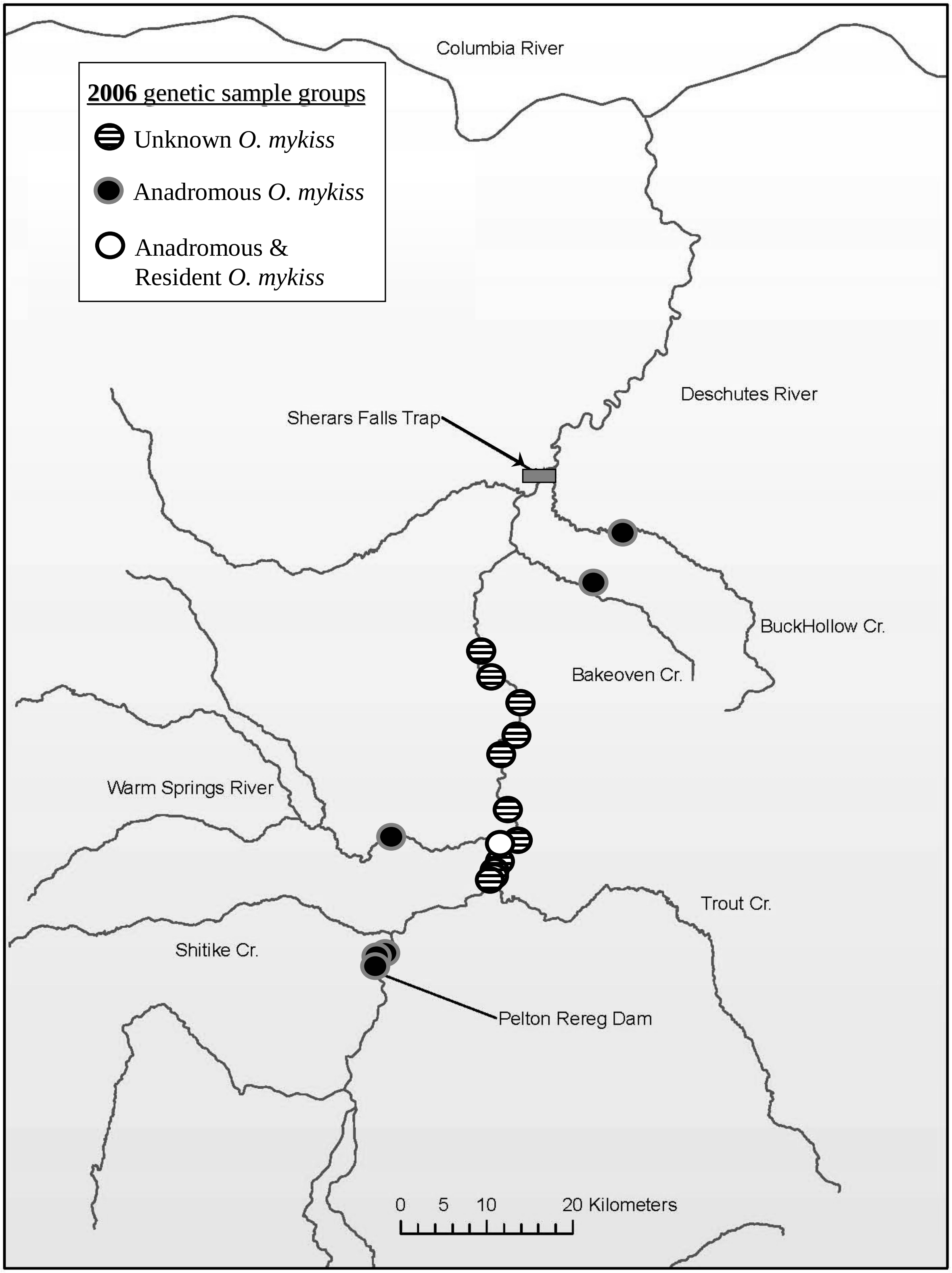


Figure 3a. Pairwise-F_{st} plot for among-region comparisons (E-eastside, W-westside, M-mainstem). Westside specifies all Shitke Creek and Warm Springs River collections (excluding strays), and eastside specifies all BuckHollow and BakeOven Creek collections.

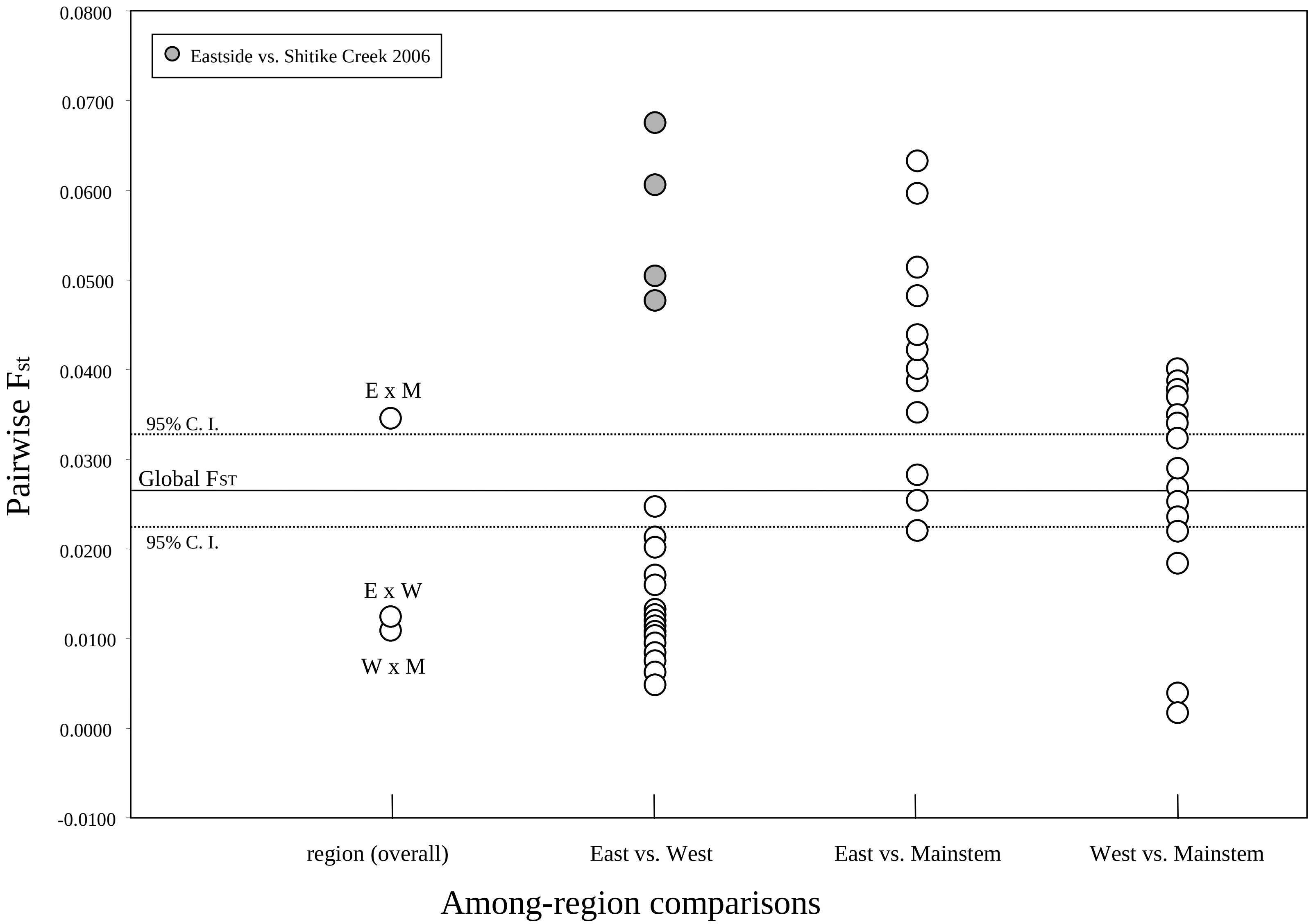


Figure 3b. Pairwise-F_{st} plot for within-region comparisons (L-lower mainstem, U-upper mainstem). The figure also displays results for comparisons between all Deschutes River putative natural-origin collections versus hatchery-origin collections.

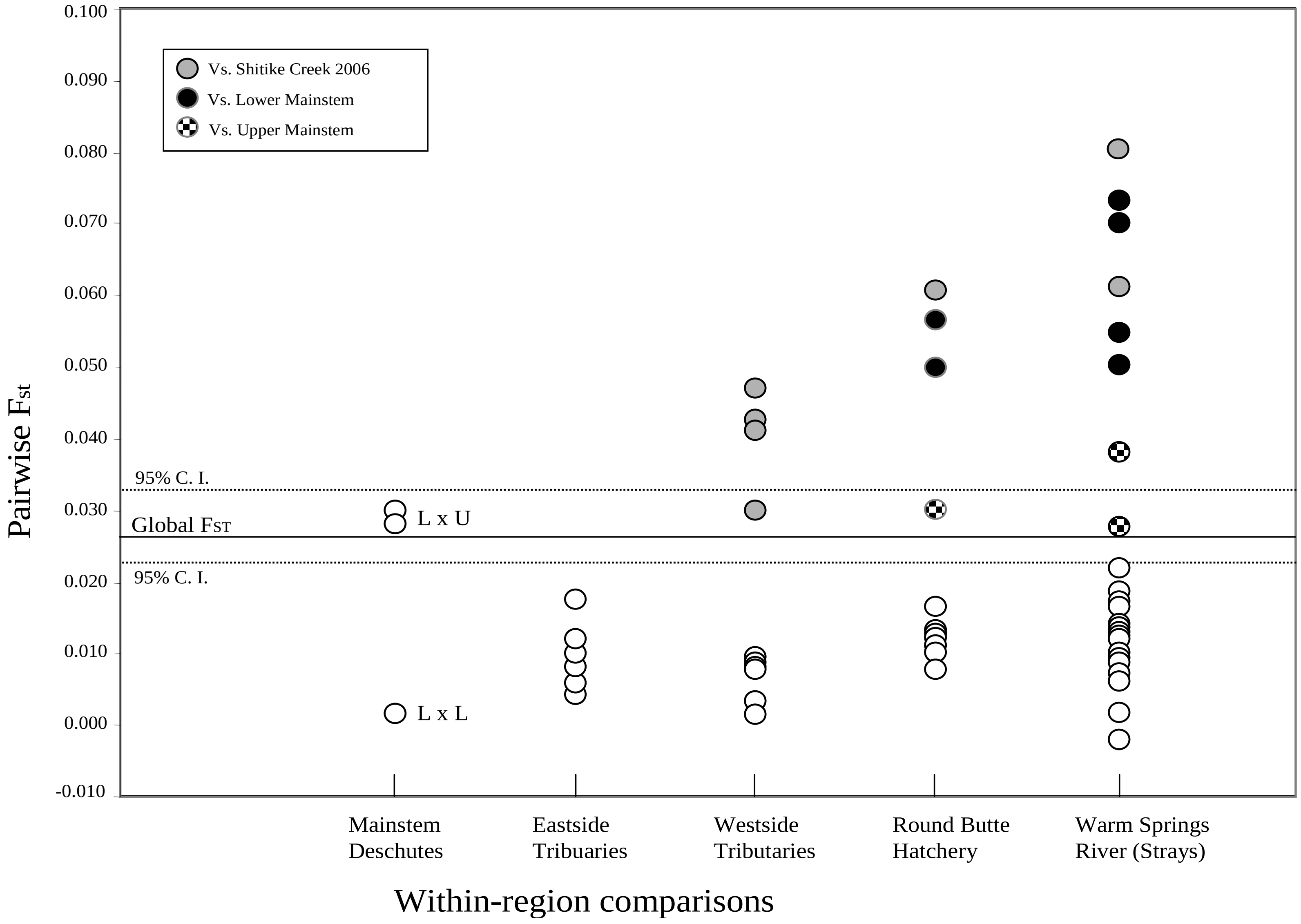


Figure 4. Un-rooted neighbor-joining tree: The phylogram topology was constructed from pairwise genetic (chord) distance measurements (Cavalli-Sforza & Edwards 1967). Juvenile collections (age 0+) are designated STH-anadromous, Omy-resident or unknown. Bootstrap support among 1000 replicate data sets is shown between branch nodes, indicates concordance among loci for each branch in the topology.

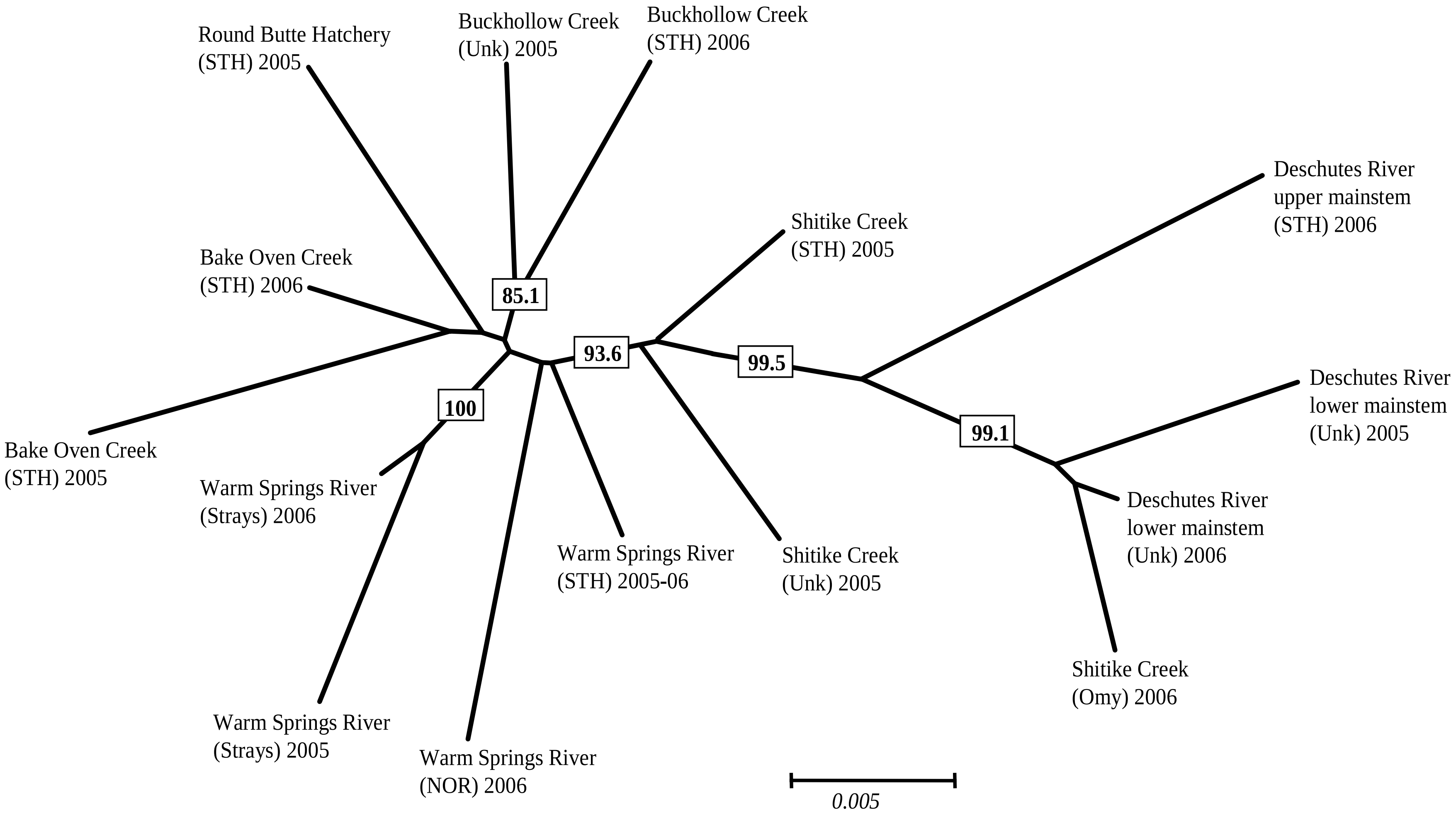
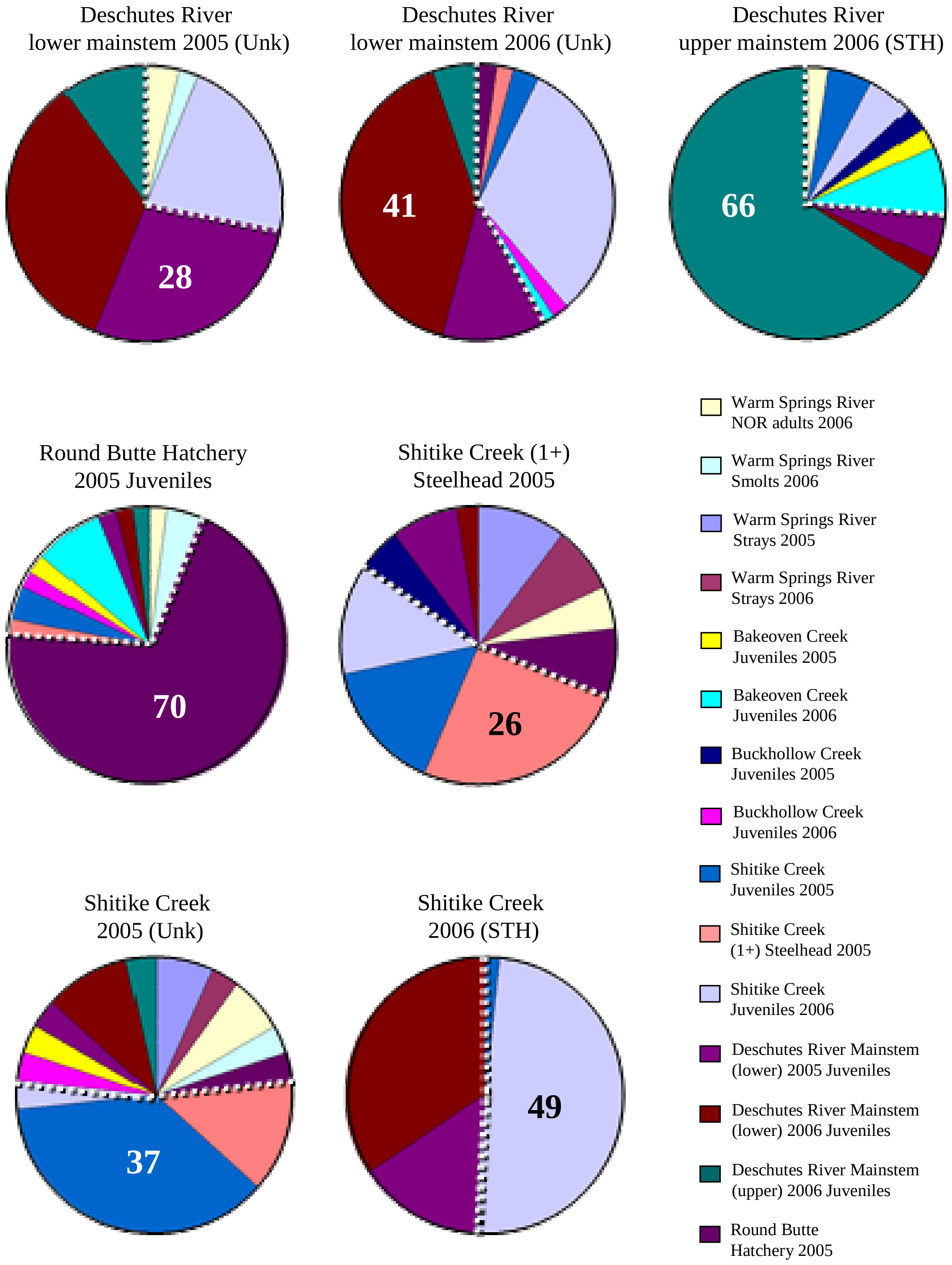


Figure 5. Pie charts showing population assignment results. The proportion of correct assignments to collection of origin is given in each chart, and dotted lines delineate proportion among replicates that assigned to the same tributary of origin.



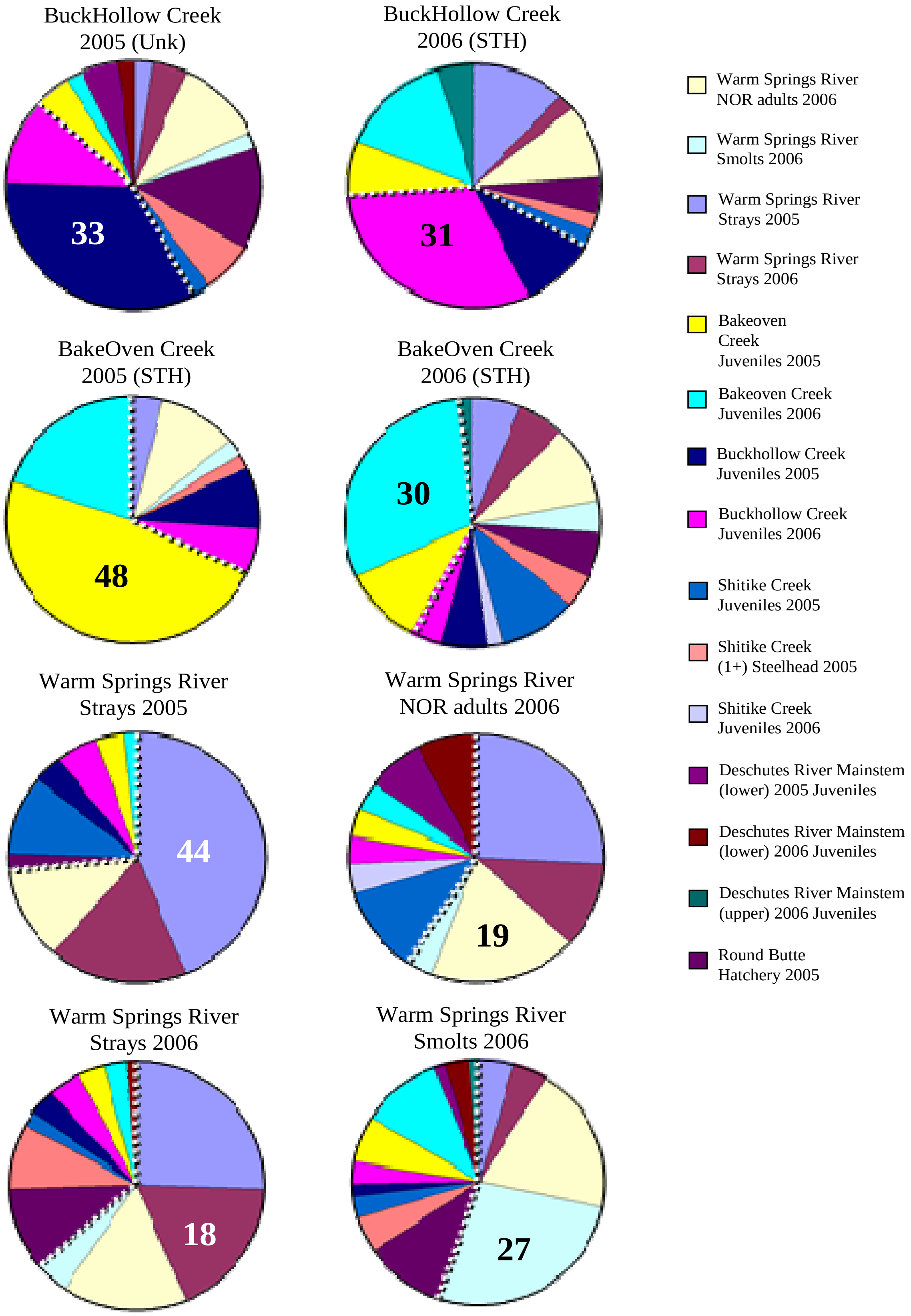

BuckHollow Creek
2005 (Unk)
33
BuckHollow Creek
2006 (STH)
31
BakeOven Creek
2005 (STH)
48
BakeOven Creek
2006 (STH)
30
Warm Springs River
Strays 2005
44
Warm Springs River
NOR adults 2006
19
Warm Springs River
Strays 2006
18
Warm Springs River
Smolts 2006
27
Warm Springs River NOR adults 2006
Warm Springs River Smolts 2006
Warm Springs River Strays 2005
Warm Springs River Strays 2006
Bakeoven Creek Juveniles 2005
Bakeoven Creek Juveniles 2006
Buckhollow Creek Juveniles 2005
Buckhollow Creek Juveniles 2006
Shitike Creek Juveniles 2005
Shitike Creek (1+) Steelhead 2005
Shitike Creek Juveniles 2006
Deschutes River Mainstem (lower) 2005 Juveniles
Deschutes River Mainstem (lower) 2006 Juveniles
Deschutes River Mainstem (upper) 2006 Juveniles
Round Butte Hatchery 2005

Figure 6. Bar plot of proportional population membership. The *K*=6 inferred population clusters (see table 3) are each represented by a different color. Proportional membership is displayed within each of 15 collections evaluated, where the x-axis is individual fish.

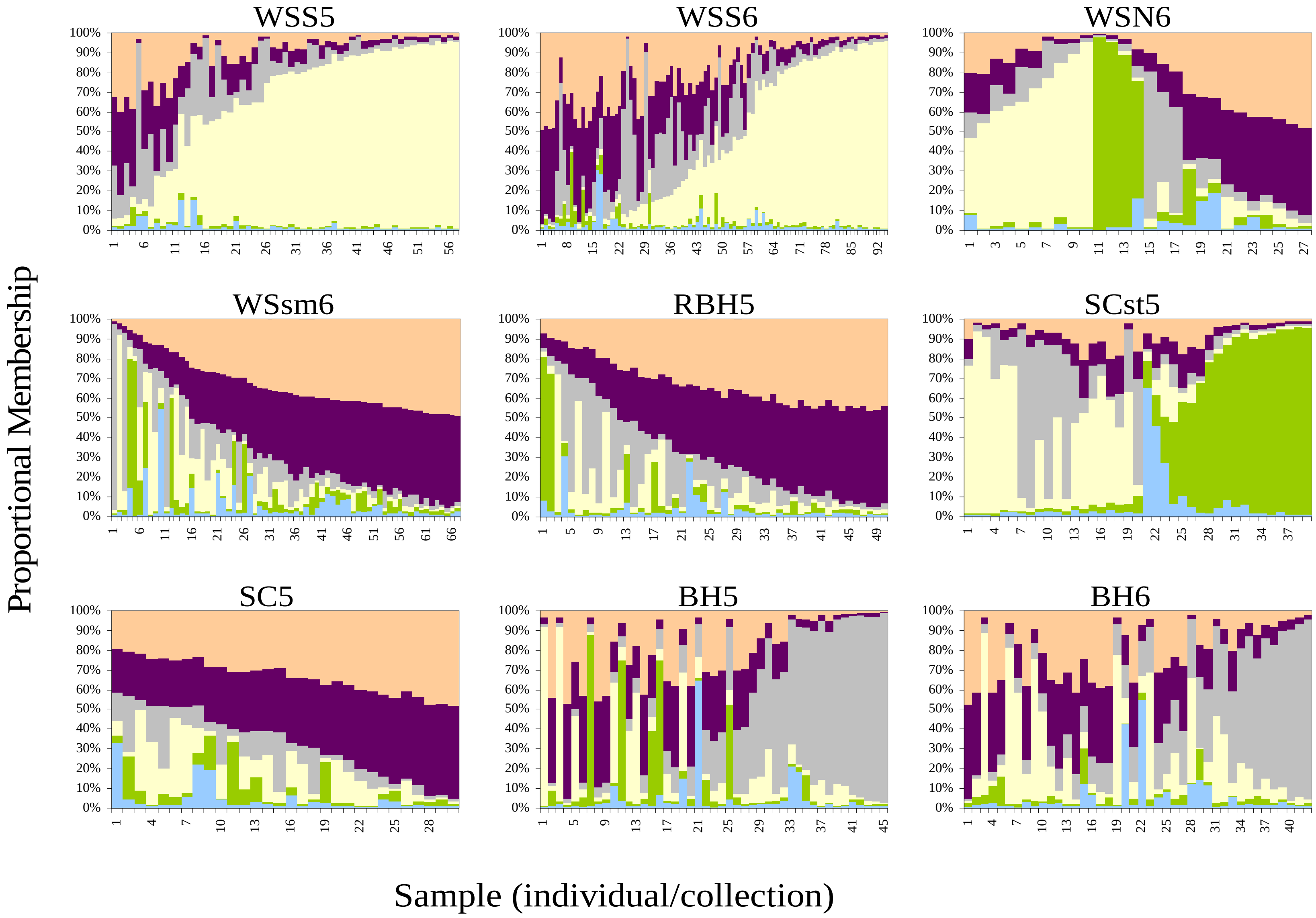
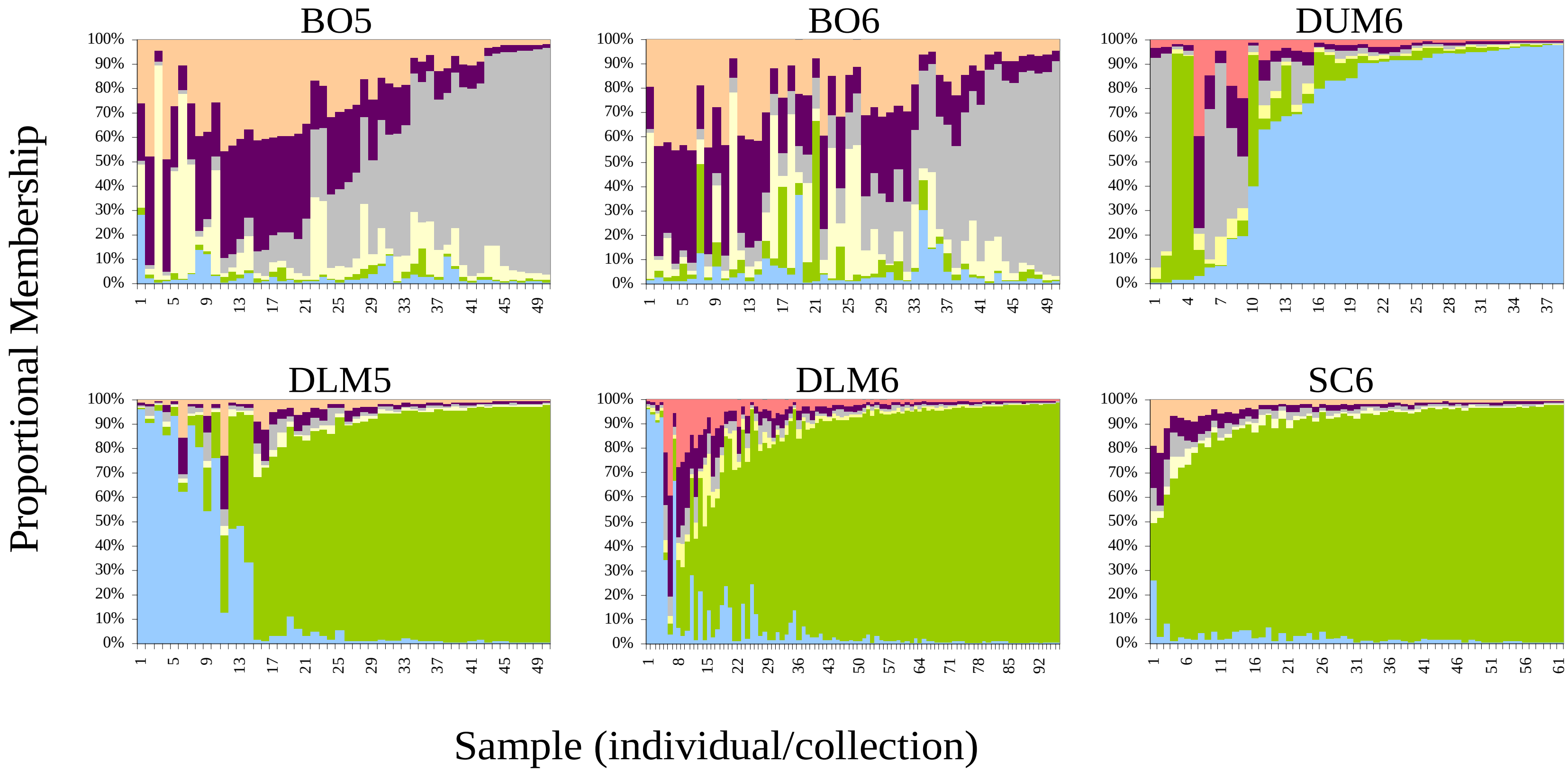


Figure 6 continued.



Appendix 1. List of Loci used for genetic structure analysis. Loci in bold are included in the SPAN-Columbia River Basin microsatellite standardization database for steelhead trout, organized by NOAA fisheries. The annealing temperatures and $MgCl_2$ concentrations for PCR are optimized conditions used at the Conservation Genetics Program Laboratory at Abernathy Fish Technology Center.

Locus	Cite/Source	Annealing °C	$[MgCl_2]$
1. ***µSsa407***	Cairney *et al.* 2000	60	2.0
2. ***µOmy1001UW***	Spies *et al.* 2005	50	1.5
3. ***µOke4***	Buchholz *et al.* 2001	54	2.0
4. *µOts3*	Banks *et al.* 1999	48	2.0
5. ***µOgo4***	Olsen *et al.* 1998	59	1.5
6. ***µOmy1011UW***	Spies *et al.* 2005	59	2.0
7. ***µOmy7iNRA***	K. Gharbi, and R. Guyomard, IRNA, France	59	2.0
8. ***µSsa289***	McConnell *et al.*1995	50	2.0
9. ***µOne14***	Scribner *et al.* 1996	60	2.0
10. ***µOts100***	Banks *et al.* 1999	57	2.0
11. ***µOts4***	Banks *et al.* 1999	53	2.0
12. *µOcl1*	Condrey & Bentzen 1998	59	1.5
13. ***µOki23***	Smith *et al.* 1998	59	2.0
14. *µOmy77*	Morris *et al.* 1996	59	2.0
15. ***µSsa408***	Cairney *et al.* 2000	59	2.0
16. *µOgo3*	Olsen *et al.* 1998	59	2.0
17. *µOts1*	Banks *et al.* 1999	59	2.0

Appendix 2. Allele frequency distribution across 16 loci for each of 15 genetic sample collections. The population designations are: WSS5-Warm Springs River Strays 2005, WSS6-Warm Springs River Strays 2006, WSN6-Warm Springs River NOR 2006, WSsm6-Warm Springs River smolts 2006, BH5-Buckhallow Creek 2005 (Unk), BH6-BuckHollow Creek 2006 (STH), BO5-BakeOven Creek 2005 (STH), BO6-BakeOven Creek 2006 (STH), SCst5-Shitike Creek (1+) steelhead 2005, SC5-Shitike Creek 2005 (Unk), SC6-Shitike Creek 2006 (Omy), DLM5-Deschutes River lower mainstem 2005 (Unk), DLM6-Deschutes River lower mainstem 2006 (Unk), DUM6-Deschutes River upper mainstem 2006 (STH), and RBH5-Round Butte hatchery juveniles 2005. The symbol (*) designates a private allele.

Locus	***Allele (bp)***	WSS5	WSS6	WSN6	WSsm6	BH5	BH6	BO5	BO6	SCst5	SC5	SC6	DML5	DML6	DMU6	RBH5
μOcl1	***154***	0	0	0	0.0149	0	0	0	0	0.0128	0	0	0	0	0	0
	176	0	0.0053	0	0.0075	0	0	0	0	0.0128	0	0	0	0.0053	0.0132	0.0100
	184	0	0	0.0556	0.0075	0	0	0	0	0	0	0	0	0	0	0
	188	0.0089	0.0266	0	0	0.0111	0.0119	0	0	0	0	0	0	0	0	0
	192	0.0268	0.0160	0.0185	0.0522	0.0111	0.0119	0.0400	0.0102	0.0128	0.0167	0.0410	0	0.0474	0.0395	0.0200
	196	0.1250	0.0851	0.0926	0.0299	0.1333	0.1071	0.0400	0.0510	0.0641	0.0667	0.0164	0.0300	0.0263	0.2105	0.0200
	200	0.1786	0.1223	0.1667	0.2239	0.2556	0.1310	0.1600	0.2755	0.2949	0.3000	0.4098	0.4200	0.3526	0.2895	0.1800
	204	0.3750	0.4255	0.4074	0.3731	0.3222	0.4762	0.3300	0.3878	0.2821	0.2667	0.1721	0.2600	0.2474	0.2500	0.3800
	208	0.0446	0.0479	0.0556	0.0896	0.0222	0.0238	0.0500	0.0408	0.0769	0.0667	0.2295	0.1900	0.2000	0.1184	0.1600
	212	0.0804	0.0904	0.0741	0.0746	0.0444	0.0238	0.0600	0.0612	0.0897	0.0667	0.0410	0.0500	0.0474	0.0395	0.0600
	216	0	0.0106	0	0.0075	0	0.0595	0.0700	0.0102	0.0128	0	0	0	0.0053	0.0132	0.0500
	220	0.0268	0.0213	0.0185	0.0373	0.0222	0.0238	0.0600	0.0408	0.0256	0.0167	0.0246	0.0300	0.0158	0.0263	0.0300
	224	0.0625	0.1064	0.0556	0.0373	0.1444	0.0952	0.1700	0.1122	0.1026	0.0833	0.0574	0.0100	0.0316	0	0.0700
	228	0.0446	0.0266	0.0185	0.0448	0.0222	0.0357	0.0200	0.0102	0	0.0667	0.0082	0.0100	0.0211	0	0.0200
	230	0.0268	0.0160	0.0370	0	0.0111	0	0	0	0.0128	0.0500	0	0	0	0	0
μOgo4	***115***	0.0877	0.1596	0.2308	0.2761	0.2889	0.1429	0.1400	0.2200	0.2308	0.3000	0.3390	0.3400	0.3474	0.3026	0.2041
	117	0.0263	0.0160	0.0192	0.0597	0.0444	0.0238	0.0400	0.0200	0.0256	0	0.0339	0	0.0421	0.0395	0.0816
	119	0.0439	0.0266	0	0.0075	0.1000	0.0238	0.0400	0	0.0513	0.0667	0.0085	0.0200	0.0053	0	0.0204
	121	0.0088	0	0	0.0075	0	0	0	0	0	0	0	0	0	0	0
	123	0	0	0	0	0.0333	0	0	0	0.0128	0	0	0	0	0	0
	125	0.0175	0.0053	0	0.0149	0.0111	0.0238	0	0	0.0128	0.0167	0	0.0100	0	0	0

	127	0.0614	0.1170	0.0769	0.0597	0.1000	0.1310	0.0300	0.0200	0.0128	0	0.0085	0	0	0.0395	0.1122
	129	0.2895	0.2553	0.2500	0.2836	0.2222	0.2738	0.3200	0.3400	0.3974	0.2333	0.4831	0.4200	0.4684	0.3158	0.2755
	131	0.2018	0.1543	0.1346	0.1194	0.0667	0.1548	0.2000	0.0900	0.0897	0.0333	0.0593	0.1300	0.0842	0.2368	0.1020
	133	0.0965	0.0851	0.1154	0.0373	0.0111	0.0833	0.0100	0.1300	0.0641	0.1667	0	0.0100	0.0053	0.0132	0.0918
	135	0.1404	0.1489	0.1346	0.1045	0.1111	0.1429	0.1700	0.1800	0.0769	0.1667	0.0508	0.0700	0.0316	0.0395	0.1122
	137	0.0263	0.0160	0	0.0149	0.0111	0	0	0	0.0128	0.0167	0.0169	0	0.0158	0.0132	0
	139	0	0.0160	0.0385	0.0149	0	0	0	0	0	0	0	0	0	0	0
	145	0	0	0	0	0	0	0.0500	0	0.0128	0	0	0	0	0	0
μOmy7i	***234***	0.0702	0.0691	0	0.0746	0.0444	0.0119	0.0500	0.0500	0.0385	0.0667	0	0.0200	0.0052	0	0
	238	0	0.0160	0	0.0149	0	0	0	0	0	0	0	0	0	0	0.0400
	242	0.0175	0.0319	0	0.0075	0.0222	0	0.0100	0	0	0	0	0	0	0	0.0200
	244	0	0.0160	0.1538	0.0522	0.0444	0.0476	0.0400	0.0300	0.0897	0.0500	0.2712	0.2200	0.1354	0.0658	0.0200
	246	0.0789	0.0691	0.0385	0.0299	0.0667	0.0119	0.0400	0.0800	0.1410	0.0500	0.0169	0	0.0208	0.1053	0.0300
	248	0.1491	0.1330	0.1538	0.0672	0.1111	0.0476	0.1400	0.0500	0.0769	0.0667	0.0508	0.0400	0.0312	0.1579	0.1000
	250	0.1228	0.1223	0.1731	0.0970	0.2333	0.1548	0.1900	0.2200	0.1282	0.1500	0.1610	0.1200	0.1042	0.1974	0.2600
	252	0.1228	0.0957	0.0769	0.0970	0.1000	0.3214	0.1800	0.2000	0.0513	0.0500	0.1186	0.1000	0.0990	0.1184	0.1700
	254	0.2368	0.2553	0.2500	0.2687	0.2111	0.2024	0.1800	0.2200	0.2949	0.2833	0.0593	0.0600	0.1250	0.1842	0.1800
	256	0.0789	0.0638	0.0385	0.1194	0.0444	0.0238	0.0400	0.0300	0.0513	0.0667	0.1356	0.1500	0.1927	0.0526	0.1200
	258	0.0702	0.0426	0.0192	0.0075	0.0222	0.0119	0.0300	0.0300	0.0641	0.1500	0.0254	0	0.0260	0.0132	0.0100
	260	0	0	0	0.0149	0	0	0	0	0.0128	0	0	0	0	0	0
	262	0.0263	0.0745	0.0577	0.1269	0.1000	0.1667	0.0800	0.0900	0.0385	0.0667	0.1186	0.2700	0.2292	0.1053	0.0500
	266*	0	0	0	0	0	0	0.0200	0	0	0	0	0	0	0	0
	268	0.0263	0.0053	0.0385	0.0075	0	0	0	0	0.0128	0	0.0424	0.0200	0.0312	0	0
	272	0	0.0053	0	0.0149	0	0	0	0	0	0	0	0	0	0	0
μOts100	***166***	0.1273	0.1064	0.1154	0.1194	0.1444	0.1429	0.1700	0.0500	0.0263	0.1500	0.1475	0.1600	0.2396	0.0946	0.1100
	170	0.2091	0.1543	0.2115	0.0821	0.1444	0.1667	0.0800	0.1300	0.1316	0.1833	0.0984	0.1100	0.1302	0.0541	0.2000
	172	0	0	0	0.0149	0	0	0	0	0	0	0.0082	0	0	0	0
	174	0.0545	0.0585	0.0962	0.0597	0.0444	0.0476	0.0700	0.0400	0.1711	0.0500	0.0246	0.0600	0.0208	0.0135	0.0300
	178	0.3545	0.2660	0.2115	0.2015	0.2222	0.2024	0.2100	0.1400	0.1711	0.1500	0.0656	0.0500	0.0885	0.0405	0.2300
	180	0	0.0053	0.0192	0	0	0	0	0	0	0	0.0082	0	0	0	0

	182	0.1273	0.1809	0.1154	0.1119	0.0778	0.0952	0.1200	0.1700	0.0789	0.1000	0.1230	0.0800	0.0885	0.1757	0.0700
	184	0.0091	0.0691	0.0577	0.0522	0.0333	0.0119	0.0300	0.0500	0.0132	0.0667	0.0492	0.0300	0.0625	0.0811	0.0300
	186	0.0091	0.0319	0.0577	0.0299	0.0556	0.0357	0.0100	0.0800	0.0263	0	0.0246	0.0100	0	0	0.0600
	188	0	0	0	0.0224	0	0	0.0200	0	0	0	0	0	0	0	0
	190	0.0091	0.0266	0	0.0299	0.0444	0.0476	0.0400	0.0800	0	0	0	0.0100	0.0104	0.0135	0.0900
	192	0	0	0.0192	0.0075	0.0111	0.0119	0.0100	0.0200	0	0	0	0.0100	0	0.0405	0
	194	0.0273	0.0266	0.0769	0.1493	0.1556	0.1548	0.1400	0.1200	0.2632	0.2500	0.4180	0.3900	0.3177	0.2432	0.1500
	196	0	0	0	0	0	0	0.0200	0	0.0132	0	0	0.0200	0	0.0270	0
	198	0.0364	0.0213	0	0.0522	0.0333	0.0119	0.0400	0.0800	0.0658	0.0167	0.0246	0.0100	0.0208	0.0405	0
	200	0.0091	0	0	0	0	0	0	0.0200	0.0132	0	0	0	0.0104	0.0270	0.0300
	202	0	0.0372	0.0192	0.0597	0	0	0	0	0	0	0	0.0100	0	0	0
	204*	0	0	0	0	0	0	0	0	0.0132	0	0	0	0	0	0
	206	0	0.0106	0	0	0.0222	0.0119	0.0400	0	0.0132	0.0333	0	0.0100	0	0	0
	210	0.0273	0.0053	0	0.0075	0	0.0238	0	0	0	0	0	0	0	0	0
	212	0	0	0	0	0	0.0238	0	0.0200	0	0	0.0082	0	0	0.0541	0
	216	0	0	0	0	0	0	0	0	0	0	0	0.0400	0.0104	0.0946	0
	220	0	0	0	0	0.0111	0.0119	0	0	0	0	0	0	0	0	0
μOts3	***73****	0	0	0	0	0	0	0	0	0	0.0500	0	0	0	0	0
	75	0.0702	0.0638	0.0185	0.0152	0.0444	0.0238	0.0500	0.0300	0.0256	0.0167	0.0082	0	0.0158	0.0526	0.0400
	77	0.3772	0.3777	0.4630	0.4697	0.5333	0.3929	0.4000	0.4900	0.4231	0.5167	0.5738	0.7100	0.5684	0.3684	0.3800
	79	0.3509	0.3457	0.3333	0.3409	0.2556	0.3214	0.3300	0.3700	0.4872	0.3500	0.3934	0.2800	0.3526	0.5132	0.4200
	81	0.1228	0.1223	0.0741	0.0909	0	0.0714	0.0200	0.0100	0.0513	0.0667	0	0	0.0368	0	0.0500
	83	0.0614	0.0851	0.0926	0.0606	0.1556	0.1786	0.1900	0.1000	0.0128	0	0.0164	0.0100	0.0263	0.0658	0.1100
	85	0	0.0053	0.0185	0.0076	0.0111	0.0119	0.0100	0	0	0	0	0	0	0	0
	87	0.0175	0	0	0.0152	0	0	0	0	0	0	0	0	0	0	0
	93*	0	0	0	0	0	0	0	0	0	0	0.0082	0	0	0	0
μOts4	***105***	0.1579	0.1223	0.0769	0.1343	0.0778	0.1429	0.0500	0.1000	0.1538	0.2069	0.0750	0.0800	0.0789	0.2237	0.1327
	117	0.1754	0.1702	0.0962	0.1194	0.1889	0.2024	0.1500	0.1800	0.0897	0.0345	0.0417	0.0700	0.0211	0.1579	0.1224
	119	0.0789	0.0638	0.0192	0.0746	0.0667	0.0357	0.1600	0.1400	0.0769	0.1034	0.1167	0.0500	0.0789	0.0789	0.1837
	121	0.0088	0.0319	0.0577	0.0224	0.0111	0.0119	0.0500	0.0500	0.0256	0	0	0.0200	0.0158	0.0789	0.0306

	123	0.3421	0.4202	0.5385	0.4627	0.5444	0.4167	0.2400	0.3000	0.6026	0.4310	0.6667	0.7200	0.7263	0.4342	0.3980
	125	0.2281	0.1862	0.1731	0.1716	0.1111	0.1905	0.3400	0.2200	0.0385	0.2241	0.0917	0.0600	0.0737	0.0132	0.1224
	127	0.0088	0.0053	0.0385	0.0149	0	0	0.0100	0.0100	0.0128	0	0.0083	0	0.0053	0.0132	0.0102
μOgo3	***77****	0	0	0	0	0	0	0	0	0	0	0	0	0	0.0132	0
	79	0	0.0053	0.0185	0	0	0	0	0	0	0	0	0	0	0	0
	81	0	0.0053	0.0185	0.0299	0.0111	0.0119	0.0200	0.0100	0.0513	0	0.0492	0.0100	0.0052	0.0132	0.0300
	83	0.2456	0.2021	0.1667	0.2463	0.3000	0.2143	0.2000	0.2600	0.2179	0.1500	0.1393	0.1300	0.1458	0.1316	0.3100
	85	0	0.0053	0	0.0149	0	0.0238	0	0	0.0256	0.0167	0	0.0100	0.0104	0.0658	0.0100
	87	0.3158	0.2819	0.2593	0.2388	0.4444	0.2381	0.3100	0.2500	0.3462	0.3333	0.1066	0.1500	0.1146	0.1842	0.2400
	89	0.0088	0.0426	0.0370	0.0299	0.0333	0.0595	0.0600	0.0600	0.0641	0.0333	0.2049	0.2500	0.1562	0.1053	0.0300
	91	0.4035	0.3989	0.3889	0.4030	0.2111	0.4167	0.3500	0.3800	0.2821	0.4167	0.3770	0.3500	0.4688	0.4474	0.3800
	93	0.0175	0.0426	0.1111	0.0373	0	0.0357	0.0500	0.0300	0.0128	0.0500	0.1230	0.0900	0.0990	0.0395	0
	95	0.0088	0.0160	0	0	0	0	0.0100	0.0100	0	0	0	0.0100	0	0	0
μOki23	***116***	0.0263	0.0266	0.0556	0.0373	0.0778	0.0238	0	0.0200	0.0256	0	0.0082	0	0	0.0405	0.0306
	120	0.0439	0.0426	0.0185	0	0.0111	0.0119	0.0200	0.0300	0.0256	0	0.0328	0.0500	0.0469	0.0270	0.0408
	122*	0.0088	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	124	0.4035	0.3351	0.2778	0.2761	0.2444	0.4524	0.5000	0.4400	0.3205	0.3667	0.2787	0.2600	0.3281	0.3649	0.5000
	128	0.2018	0.1543	0.2593	0.1418	0.2444	0.1548	0.1600	0.2400	0.1795	0.3167	0.2131	0.2000	0.1771	0.1216	0.1633
	132	0.0614	0.0585	0	0.0224	0.0778	0.0595	0.0300	0.0400	0.0128	0.0500	0.0082	0	0.0052	0.0541	0.0408
	136	0.0526	0.0585	0	0.0448	0.0444	0.0238	0.0500	0.0100	0.0385	0.0667	0.0082	0	0.0104	0	0.0204
	140	0.0526	0.0691	0.0370	0.0448	0.0778	0.0357	0.0400	0.0100	0.0385	0	0.0082	0	0.0156	0.1216	0.0102
	144	0.0702	0.0798	0.1111	0.1343	0.0333	0.0833	0.0600	0.0700	0.0769	0.0500	0	0.0300	0.0260	0.0135	0.0612
	148	0.0526	0.0372	0.0370	0.0448	0.0444	0	0.0100	0.0500	0.0256	0	0.0410	0.0200	0.0104	0	0.0306
	152	0.0175	0.0426	0.0741	0.0896	0.0444	0.0357	0	0.0400	0.1795	0.0833	0.2131	0.2000	0.1771	0.0541	0.0306
	156	0	0.0106	0.0370	0.0075	0.0444	0.0952	0	0.0300	0.0385	0.0167	0.0574	0.0900	0.1042	0.0270	0.0714
	160	0	0.0160	0	0.0373	0.0111	0	0.0300	0.0200	0.0128	0.0500	0.1066	0.0900	0.0677	0.0135	0
	164	0	0.0213	0.0370	0.0746	0	0	0.0300	0	0	0	0	0.0100	0.0052	0	0
	168	0	0.0053	0.0370	0.0075	0.0111	0	0.0100	0	0	0	0	0.0200	0.0104	0.0270	0
	172	0.0088	0.0106	0	0.0224	0	0.0119	0.0200	0	0.0128	0	0.0164	0.0100	0.0156	0.0541	0
	176*	0	0	0	0	0	0	0	0	0	0	0.0082	0	0	0	0

	184	0	0	0	0	0.0111	0	0.0200	0	0	0	0	0	0	0.0811	0
	188	0	0.0053	0	0	0	0	0	0	0.0128	0	0	0.0200	0	0	0
	192*	0	0.0053	0	0	0	0	0	0	0	0	0	0	0	0	0
	196	0	0.0213	0.0185	0.0149	0.0222	0.0119	0.0200	0	0	0	0	0	0	0	0
μOmy1011	134	0	0	0	0.0075	0	0	0	0	0	0	0	0.0200	0.0053	0.1316	0
	138	0.0089	0.0053	0.0185	0.0299	0.0111	0	0	0	0	0	0	0	0	0	0
	146	0.0268	0	0	0.0075	0	0	0.0100	0	0	0.0167	0.0082	0.0100	0	0	0.0600
	150	0.0089	0.0266	0.0370	0.0149	0	0	0.0300	0.0100	0.0513	0.0167	0	0	0.0053	0.0132	0.0300
	154	0.0625	0.0585	0.0926	0.0970	0.1222	0.0119	0.0900	0.0900	0.0256	0	0	0.0100	0	0	0.0300
	158	0.1250	0.0745	0.0926	0.1119	0.0333	0.0595	0.0900	0.0800	0.0128	0.1000	0.0082	0.0200	0.0316	0.0526	0.0900
	162	0.0089	0.0426	0.0741	0.0075	0.0667	0.0714	0.0300	0.0300	0.0128	0.0500	0.0328	0.0200	0.0263	0.0789	0.0500
	166	0.0804	0.0957	0.0926	0.0746	0.1333	0.0476	0.0800	0.0800	0.1410	0.1500	0.2131	0.1600	0.1632	0.0789	0.1200
	170	0.2411	0.2074	0.2778	0.2239	0.1556	0.2500	0.2500	0.2400	0.1538	0.2000	0.1230	0.1700	0.1421	0.1316	0.1400
	174	0.0982	0.1436	0.0556	0.1418	0.0889	0.1071	0.1500	0.1400	0.1667	0.0500	0.0246	0.0300	0.0526	0.0658	0.2200
	178	0.1339	0.1330	0.0741	0.0224	0.0111	0.0595	0.0300	0.0200	0.0385	0.0333	0.0410	0.0500	0.0526	0.0132	0.0900
	182	0	0.0319	0.0185	0.0448	0.0667	0.0238	0.0100	0.0400	0.0769	0.0167	0.0902	0.1200	0.1053	0.0263	0.0100
	186	0.0536	0.0532	0.0185	0.0448	0.1333	0.2500	0.0800	0.0900	0.1282	0.1333	0.2131	0.2600	0.2316	0.1842	0.0700
	190	0.0536	0.0532	0.0370	0.0746	0.0556	0.0357	0.0500	0.0800	0.0769	0	0.0738	0.0500	0.0474	0.1184	0.0400
	194	0.0357	0.0266	0	0.0448	0.0222	0.0238	0.0200	0.0400	0.0513	0.0833	0.0984	0.0500	0.0684	0.0526	0.0200
	198	0	0.0213	0.0556	0.0224	0.0444	0.0476	0.0300	0.0500	0.0128	0.0333	0.0328	0.0100	0.0105	0.0395	0.0300
	202	0.0625	0.0266	0.0370	0.0299	0.0444	0.0119	0.0100	0.0100	0.0256	0.0833	0.0410	0.0200	0.0526	0.0132	0
	206	0	0	0.0185	0	0	0	0.0300	0	0	0	0	0	0	0	0
	210	0	0	0	0	0	0	0.0100	0	0.0256	0.0333	0	0	0	0	0
	230	0	0	0	0	0.0111	0	0	0	0	0	0	0	0.0053	0	0
μOmy77	96*	0	0	0	0	0	0	0.0100	0	0	0	0	0	0	0	0
	98	0.0091	0	0	0	0	0	0	0	0	0	0	0.0800	0.0158	0.2237	0
	102	0.0273	0.0160	0.0556	0.0076	0.0556	0.0250	0	0	0.0385	0.0167	0	0.0100	0	0	0
	110	0	0.0160	0.0185	0.0076	0	0.0125	0	0	0.0385	0.1000	0	0.0100	0	0	0.0521
	112	0.0091	0.0106	0	0.0227	0.0222	0.0125	0	0.0700	0	0	0	0.0100	0	0	0.0104
	114	0.0364	0.0160	0.0185	0.0152	0.0222	0.0125	0.0400	0	0	0	0.0164	0.0200	0.0368	0.0132	0

	116	0.1091	0.1702	0.1667	0.0758	0.0667	0.0500	0.0600	0.0900	0.1154	0.1167	0.0984	0.1300	0.1368	0.0526	0.1354
	118	0.0273	0.0479	0.0926	0.1212	0.0667	0.0125	0.1300	0.0900	0.0897	0.0667	0.0820	0.1500	0.1316	0.1184	0.1771
	120	0.0455	0.0691	0.0185	0.0379	0.0333	0.0375	0.0500	0.0300	0.0128	0.0167	0.0082	0.0200	0.0211	0	0.0312
	122	0.2182	0.1064	0.0556	0.0909	0.0667	0.1250	0.1000	0.1100	0.0641	0.0167	0.0164	0	0	0.0132	0.0208
	124	0.0818	0.0904	0.0556	0.1364	0.1778	0.1625	0.1000	0.1500	0.1154	0.1000	0.0328	0.0200	0.0368	0.0526	0.1458
	126	0.1364	0.1117	0.0741	0.1136	0.1333	0.0625	0.1300	0.1300	0.1923	0.1833	0.1557	0.1100	0.0684	0.1053	0.0833
	128	0.0273	0.0851	0.0370	0.0909	0.0556	0.0875	0.0600	0.0800	0.0385	0.0500	0.0902	0.0600	0.0737	0.0789	0.1667
	130	0.0364	0.0426	0.1296	0.1212	0.0667	0.1375	0.0100	0.0600	0.0641	0.1000	0.2049	0.1200	0.1789	0.0395	0.0521
	132	0.1909	0.1755	0.1852	0.1212	0.1333	0.1375	0.2100	0.1200	0.1795	0.2000	0.2131	0.2300	0.2211	0.1974	0.0938
	134	0.0182	0.0372	0.0926	0.0303	0.0778	0.0125	0.0400	0	0.0385	0.0333	0.0820	0.0300	0.0737	0.0658	0.0104
	136	0	0	0	0.0076	0.0222	0.0875	0.0500	0.0500	0	0	0	0	0	0.0395	0.0104
	138	0.0091	0.0053	0	0	0	0.0250	0.0100	0.0200	0.0128	0	0	0	0	0	0.0104
	140	0.0182	0	0	0	0	0	0	0	0	0	0	0	0.0053	0	0
μSsa289	103*	0	0	0	0	0	0	0	0	0.0128	0	0	0	0	0	0
	105	0	0.0160	0.0185	0.0149	0.0222	0.0119	0	0.0200	0	0	0	0.0400	0.0104	0.0921	0
	107	0.5625	0.7181	0.6852	0.8209	0.7444	0.6667	0.8000	0.8600	0.8205	0.6500	0.8689	0.8600	0.9115	0.6974	0.7500
	109	0.2857	0.1649	0.2407	0.0597	0.1556	0.2262	0.1600	0.0800	0.0513	0.1667	0.0410	0.0400	0.0156	0.0395	0.1000
	111	0	0	0	0.0075	0.0111	0.0119	0	0.0100	0	0.0500	0.0492	0.0200	0.0312	0.0263	0.0400
	113	0.0357	0.0426	0.0556	0.0299	0.0556	0.0357	0.0300	0.0100	0	0.0500	0	0	0	0	0
	115	0.1071	0.0532	0	0.0597	0.0111	0.0357	0.0100	0.0200	0.0256	0.0333	0.0328	0.0200	0.0208	0.1316	0.0500
	117	0	0	0	0	0	0	0	0	0.0641	0.0333	0	0.0200	0.0052	0.0132	0.0500
	119	0.0089	0.0053	0	0.0075	0	0.0119	0	0	0.0256	0.0167	0.0082	0	0.0052	0	0.0100
Ssa407	159	0	0.0053	0	0	0	0.0119	0	0	0	0	0.0083	0	0.0052	0	0.0300
	163	0.0179	0.0053	0	0.0149	0	0	0	0.0200	0	0.0167	0	0.0300	0	0	0
	167	0.0714	0.0479	0.0926	0.0448	0.0556	0.1310	0.0600	0.0900	0.0263	0.0500	0.0167	0.0400	0.0521	0.0263	0.0600
	171	0.1071	0.1755	0.1296	0.1269	0.1889	0.1786	0.1600	0.1700	0.1579	0.1500	0.2917	0.2400	0.2969	0.1447	0.1700
	175	0.1518	0.1436	0.0185	0.0821	0.0778	0.0714	0.1500	0.1100	0.1184	0.1167	0.0167	0.0600	0.0365	0.0395	0.0600
	179	0.1875	0.1915	0.2037	0.0896	0.1778	0.1905	0.1200	0.1600	0.1447	0.0500	0.0583	0.1100	0.0573	0.1316	0.1300
	183	0.1786	0.1755	0.1667	0.1343	0.1667	0.1310	0.0900	0.1700	0.2237	0.1833	0.2083	0.2400	0.1615	0.2763	0.2200
	187	0.1339	0.1117	0.1481	0.2910	0.1111	0.1071	0.1400	0.1000	0.1579	0.1833	0.2167	0.1300	0.1615	0.1316	0.0800

	191	0.0268	0.0160	0.0741	0.0299	0.0333	0.0238	0.0300	0.0300	0	0.0333	0.0250	0.0100	0.0260	0.0395	0.0400
	195	0.0446	0.0160	0.0185	0.0149	0.0556	0.0357	0.0900	0.0500	0.0263	0	0.0250	0.0100	0.0104	0.0395	0.0300
	199	0.0179	0.0319	0.0185	0.0522	0.0222	0.0119	0.0300	0.0100	0.0263	0.0667	0.0083	0.0300	0.0156	0.0395	0.0300
	203	0.0089	0.0106	0	0.0224	0.0111	0.0238	0.0100	0.0200	0	0	0	0.0100	0	0.0132	0
	207	0.0089	0	0	0	0.0333	0	0.0100	0	0.0132	0.0167	0	0.0100	0	0	0.0100
	211	0.0179	0.0372	0.0185	0.0149	0.0111	0.0357	0.0500	0	0.0263	0	0.0167	0.0200	0.0417	0.0395	0.0200
	215	0.0089	0	0.0556	0.0448	0.0111	0.0119	0	0.0200	0.0263	0.1167	0.0500	0.0500	0.1042	0.0526	0.0900
	219	0	0.0160	0.0370	0.0299	0	0.0238	0.0600	0.0200	0.0395	0	0	0.0100	0.0052	0	0
	223	0.0089	0.0053	0	0.0075	0.0111	0	0	0.0100	0.0132	0	0.0250	0	0.0156	0.0263	0.0300
	227	0	0	0	0	0	0	0	0.0200	0	0	0.0333	0	0.0104	0	0
	231	0.0089	0.0106	0.0185	0	0	0	0	0	0	0	0	0	0	0	0
	235	0	0	0	0	0.0333	0.0119	0	0	0	0	0	0	0	0	0
	247*	0	0	0	0	0	0	0	0	0	0.0167	0	0	0	0	0
μSsa408	169	0	0.0106	0	0	0.0556	0.0119	0	0.0100	0	0	0	0	0	0.0395	0
	173	0.0526	0.0957	0.0741	0.0896	0.0333	0.0714	0.0700	0.1400	0.1026	0.1333	0.0167	0.0100	0.0260	0.0395	0.2021
	177	0.1316	0.0904	0.0926	0.0970	0.1444	0.0476	0.0600	0.1200	0.0641	0.0833	0.0167	0.0200	0.0521	0.1316	0.0957
	181	0.0351	0.0691	0.0556	0.0448	0.0111	0.0238	0.0200	0.0200	0.0256	0.0167	0.0333	0.0200	0.0156	0.0658	0.0213
	185	0.1228	0.0745	0.0741	0.0746	0.1333	0.1786	0.1600	0.0900	0.0128	0.0333	0.0583	0.0900	0.0833	0.0263	0.0851
	189	0.0351	0.0479	0.0370	0.1045	0.0667	0.0714	0.1100	0.0800	0.1026	0.1500	0.0333	0.0600	0.0521	0.1316	0.0426
	193	0.0965	0.1383	0.1296	0.0672	0.1000	0.0476	0.0100	0.0600	0.0769	0.2333	0.1083	0.1200	0.1667	0.1184	0.1383
	197	0.1053	0.0585	0.0556	0.1343	0.1222	0.1429	0.0900	0.0900	0.0897	0.1167	0.2000	0.2400	0.1823	0.1184	0.0532
	201	0.0789	0.0319	0.0370	0.0597	0.0444	0.0595	0.0100	0.0300	0.0513	0.0167	0.0333	0	0.0104	0.0132	0.0319
	205	0.2105	0.1543	0.1296	0.0597	0.0778	0.0833	0.2500	0.1100	0.1538	0.0500	0.0417	0.0100	0.0104	0	0.1489
	209	0.0614	0.0266	0.0741	0.0224	0.0111	0.0476	0	0	0.0385	0	0.0250	0.0300	0.0156	0.0132	0
	213	0	0.0372	0.0185	0.0448	0.0111	0.0476	0	0.0300	0.0256	0.0167	0.0083	0.0100	0.0052	0	0.0319
	217	0.0088	0.0319	0	0.0224	0.0111	0.0238	0	0.0300	0.0128	0.0167	0.0083	0	0	0	0.0106
	221	0.0088	0.0319	0.0556	0.0299	0.0111	0.0119	0.1100	0.0700	0.0641	0.0333	0.1917	0.1100	0.1302	0.0526	0.0638
	225	0.0439	0.0372	0	0	0.0556	0.0238	0	0.0400	0.0769	0.0167	0.0333	0.0700	0.0573	0.0263	0.0106
	227	0	0	0	0	0	0.0119	0.0200	0.0100	0	0	0	0	0	0	0
	229	0.0088	0.0426	0.1111	0.0522	0.0667	0.0833	0.0900	0.0600	0.0897	0.0667	0.1583	0.1900	0.1719	0.1447	0.0638
	233	0	0.0160	0.0556	0.0597	0.0333	0.0119	0	0	0	0.0167	0.0333	0.0100	0.0208	0.0395	0

	237	0	0	0	0.0075	0.0111	0	0	0.0100	0	0	0	0.0100	0	0	0
	241	0	0.0053	0	0	0	0	0	0	0.0128	0	0	0	0	0	0
	245	0	0	0	0.0299	0	0	0	0	0	0	0	0	0	0.0395	0
μOke4	234	0.0088	0.0165	0	0.0075	0.0222	0	0	0	0.0128	0.0667	0	0.0100	0.0052	0	0
	236	0.0526	0.0220	0.0370	0.0299	0.0444	0.0357	0.0900	0.0900	0.0256	0.0500	0.0082	0	0	0.0270	0.1735
	240	0	0	0	0	0	0	0	0	0.0128	0	0.0164	0	0.0573	0	0
	242	0.1053	0.2308	0.2593	0.3284	0.2444	0.2143	0.2100	0.1600	0.2436	0.1500	0.4508	0.3100	0.3542	0.2703	0.2551
	244	0.1842	0.2253	0.2593	0.1119	0.1111	0.1190	0.3400	0.2300	0.1026	0.2667	0.0656	0.1600	0.0833	0.1081	0.1429
	245*	0	0	0	0	0	0.0119	0	0	0	0	0	0	0	0	0
	246	0.0702	0.0659	0.1481	0.1119	0.0889	0.1071	0.0900	0.1000	0.0769	0.1167	0.0246	0.0900	0.0625	0.0270	0.1531
	248	0.1404	0.0824	0.0926	0.1642	0.1444	0.1905	0.0300	0.1900	0.2051	0.1500	0.3689	0.3600	0.3333	0.2973	0.0918
	250	0.1316	0.0879	0.0556	0.0224	0.0556	0.0833	0.0500	0.0300	0.0513	0.0667	0	0.0100	0.0052	0.0135	0.0510
	252	0	0	0	0	0	0	0	0	0.0256	0	0.0082	0	0	0	0
	254	0.2456	0.2143	0.1296	0.1194	0.2222	0.2262	0.1500	0.1400	0.2308	0.1000	0.0574	0	0.0677	0.0270	0.1224
	256	0	0.0055	0.0185	0.0597	0.0111	0	0.0100	0.0300	0	0.0167	0	0	0	0	0
	257	0	0	0	0.0373	0	0	0	0	0	0	0	0	0.0104	0	0
	258	0.0439	0.0385	0	0	0	0	0.0300	0.0100	0.0128	0.0167	0	0	0	0	0
	262	0	0	0	0	0.0111	0.0119	0	0	0	0	0	0	0	0	0
	264	0.0175	0.0110	0	0.0075	0.0333	0	0	0.0100	0	0	0	0	0.0052	0.0541	0.0102
	272	0	0	0	0	0.0111	0	0	0.0100	0	0	0	0.0400	0.0052	0.0676	0
	274	0	0	0	0	0	0	0	0	0	0	0	0.0200	0.0104	0.1081	0
μOmy1001	168	0.0263	0.0330	0.0192	0.0075	0.0222	0	0	0	0.0132	0	0	0	0.0052	0	0.0204
	172	0	0	0	0	0	0	0.0300	0.0100	0	0	0	0	0	0	0
	174*	0	0	0	0	0	0	0.0100	0	0	0	0	0	0	0	0
	176	0.0439	0.0495	0.0192	0.0522	0.0444	0.0119	0.1100	0.0400	0	0.0333	0	0	0.0052	0.0658	0.0510
	180	0.0351	0.0330	0	0.0149	0.0333	0.0357	0.0800	0.0400	0	0.0167	0	0.0400	0.0052	0.1447	0.0102
	182	0.0351	0.0604	0.0385	0.0448	0.1000	0.0357	0.1600	0.0800	0.1316	0.0333	0.2131	0.1200	0.2135	0.0658	0.0612
	184	0.1140	0.0769	0.0192	0.1269	0.0778	0.0476	0.0300	0.0900	0.0658	0.1000	0.0082	0.0400	0.0312	0.0658	0.0306
	186	0.0088	0.0330	0.0192	0.0299	0.0333	0.0238	0	0.0300	0.0395	0	0.0082	0.0600	0.0208	0.0395	0.0612
	188	0.1404	0.1264	0.1538	0.1269	0.1111	0.1905	0.0700	0.1100	0.1316	0.0833	0.0984	0.1300	0.1302	0.0921	0.0918

	190	0.1140	0.1099	0.1154	0.0746	0.1444	0.1310	0.1800	0.1300	0.1184	0.1167	0.0328	0	0.0469	0.1447	0.0612
	192	0.0965	0.0385	0.0962	0.0448	0.0333	0.0357	0.0200	0.0600	0.1184	0.1000	0.0246	0.0500	0.0312	0.0263	0.0306
	194	0.0088	0.0165	0.0385	0.0075	0.0111	0.0238	0.0200	0.0500	0.0132	0.0333	0.0410	0.0600	0.0208	0	0.0204
	196	0.1316	0.1154	0.1731	0.0597	0.0556	0.1071	0.0300	0.1200	0.0263	0.1667	0.0164	0.0500	0.0104	0.0526	0.1122
	198	0.0263	0.0275	0	0.0299	0.0778	0.0714	0.0100	0.0100	0.0132	0	0.0164	0.0300	0	0	0.0408
	200	0.0351	0.0440	0.0385	0.0597	0.0222	0.0357	0.0100	0.0100	0.0263	0	0.0164	0.0100	0.0312	0.0526	0.1939
	202	0.0263	0.0714	0.1346	0.0597	0.0444	0.0238	0.0300	0.0700	0.1579	0.1500	0.3934	0.2300	0.3125	0.1053	0
	204	0.0877	0.0769	0.0385	0.1269	0.0444	0.0833	0.0900	0.0600	0.0263	0.0667	0.0574	0.0400	0.0312	0.0789	0.1122
	206	0	0	0	0.0224	0	0.0119	0.0100	0	0.0263	0	0	0.0800	0.0312	0.0395	0
	208	0.0088	0.0495	0.0192	0.0373	0.0556	0.0476	0.0300	0.0900	0.0658	0.0667	0.0082	0.0100	0.0104	0.0263	0.0714
	210	0	0.0055	0.0385	0.0373	0.0556	0.0238	0	0	0	0.0167	0.0492	0.0400	0.0521	0	0.0306
	212	0.0088	0.0110	0	0.0224	0.0222	0.0119	0.0400	0	0	0	0.0164	0	0	0	0
	214*	0	0	0	0	0	0	0	0	0	0	0	0	0.0104	0	0
	216	0	0	0	0	0	0.0119	0	0	0	0.0167	0	0	0	0	0
	220	0.0088	0	0	0	0	0	0.0400	0	0.0132	0	0	0	0	0	0
	224	0.0439	0.0220	0.0385	0.0149	0.0111	0.0357	0	0	0.0132	0	0	0.0100	0	0	0
μOne14	146	0.1842	0.0934	0.0926	0.1045	0.0778	0.0952	0.1000	0.0500	0.0769	0.1333	0.0246	0.0200	0.0365	0	0
	150	0.1053	0.0989	0.0741	0.0896	0.0333	0.0476	0.1600	0.1300	0.0641	0.0500	0.0246	0.0200	0.0104	0.0658	0.0300
	152*	0	0.0055	0	0	0	0	0	0	0	0	0	0	0	0	0
	154	0.2281	0.2363	0.2593	0.2313	0.2111	0.2262	0.1900	0.1800	0.2308	0.2167	0.0656	0.0700	0.1094	0.0526	0.4300
	156	0	0	0.0185	0	0	0.0119	0	0	0	0	0	0	0	0	0
	158	0.4649	0.5385	0.5556	0.5299	0.6222	0.5119	0.5200	0.6100	0.6026	0.5667	0.8525	0.8700	0.8073	0.7763	0.5400
	160	0.0088	0.0110	0	0.0149	0.0111	0.0119	0.0200	0	0	0.0167	0.0082	0.0100	0.0208	0.0921	0
	162	0.0088	0.0110	0	0.0224	0.0222	0.0952	0.0100	0.0100	0.0256	0.0167	0.0246	0.0100	0.0156	0.0132	0
	164	0	0	0	0.0075	0	0	0	0.0200	0	0	0	0	0	0	0
	168*	0	0	0	0	0.0111	0	0	0	0	0	0	0	0	0	0
	180	0	0.0055	0	0	0.0111	0	0	0	0	0	0	0	0	0	0

Appendix 3. Pairwise F_{st} comparisons for 15 genetic sample collections. The population designations are: WSS5-Warm Springs River Strays 2005, WSS6-Warm Springs River Strays 2006, WSN6-Warm Springs River NOR 2006, WSsm6-Warm Springs River smolts 2006, BH5-Buckhallow Creek 2005 (Unk), BH6-BuckHollow Creek 2006 (STH), BO5-BakeOven Creek 2005 (STH), BO6-BakeOven Creek 2006 (STH), SCst5-Shitike Creek (1+) steelhead 2005, SC5-Shitike Creek 2005 (Unk), SC6-Shitike Creek 2006 (Omy), DLM5-Deschutes River lower mainstem 2005 (Unk), DLM6-Deschutes River lower mainstem 2006 (Unk), DUM6-Deschutes River upper mainstem 2006 (STH), and RBH5-Round Butte hatchery juveniles 2005.

Collection	WSS5	WSS6	WSN6	WSsm6	RBH5	SCst5	SC5	SC6	BH5	BH6	BO5	BO6	DLM5	DLM6
WSS6	0.0018													
WSN6	0.0065	-0.0012												
WSsm6	0.0169	0.0073	0.0037											
RBH5	0.0191	0.0104	0.0105	0.0125										
SCst5	0.0222	0.0125	0.0084	0.0080	0.0166									
SC5	0.0146	0.0106	0.0018	0.0091	0.0165	0.0078								
SC6	0.0811	0.0619	0.0475	0.0416	0.0613	0.0302	0.0429							
BH5	0.0173	0.0098	0.0053	0.0093	0.0167	0.0081	0.0113	0.0476						
BH6	0.0087	0.0064	0.0057	0.0115	0.0124	0.0197	0.0166	0.0608	0.0103					
BO5	0.0131	0.0095	0.0128	0.0162	0.0166	0.0240	0.0194	0.0680	0.0182	0.0122				
BO6	0.0135	0.0065	0.0063	0.0069	0.0084	0.0104	0.0080	0.0498	0.0091	0.0067	0.0051			
DLM5	0.0736	0.0553	0.0397	0.0368	0.0572	0.0290	0.0365	0.0037	0.0391	0.0514	0.0634	0.0433		
DLM6	0.0706	0.0509	0.0380	0.0323	0.0503	0.0260	0.0349	0.0018	0.0403	0.0489	0.0603	0.0426	0.0019	
DUM6	0.0387	0.0280	0.0245	0.0217	0.0305	0.0185	0.0233	0.0345	0.0258	0.0279	0.0353	0.0219	0.0286	0.0298