



Migration patterns of anadromous Cutthroat Trout in South Puget Sound: A fisheries management perspective



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ABSTRACT

In Washington State, anadromous Cutthroat Trout are targeted by sport fishermen in the marine environment, year round in catch and release fisheries, however little is known regarding marine stock distribution and migration patterns. The current study was designed to (1) describe the size, age and stock structure of Cutthroat Trout captured in marine waters of South Puget Sound, (2) estimate travel distances of individual Cutthroat Trout and (3) evaluate factors that determine travel distances. Genetic assignment of fish captured in inlets to their population of origin was performed, and marine migration patterns were inferred from the genetic assignments. Cutthroat Trout in South Puget Sound were frequently recovered outside of their natal inlet. Fish originating from Skookum Creek were disproportionately represented in the study area representing 78.8% of the total catch and were found in every marine sampling area while 90% of McLane and 100% of Kennedy Creek fish were found in their natal inlet. Travel distances were greatest during summer months (Mean: 18.9 km \pm 4.9 S.D.) and shortest during fall (Mean: 6.0 km \pm 7.9 S.D.), prior to spawning. Complex migration patterns of Coastal Cutthroat Trout resulted in a mixed stock fishery for most of the year and have the potential to make protection of smaller populations difficult in the marine environment. Catch and release regulations in marine waters have likely had a positive effect on the total abundance of anadromous Cutthroat Trout in Washington State however, managers should focus population specific recovery efforts in the freshwater and estuarine environments where Cutthroat Trout populations segregate naturally as they return to natal waters.

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1. Introduction

Two management types provide the framework for most marine salmon fisheries: Mixed-Stock and Terminal Fishery Management. Mixed Stock Fisheries are those that are known to exploit multiple stocks in one area (Lloyd, 1996). Mixed stock fisheries management principles have been especially useful among salmon fisheries when one or more, less numerous stocks overlap spatially and temporally with more numerous stocks or species. To meet the desired outcome in a mixed stock fishery, managers typically set harvest rates based on the abundance or available harvest of those stocks or species that are limited in number. In contrast, stocks that do not overlap with stocks or species of concern are typically managed independently of one another as a Terminal Fishery (Healey, 1982). For salmon, Terminal Fisheries typically exist near the mouth of

rivers where stocks segregate naturally by population as the adults migrate back to natal spawning grounds (Fujita et al., 1998). While these two management types provide the framework for most marine salmon fisheries, both require high quality data describing migratory patterns, stock structure and abundance. For species which exhibit diverse life history patterns or are not commercially important, these types of information are often lacking or difficult to obtain.

An economically important (~1.1 million dollars economic value annually) sport fishery exists in Washington State for the anadromous form of Coastal Cutthroat Trout *Oncorhynchus clarkii clarkii* (Lothrop and Losee, 2016) however neither the stock status (i.e. abundance) nor genetic stock structure is well understood. Historically, managers have relied on counts of live fish at dams or upstream traps to estimate abundance of individual populations. While these types of data along with anecdotal reports are helpful in signaling broad scale patterns in Cutthroat Trout abundance such as a range-wide decline of Coastal Cutthroat stocks observed in the 1980's (Johnson et al., 1999); they are not efficient in evaluating

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stock-specific management goals where long-term time series are not present.

In the absence of definitive information on the status of Coastal Cutthroat Trout, managers have relied on conservative management approaches to minimize fishing mortality in hopes of maintaining or increasing the number of Cutthroat Trout while continuing to offer fishing opportunity. While harvest is permitted in selected rivers in Washington State current sport fishing regulations for Cutthroat Trout in marine waters require barbless hooks and prohibit harvest year-round. Unlike harvest fisheries, where the majority of fish captured are removed from the population, catch and release fisheries assume that the majority of fish captured are successfully returned to the water alive and thus remain part of the affective population. Hooking mortality associated with catch and release fisheries is thought to be low (Schill et al., 1986), however, mortality rates may vary widely depending on a variety of factors (e.g., gear type, angler experience and environmental conditions; Gresswell and Harding, 1997). Under a high mortality rate scenario and where stocks of concern are frequently encountered by anglers, fishing pressure could conflict with conservation concerns, regardless of special angling regulations such as catch and release.

Puget Sound Cutthroat Trout in marine waters are managed assuming a mixed-stock management type, but the degree of mixing is unknown. Cutthroat Trout exhibit high site fidelity during spawning (Wenburger and Bentzen, 2001) forming genetic stock structure organized at the stream level (Campton and Utter, 1987; Blakley et al., 2000; Guy et al., 2008). In addition, results from tagging studies in Hood Canal, a large fjord of Puget Sound, suggests that Cutthroat Trout rarely migrate far from their natal stream in the marine environment (Moore et al., 2010; Goetz et al., 2013). It is unknown, however, whether or not the fidelity Cutthroat Trout exhibit to their natal inlet in Hood Canal is characteristic of Cutthroat Trout throughout Puget Sound. If so, the popular sport fishery concentrated near estuaries adjacent to Cutthroat Trout spawning streams may be best managed as a series of inlet-specific terminal fisheries where angling regulations can be applied to marine waters based on the status of the associated population. Conversely, if longer distance migrations that are common for other species of anadromous trout (i.e. Bull Trout, Brown Trout, Arctic Char etc.; Quinn and Myers, 2004) are observed for Cutthroat Trout, inlets of Puget Sound may be best characterized as mixed stock fisheries. In this case, angling regulations applied across a broad geographic region may be appropriate to protect small, independent populations mixed with larger ones.

The goal of this study was to characterize Cutthroat Trout found in the marine environment of south Puget Sound. Specifically, we sought to (1) describe the size, age and stock structure of Cutthroat Trout captured in the marine sport fishery, (2) identify population of origin of fish caught in the marine sport fishery using genetic stock identification, and with which estimate migration distances of individual Cutthroat Trout and (3) evaluate factors that may influence migration distances. With new information describing size, age and migration behavior of Coastal Cutthroat Trout managers may be better able to design fisheries to address stocks of concern.

2. Methods

2.1. Overview of experiment

Fish of unknown population of origin were sampled by angling in Skookum, Totten and Eld Inlets of south Puget Sound, Washington each with one stream known to have a spawning population of Cutthroat Trout (Fig. 1). Using genetic stock identification, fish

were genetically assigned to their population of origin. From that information, the minimum marine migration distance was calculated.

2.2. Study area

Puget Sound is characterized by numerous fjord-like inlets which as a whole have water chemistry properties resembling partially mixed estuaries (Sutherland et al., 2011). The current study was conducted in nearshore waters of South Puget Sound that represent high-use fishing areas for those targeting Cutthroat Trout (Lothrop and Losee, 2016), comprising Skookum, Totten and Eld inlets as well as the area where these three inlets meet (Squaxin Passage, Fig. 1). Skookum Inlet, represents the shortest (5.86 km) and narrowest inlet (<0.5 km) in the study area with a maximum depth of 22 m. Skookum Inlet receives freshwater input from Skookum Creek and flows eastward where it meets Totten Inlet. Totten Inlet is 15.8 km long and 2.3 km wide at the widest point. Totten Inlet has the greatest maximum depth (65 m) of the three inlets in the study area and contains numerous small tributaries. Kennedy Creek represents the largest tributary of Totten Inlet. Immediately east of Totten Inlet, Eld Inlet (1.5 km wide, 15.4 km long) receives freshwater input from one major tributary, McLane creek.

2.3. Collection of coastal Cutthroat for genetic baseline

Fork lengths (FL), scales and tissue samples were collected from 30 juvenile Cutthroat Trout each from three south Puget Sound streams; Skookum Creek, Kennedy Creek and McLane Creek, in the spring of 2014 by electrofishing. Cutthroat Trout life history is quite variable, including migrations to and from non-natal streams (USFWS, 2008). To ensure that tissue collections from putative source populations represented the spawning population, only young fish that had not been to sea were used in baseline collections. To determine life history status, scales collected from the preferred area above the lateral line midway between the dorsal and adipose-fins were analyzed for age and saltwater entry (Scarnecchia, 1979) at the WDFW marine aging lab. The scales were mounted on scale cards, lightly dyed for visibility and analyzed under 40× magnification. Only fish without a marine entry “check” were used in baseline.

2.4. Collection of Cutthroat of unknown origin in marine inlets

Cutthroat Trout of unknown source population were sampled year-round in 1999, 2001, and 2002 using hook and line from boat and shore with the objective of sampling 30 fish from each inlet across all months. Sampling was focused around high slack tides when catch rates of Cutthroat Trout were highest. FL, scales from the preferred body area and tissue samples were collected from Cutthroat Trout sampled in inlets into which each of the baseline streams flows (Skookum, Totten and Eld Inlets, Fig. 1). To evaluate the effect of age on migration distance, scales were aged according to standard procedures (Scarnecchia, 1979).

2.5. Genetic processing and analysis

To extract and isolate DNA from fin tissue, Qiagen DNEasy® kits (Qiagen Inc., Valencia, CA) were used, following the recommended protocol for animal tissues. Single-nucleotide polymorphisms (SNPs) and microsatellite loci were amplified using polymerase chain reaction (PCR). Cutthroat Trout were genotyped at a panel of 96 SNP loci, three of which were designed to distinguish *O. mykiss*, *O. clarki*, and their F1 hybrids (Table S1). Hybrid individuals were identified as heterozygous at two or three of the three loci. Cutthroat Trout were also genotyped at 7 microsatellite loci (Table

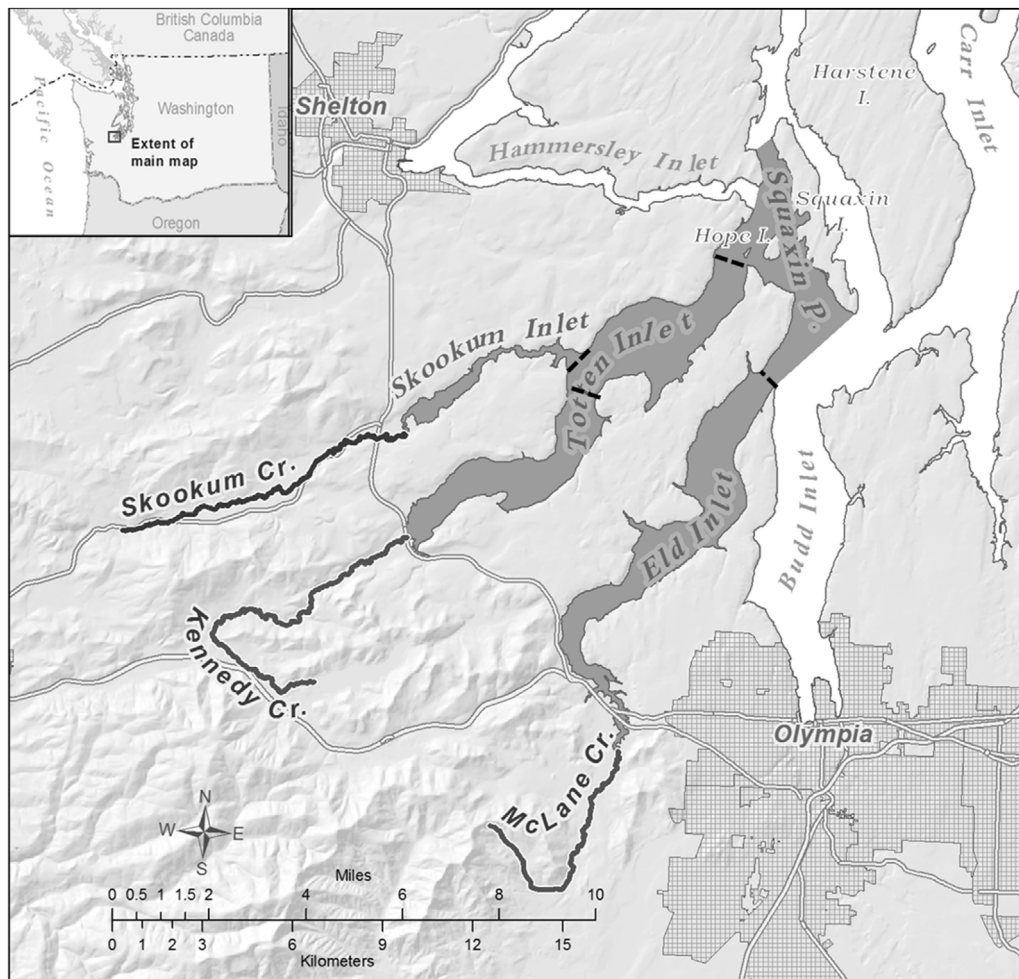


Fig. 1. Locations of Coastal Cutthroat Trout (*Oncorhynchus clarkii clarkii*) stream (black) and marine (shaded) collection areas in South Puget Sound, Washington. Dashed black lines represent sampling sub-areas.

S2). Microsatellite alleles were PCR-amplified using fluorescently labeled primers. Further details of the DNA extraction, PCR amplification, and visualization steps can be found in the supplementary materials.

2.6. Evaluation of loci

To evaluate genetic qualities of SNP and microsatellite loci, we estimated several genetic parameters using baseline collections. To check for systematic scoring issues, we performed a two-tailed exact test of Hardy–Weinberg equilibrium (HWE) for each locus in each collection using the Markov Chain method implemented in GENEPOP 4.2 (dememorization number 1000, batches 100, 1000 iterations per batch; (Raymond and Rousset, 1995; Rousset, 2008)). Significance of probability values was adjusted for multiple tests using false discovery rate (Verhoeven et al., 2005). F_{IS} , a measure of the fractional reduction in heterozygosity due to inbreeding in individuals within a subpopulation and an additional indicator of scoring issues in baseline collections was calculated according to Weir and Cockerham (1984) using GENEPOP 4.2. Expected heterozygosity was calculated using GENETIX 4.05 software (Belkhir et al., 2001). Inclusion of many related individuals may bias population structure results (Garza, 2014), thus baseline collections were further analyzed for patterns of family structure within collections by calculating pairwise R_{xy} values (Queller and Goodnight, 1989) as estimated using the software IDENTIX (Belkhir et al., 2002) and by performing sibship analysis using COLONY2 (Wang, 2004; Wang,

2013; Wang and Santure, 2009). In order to balance the needs of eliminating bias and sample size, when full-sibling families of more than three members were inferred, members were randomly removed until only three members remained in the dataset for further analysis.

2.7. Evaluation of baseline samples

In order to evaluate the power of the full suite of loci to distinguish among baseline collections we calculated pairwise F_{ST} estimates among baseline collections including, for comparison, collections of Coastal Cutthroat Trout from north Puget Sound and coastal Washington State (WDFW collections). F_{ST} estimates were calculated and statistical significance was estimated by permutation tests using FSTAT (Goudet, 1995) with 1000 permutations. The power of the marker set for individual assignment tests was evaluated by performing realistic fishery simulation analysis using the algorithms employed by the software ONCOR (Anderson et al., 2008).

2.8. Individual assignment tests

To estimate the source population of the Cutthroat Trout captured in the inlets, we performed individual assignment tests using the partial Bayesian algorithms employed by the software ONCOR (Anderson et al., 2008; Rannala and Mountain, 1997). Population assignments were finalized with a threshold assignment

Table 1Locations and sample sizes of collections of Coastal Cutthroat Trout (*Oncorhynchus clarkii clarkii*) in south Puget Sound, WA.

Purpose	Collection year	Location	N Processed	N <i>O. mykiss</i> /hybrid	N Incomp./matching	N Final
Baseline	2014	Kennedy Creek	36	3	1	32
	2014	McLane Creek	34	0	1	33
	2014	Skookum Creek	36	1	0	35
Unknown	1999	Squaxin Passage	13	0	0	13
	2001–2002	Totten Inlet	30	0	4	26
	2001–2002	Eld Inlet	30	0	0	30
	2001–2002	Skookum Inlet	30	0	0	30

posterior probability of >0.85 resulting in a subset of individuals designated “unassigned” when the probability was <0.85. An assumption of individual assignment tests is that all source populations were sampled, however, Cutthroat Trout caught in the inlets may have originated from nearby un-sampled populations. To test this assumption, the probability of inclusion was calculated for all individuals of unknown source population using the algorithms employed by the software GENECLASS2 (Piry, 2004) using the methods of Paetkau et al. (2004). Ten thousand individuals were simulated with $\alpha = 0.001$. To compare stock distribution by catch location, fish were grouped by the inlet in which they were caught (sub-area). To increase resolution Totten Inlet was divided into two sub-areas (north vs. south of entrance to Skookum Inlet).

2.9. Migration distance

Migration distance (straight line open-water route) was calculated for each fish as the shortest distance (km) between the catch location in the marine environment and the mouth of the genetically assigned natal stream. Migration distance was compared to several variables shown to effect migration patterns of anadromous trout: FL, age, stock, lunar season and sex (Daly et al., 2014; Eldøy et al., 2015; Spares et al., 2015; Bond et al., 2015; USFWS, 2008). Prior to further analysis, an F-test for equality of variances was conducted to determine the need for transformations. Fork length (continuous variable) was tested against migration distance using correlation analysis. Multi-factor analysis of variance (ANOVA) was used to test for an effect of each categorical variable (age, source population, season and sex) on migration distance. Difference in migration distance across seasons (fall, winter, summer, spring) were investigated further using one-way ANOVA followed by Fisher’s protected least significant difference post hoc test using R statistical software (R Core Team; www.r-project.org).

3. Results

3.1. Sample collections

A total of 106 juvenile Cutthroat Trout were collected. These samples originated from the three creeks (Skookum, Kennedy, McLane creeks) representing south Puget Sound Cutthroat Trout putative source populations (baseline collections, Table 1). Age of fish collected for baseline ranged from zero to three years, representing four brood years (2009–2012) and mean length was 150 mm \pm 4.2 S.D. (Fig. 2a). *O. mykiss*/*O. clarkii* hybrids (Kennedy and Skookum creeks, $n = 4$) and fish that exhibited a marine entry check on scales (McLane creek, $n = 1$) were removed from further analysis. Siblings were found in all south Puget Sound baseline collections. One full sibling family in Kennedy Creek consisted of four individuals, so one randomly chosen member was removed.

A total of 103 fish of unknown source population were sampled from South Puget Sound inlets. These fish ranged in size from 195 to 485 mm (mean: 324 \pm 63.1 S.D., Fig. 2b). Two fish sampled had

identical genotypes and are assumed to be the same fish sampled twice in the marine environment. This fish was included only in analysis of migration distances. Freshwater age (age at the time of ocean entry “check”) for Coastal Cutthroat Trout captured in the marine water was one, two and three (16.6%, 75.6% and 7.8% respectively) while total age ranged from (Fig. 2b) one to five years old. Length and age were significantly correlated (Pearson’s $R = 0.559$ $P < 0.0001$) therefore we included only age as a factor in analysis of migration distance. No *O. mykiss*/*O. clarkii* hybrids were detected among marine-caught fish.

3.2. Evaluation of baseline

Twenty-three SNP loci, in addition to the three species ID loci, were dropped from further analysis (Table S3). Most were uninformative due to fixation of the same allele in all baseline collections; too much data were missing from a few others. One microsatellite locus (*Ogo-3*) and several SNP loci were fixed for the same allele in all south Puget Sound Cutthroat Trout collections. Although they were uninformative for assignment tests, they were included in further analyses because they were variable among all baseline collections. Only one locus (*AOmy258*) in one baseline collection (Skookum Creek) was out of HWE after correction for multiple tests using FDR. Three loci (*AOcl032*, *AOmy063*, and *AOmy258*) showed evidence of deviation from HWE in two of the three south Puget Sound populations before correction for multiple tests, suggesting that there might be some amplification or scoring issues with those loci. However, F_{IS} values for these loci varied from negative to positive values among populations, suggesting it was not a systematic scoring issue.

Pairwise F_{ST} values among all six baseline collections were relatively large (>0.02) and all statistically significant at $\alpha = 0.05$ after corrections for multiple tests (Table S7). Patterns in F_{ST} values corresponded to expectations based on geographic proximity of collections and relationships seen in congeneric salmonids from roughly the same locations; the F_{ST} s of geographically proximate populations were smaller than those from geographically distant populations. Thus, the use of the SNP and microsatellite panel for further analysis was supported.

Assignment success of south Puget Sound baseline collections using the realistic fishery simulations in ONCOR was high. Over 95% of simulated individuals correctly assigned to their source population. Simulated McLane Creek individuals were misassigned at a slightly higher rate than individuals from the other two collections (~3% vs. ~2%) and most of those misassignments were to Kennedy Creek. This pattern roughly follows the patterns of F_{ST} among the baseline populations, with the smallest F_{ST} being that of the pairwise comparison of McLane and Kennedy Creeks.

3.3. Marine distribution

Most (78.8%, 67/85) of the Cutthroat Trout sampled in marine waters assigned to Skookum Creek (Table 2) and were distributed

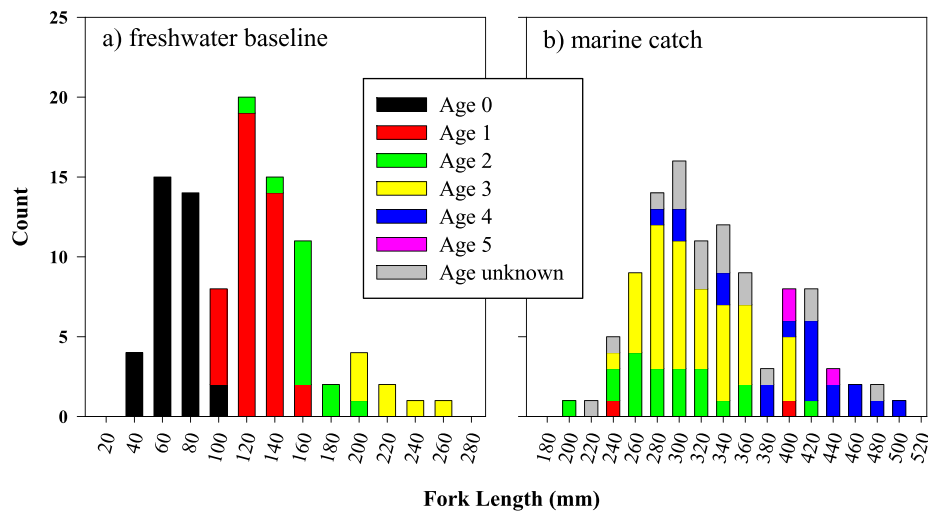


Fig. 2. Length frequency distribution and age composition (stacked bars) of (a) Coastal Cutthroat Trout (*Oncorhynchus clarkii clarkii*) captured in freshwater for baseline sample and (b) adults of unknown origin captured in marine water. Bins are 20 mm.

Table 2

Individual genetic assignments to putative source population of Coastal Cutthroat Trout (*Oncorhynchus clarkii clarkii*) sampled in south Puget Sound inlets.

Assigned Source Population	Sampling Location					Total
	Skookum Inlet	North Totten Inlet	South Totten Inlet	Eld Inlet	Squaxin Passage	
Skookum Creek	26	11	11	10	9	67
Kennedy Creek	0	1	1	0	0	2
McLane Creek	1	0	0	11	1	13
Unsampled source	0	1	1	0	1	3
Total	27	13	13	21	11	85

Table 3

Multi-factor analysis of variance (ANOVA) for main effects (marine age, source population, sex and season) on natural log transformed migration distance of Coastal Cutthroat Trout (*Oncorhynchus clarkii clarkii*) sampled in South Puget Sound, Washington.

Dependent	Independent	d.f	Sum of sqrs.	Mean sqrs.	F ratio	P value
Ln	Age	4	0.04	0.04	0.10	0.751
Distance from natal stream	Source population	2	0.65	0.22	0.57	0.637
	Sex	1	0.01	0.01	0.04	0.851
	Season	3	17.88	5.96	15.76	<0.0001
	Sex × season interaction	3	0.35	0.12	0.31	0.821
	Stock × season interaction	3	0.59	0.20	0.52	0.668
	Age × season interaction	3	0.14	0.05	0.12	0.948
	Residuals	51	19.28	0.38		

throughout the study area (Fig. 3). McLane Creek was the second most frequently assigned source population with 15.3% (13/85) of the total assignments. Kennedy creek fish represented only 2.4% of the overall catch (2/85) and were not encountered outside of their natal inlet (Totten Inlet; Fig. 3).

Three individuals, one each from Hammersley Inlet, Hope Island, and Totten Inlet, had probabilities of inclusion less than 0.10 for all three source populations suggesting that these three individuals originated from unsampled source populations (Table 2). Cutthroat Trout in each sub-area were comprised of more than one population, with catch in north Totten Inlet comprising all sampled populations (Skookum, Kennedy and McLane creeks, Fig. 3).

3.4. Migration distance

Cutthroat Trout sampled in the marine environment were captured an average of 11.7 km ($9.2 \pm \text{S.D.}$) from the mouth of their natal stream. The maximum migration distance that we could observe was 32.47 km given the size of our study area. This dis-

tance was achieved by one individual. The majority (71.6%) of Cutthroat Trout captured in the marine environment were less than 15 km from the mouth of their natal stream while 14.1% were captured greater than 30 km from their natal stream (Fig. 4). Following a natural log transformation of migration distance, data used in multi-factor ANOVA were not skewed. Season of capture was associated with log transformed migration distance of individual Cutthroat Trout (Table 3; multi-factor ANOVA, $P < 0.05$). However, there was no effect of age, source population or sex on migration distance (Table 3; $P > 0.05$). In addition, fork length of Coastal Cutthroat Trout was not significantly related to migration distance (Pearson's $r = 0.126$, $P > 0.05$). Mean migration distance was significantly different between seasons (Fig. 5; ANOVA, $F = 10.3$, $d.f. = 3, 65$, $P < 0.001$). Specifically, Coastal Cutthroat Trout were significantly closer to their natal stream in the fall than those fish captured in winter, spring and summer (Fisher's PLSD, $P < 0.05$). Cutthroat Trout captured in summer months, were on average the furthest from their natal stream (18.9 ± 4.9 S.D., Fig. 5) relative to those captured in other seasons.

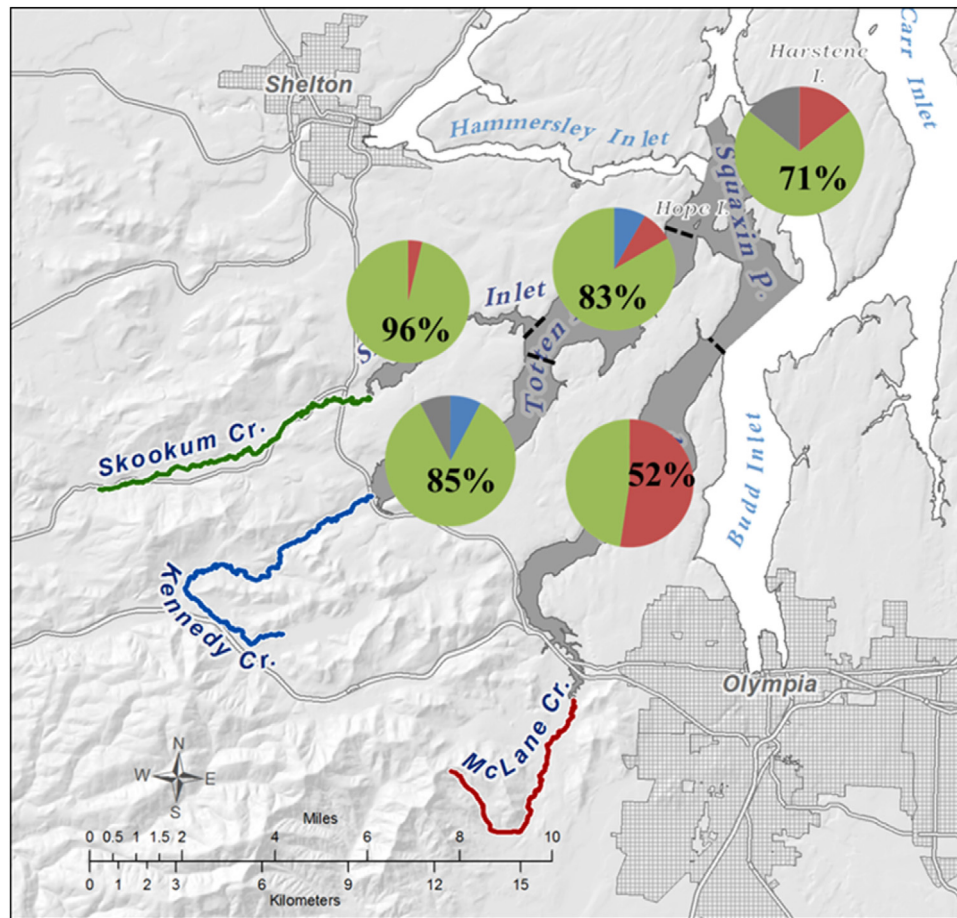


Fig. 3. Proportional contribution of genetic assignment of Coastal Cutthroat Trout (*Oncorhynchus clarkii clarkii*) by sampling region (Skookum inlet, south Totten Inlet, north Totten Inlet, Eld Inlet and Squaxin Passage) in South Puget Sound Washington. Dashed black lines represent sampling “sub-areas”. Colors within pie graphs indicate natal stream assignment; Skookum Creek: green, Kennedy Creek: blue, McLane Creek: red and unidentified source population: grey. Percentages indicate stock with greatest contribution by region. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

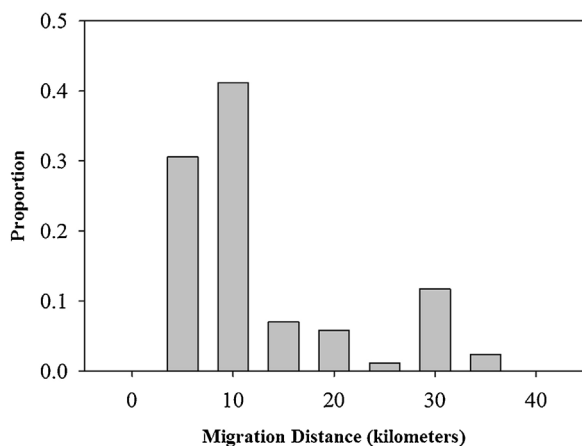


Fig. 4. Distribution of the migration distance of Coastal Cutthroat Trout (*Oncorhynchus clarkii clarkii*) in South Puget Sound, Washington. Migration distance was calculated as the shortest distance (km) between the catch location in the marine environment and the mouth of the genetically assigned natal stream.

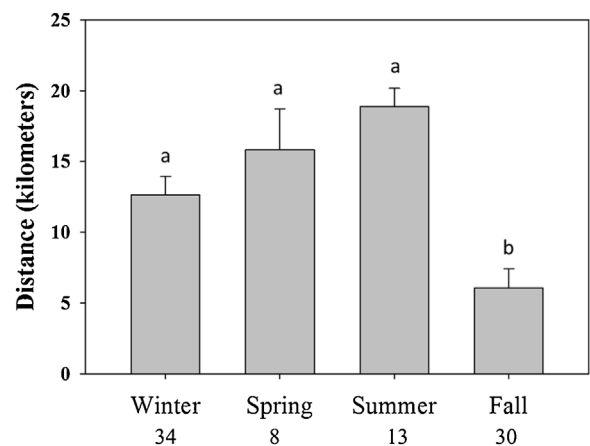


Fig. 5. Mean migration distance \pm SE of Coastal Cutthroat Trout (*Oncorhynchus clarkii clarkii*) in South Puget Sound, Washington. Samples sizes are indicated below each bar. Letters above bars are associated with pair-wise comparisons. Bars which do not share a letter are significantly different than each other ($P < 0.05$).

4. Discussion

With genetic stock identification, we showed that anadromous Coastal Cutthroat Trout regularly made marine migrations outside of natal inlets. Anadromous trout have been shown to exhibit a variety of different migration patterns from transoceanic migrations of

Steelhead (Pearcy and Masuda, 1982; Quinn and Myers, 2004; Daly et al., 2014) to short interbasin migrations of Dolly Varden (Spares et al., 2015) and Brown Trout (Eldøy et al., 2015) as well as partial expression of anadromy in Dolly Varden and Rainbow Trout (Kendall et al., 2013; Bond et al., 2015). While studies specifically focused on Cutthroat Trout in the marine environment are lim-

ited, the majority of what is known suggests that Cutthroat Trout make relatively short distance marine migrations (Giger, 1972; Goetz et al., 2013), do not migrate across large bodies of water (Jones, 1977; Jones and Seifert, 1997) and are unlikely to leave their natal inlet (Moore et al., 2010; however, longer migrations have been documented, e.g., Pearcy et al., 1990). In the current study, the majority of fish were assigned to their nearby natal streams <15 km away from the capture location however a second “mode” of longer migrating fish was observed (Fig. 4). Fish originating from Skookum and McLane creeks were recovered in high proportions on the margins of the study area suggesting that it is likely that the full extent of the marine distribution of our study populations was not observed. These results are consistent with those of Goetz et al. (2013) where most fish underwent short marine migrations (residents) while others exhibited longer migrations (migrants). Overall, information reported here suggests that, unlike Cutthroat Trout observed in Hood Canal (Moore et al., 2010), Cutthroat Trout in South Puget Sound regularly leave their natal inlet and exhibit a high degree of variability in migration distance.

The factors that affect migration patterns of anadromous fish are not well understood however migration of anadromous trout have been shown to be related to size (Haque, 2008), age (Bond et al., 2015), stock (Keefer et al., 2004), sex (USFWS, 2008) and season (Haque, 2008). Only season had a significant effect on migration distance in the current study. Fish captured during fall months (September, October and November) were closer, on average to their natal inlet, than fish captured in other seasons. This behavior could represent a period of transition from marine residency to reentry into natal streams prior to spawning in the Winter/Spring (Losee et al., 2016) and corroborate published (Wenburg, 1998) and anecdotal reports of a fall migration to freshwater that gave Cutthroat Trout the common name “Harvest Trout.” Similarly, Haque (2008) reported a freshwater migration of Cutthroat Trout associated with the spawning migration of Fall Chum salmon but suggested the period of freshwater residency was short with the majority of fish returning to marine water prior to winter. Future work identifying over-wintering behavior of Cutthroat Trout in south Puget Sound would fill an important gap in the understanding of anadromous Coastal Cutthroat Trout life history.

Few Kennedy Creek Cutthroat Trout were sampled in the marine environment. Although these low numbers could have been a result of stock specific differences in migration patterns, it was more likely a result of a lower abundance of Kennedy Creek Cutthroat Trout compared to the other two streams. In recent years (2012–2016), Kennedy Creek yielded fewer Cutthroat Trout redds than both McLane and Skookum creeks (WDFW, unpublished data). Previous studies have demonstrated the effect sportfishing regulations can have on the population size of Coastal Cutthroat Trout (Gresswell and Harding, 1997) and harvest may have contributed to the relative abundance of the three populations observed here. In Washington, while marine fisheries are managed under catch and release regulations, select freshwater fisheries are managed for harvest of Cutthroat Trout, and Kennedy Creek had the most liberal harvest regulations of the three study streams during the study period. With the knowledge that anadromous Cutthroat Trout populations mix in the marine environment, recent advances in redd-based escapement methodologies for anadromous Cutthroat Trout (Losee et al., 2016) should be combined with experimental changes to regulations in freshwater in an effort to determine factors that affect the relative contribution various Coastal Cutthroat Trout populations make to sport fisheries.

Cutthroat Trout captured in the marine environment were found mixing temporally and spatially with neighboring populations during the marine phase(s) of their lifecycle. While information describing the potential for Coastal Cutthroat Trout in the marine environment to mix is limited, our results are consistent with those

reported for similarly sized sea-run Brown Trout (Eldøy et al., 2015) and Arctic Char (Spares et al., 2015) where extra-estuarine migrations were not uncommon. These results suggest performance of Cutthroat Trout fisheries in the marine environment is likely affected by Cutthroat Trout populations originating from streams across a broad geographic area.

It is now understood that sport fishers targeting Coastal Cutthroat Trout in marine waters of South Puget Sound encounter a variety of distinct stocks. Depending on the goals of fish managers, considerations for those stocks that are limiting should be made when designing regulations, consistent with a mixed-stock management strategy. While this may seem unfeasible due to limited funds and federally mandated recovery efforts for higher priority Endangered Species Act listed stocks, methodologies for estimating abundance of Coastal Cutthroat Trout in-river are available and can be implemented with little cost. Finally, by gaining additional information on the movements of various stocks, managers may be better able to evaluate the impact sport fisheries have on Coastal Cutthroat Trout in the marine and freshwater and design fisheries to maximize long-term fishing opportunity on abundant stocks.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at <http://dx.doi.org/10.1016/j.fishres.2016.12.006>.

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