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Aligning Conservation Goals and Management Objectives for Bonneville Cutthroat Trout (*Oncorhynchus clarki utah*) in the Logan River, Utah

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ALIGNING CONSERVATION GOALS AND MANAGEMENT OBJECTIVES FOR BONNEVILLE CUTTHROAT TROUT (*ONCORHYNCHUS CLARKI UTAH*) IN THE LOGAN RIVER, UTAH

by

Harrison Mohn

A thesis submitted in partial fulfillment
of the requirements for the degree

of

MASTER OF SCIENCE

in

Fisheries Biology

Approved:

Brett Roper Major Professor	Phaedra Budy Committee Member
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UTAH STATE UNIVERSITY
Logan, Utah

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ABSTRACT

Aligning Conservation Goals and Management Objectives for Bonneville Cutthroat Trout (*Oncorhynchus clarki utah*) in the Logan River, Utah

by

Harrison E. Mohn, Master of Science

Utah State University, 2016

Major Professors: Dr. Brett Roper and Dr. Phaedra Budy
Department: Watershed Sciences

Watersheds are often managed without direct knowledge of how salmonid species use spatially-distinct spawning habitats within their watersheds, and rarely take into account the relationship between fish movement and potential population structure when making management decisions. The population of native Bonneville cutthroat trout (*Oncorhynchus clarki utah*) within the Logan River is the largest documented population remaining for this imperiled species, and still maintains extremely high densities of native fish in the upper river. Currently, fishing is not allowed in the upper 20 kilometers of the Logan River watershed during spawning, based on the assumption that cutthroat trout migrate to and spawn primarily in this section. I redetected cutthroat trout tagged (2,271) during years 2008-2012 in seven mainstem and tributary reaches of the Logan River during spawning months (April-June) of 2013 using a combination of stationary detection systems and mobile scanning techniques. Cutthroat trout in both mainstem and tributary reaches exhibit a leptokurtic movement distribution, indicating most fish spawn near to their original tagging site; however, small percentages of trout moved long distances to seek out spawning sites throughout the watershed. Growth, length, and condition estimates between mobile and non-mobile tagged fish demonstrate that while mobile fish tend to growth faster, be slightly larger, and in some cases be in relatively poorer condition, these differences are often biologically insignificant and dependent on site location within the watershed. A genetic microsatellite DNA analysis conducted on trout sampled from each study site confirms the assumption of panmixia, and I observed very little evidence of sub-population structure. Using River Styles® to assess geomorphically distinct reaches, I created a large-scale population estimate of spawning individuals, which found approximately 61% of spawning cutthroat trout are not subject to angling during the spawning season, while 39% could be susceptible to harvest in the lower basin and its tributaries. Most trout within the Logan River likely spawned very close to initial tagging locations and microsatellite analyses confirmed the population is genetically well-mixed, indicating conservation efforts should promote risk-averse management throughout the watershed, rather than focus heavily on any one section of the river.

(81 pages)

PUBLIC ABSTRACT

Aligning Conservation Goals and Management Objectives for Bonneville Cutthroat Trout (*Oncorhynchus clarki utah*) in the Logan River, Utah

Harrison E. Mohn

Rivers are often managed without informed knowledge of how sportfish use different areas of the river to reproduce, and rarely take into account the relationship between fish movement and how they are distributed within the river when making management decisions. The population of native Bonneville cutthroat trout (*Oncorhynchus clarki utah*) within the Logan River is the largest documented population remaining for this imperiled species, and still maintains extremely high numbers of fish in the upper river. Currently, fishing is not allowed in the upper 20 kilometers of the Logan River watershed during spawning, based on the assumption that cutthroat trout migrate to and spawn primarily in this section. I redetected cutthroat trout tagged (2,271) during years 2008-2012 in seven mainstem and tributary reaches of the Logan River during spawning months (April-June) of 2013 using a combination of stationary and mobile techniques. Most cutthroat trout in both mainstem and tributary reaches spawn near to their original tagging site; however, small numbers of trout moved long distances to seek out spawning sites throughout the watershed. Growth, length, and fitness estimates between mobile and non-mobile tagged fish demonstrate that while mobile fish tend to growth faster, be slightly larger, and in some cases be in relatively poorer condition, these differences appear inconsequential and depend on the location within the watershed. A genetic analysis conducted on trout sampled from each study site confirms this is one population (instead of many small populations). Using River Styles® to assess unique types of river reaches, I created a large-scale population estimate of spawning individuals, which found approximately 61% of spawning cutthroat trout are not subject to angling during the spawning season, while 39% could be susceptible to harvest in the lower basin and its tributaries. This indicates that future conservation efforts should promote risk-averse management throughout the watershed, rather than focus heavily on any one section of the river in order to protect this species for public enjoyment for future generations.

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I want to thank the many friends I've met during my time spent in Utah for making it some of the most enjoyable and broadening experiences in my life thus far, and wish to thank the greater Utah State community for their support. I would like to thank my loyal, goofy companion Klaus for always keeping me on my toes. Finally, I especially need to thank my family for their moral support and encouragement throughout this process.

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INTRODUCTION

The availability and distribution of spawning, rearing, and feeding areas within a watershed combined with the ability of fish to freely move among these habitats is critical for many stream fish to complete their life cycles (Schlosser and Angermeier 1995). How these different habitats are distributed are important in determining population structure, population dynamics, and the likelihood a population will persist at a watershed scale (Schlosser and Angermeier 1995; Fausch et al. 2002). Due to the range of population and habitat requirements present for a single species within a single river system (Harrison 1991), managers need to take into account the magnitude, timing, and distribution of interchange of individuals across both populations and habitats to best manage or conserve a species of interest.

A growing segment of research in the field of fisheries management, particularly involving stream-based salmonid species, is evaluating the metapopulation structure within larger watersheds (Rieman and Dunham 2000). The term metapopulation generally refers to a spatially-structured population, whether fish in a single watershed, or wildlife dispersed across a region (Hanski 1998). Understanding metapopulation structure requires the consideration of three conditions: (1) how patterns of discrete habitat patches support local breeding populations, (2) the synchronicity of populations among these discrete habitat patches, and (3) how the dispersal among breeding individuals within the populations affects the dynamics and/or persistence of the metapopulation or localized populations (Rieman and Dunham 2000). Due to the increasingly fragmented state of many streams, native species may be unable to utilize historically available habitats, which often alter metapopulation dynamics and persistence (Rieman and Dunham 2000).

Even if the above metapopulation conditions are not fully met, spatially-structured populations may still be present due to habitat differences, invasive species, and or habitat fragmentation. Therefore, resource managers should consider how past management actions and/or invasive species introductions have altered spatial population structures when managing or conserving an important fishery resource (Dunham and Rieman 1999).

Understanding how populations are structured across large spatial scales can inform effective resource management at the spatial scale relevant to the viability of a population, and thus species persistence (Hanski 1998; Rieman and Dunham 2000; Falke and Fausch 2009). The distribution and availability of habitat, and the differential use of these habitats by inland trout, will determine the spatial structure of a population in a watershed (Rieman and Dunham 2000). How a given trout population utilizes stream habitat within a basin should then determine the management activities permitted and the fishing regulations implemented, as these management actions can have widespread effects on population viability or persistence. For example, different management restrictions should be implemented for trout populations that spawn primarily in tributaries versus a population that spawns throughout a watershed, including within main-stem sections. Most importantly, populations that spawn only in a few specific locations will be more at risk to direct and indirect effects of management than those who spawn more uniformly across available stream habitat (Harrison 1991; Hanski 1998; Hilderbrand 2003). Evaluating spatial population structure requires the understanding and quantification of distributions, population dynamics, genetic arrangement, and movement patterns of a specific species throughout the entire watershed. This contemporary structure will then need to be considered within the context of historical conditions and connectivity of the watershed.

In addition to selective habitat use, distinct population structure can also result from habitat fragmentation. Distinct spatial structure may result when prime spawning habitat is spatially-separated from other high quality spawning habitat by patches of poor habitat (Harrison 1991). Spawning success is attributed to the presence or availability of suitable habitat (i.e., temperature, velocity, substrate size), with spawning gravel often providing the most limiting factor for inland salmonids (Chapman 1988; Budy et al. 2012). Due to the importance and limited availability of high quality spawning habitat, many subspecies of cutthroat trout, including Bonneville cutthroat trout (*Oncorhynchus clarki utah*), can demonstrate high rates of seasonal migration to and from spawning locations (Bernard and Israelsen 1982; Colyer et al. 2005). For example, within the Logan River, UT and other high-gradient mountain streams, suitable spawning habitat may be limited in much of the mainstem (Meredith 2012; Meredith et al. 2015), even though much of the stream is high quality rearing habitat for juvenile trout. Given this spatial habitat structure, cutthroat trout (particularly in the main-stem of the rivers) may be required to exhibit longer movement distances than fish directly adjacent to prime spawning habitats (Bernard and Israelsen 1982; Colyer et al. 2005), and spatial population structure may result from the spatial distribution of tributary or headwater stream sections with sufficient spawning habitat (White and Rahel 2008).

The Logan River, Utah is a typical Intermountain West river, fed by snowmelt run-off in the spring, home to a low diversity of native fishes, and characterized by cold, snowy winters and hot, dry summers (Budy et al. 2007, 2008a). The population of adult cutthroat trout within the Logan River is the largest documented population of the Bonneville subspecies remaining (Budy et al. 2007), is currently listed under a multi-agency Conservation Agreement, and is listed as a ‘species of special concern’ in Utah (Lentsch et al. 1997). Relevant to this study within the Logan River, previous studies on Bonneville cutthroat trout have evaluated fish movement patterns (Bernard and Israelsen 1982; Hilderbrand and Kershner 2000a), differences in growth and survival between stationary and mobile tributary fish (Hilderbrand and Kershner 2004; Randall 2012), native and non-native trout distributions (de la Hoz Franco and Budy 2005; Budy et al. 2007), and seasonal-based movements of tributary-residing fish (Hilderbrand and Kershner 2000a; Randall 2012). Previous work has also described hatch rates, quantified number of redds, and suggested several major tributaries contribute to the overall cutthroat population in the Logan River (Seidel 2009; Budy et al. 2012).

To better understand the potential spatial structure of cutthroat trout within the Logan River, it is important to consider the movement and timing patterns within the context of destinations associated with spawning (Bernard and Israelsen 1982; Budy et al. 2012); the time when genetic exchange occurs. Condition, size structure, and growth rates vary between habitats and can also vary between mobile and non-mobile trout (Olsson et al. 2006; Young 2011); therefore, an understanding of these differences throughout the watershed could be important for discerning spatial structure.

Understanding vital rates in different areas of the watershed by quantifying growth (especially density and the potential for dependent effects), survival of mobile and sedentary fish in mainstem and tributaries, and fecundity (which is directly related to trout size, growth, and condition) are also critical for sound management.

The timing of cutthroat trout spawning is initiated in part by increasing water temperatures, receding stream-flows following peak runoff, and increasing day length (Behnke 1992; Budy et al. 2012; Bennett et al. 2014). Seasonal movement distances associated with spawning have varied within the Bear River Basin, ranging from 5.2 river kilometers (rkm) in the upper Logan River (Hilderbrand and Kershner 2000a) to 86 rkm for large fluvial Bonneville cutthroat trout in the Bear River (Colyer et al. 2005) with dramatic increases in movement rates in the spring months (Hilderbrand and Kershner 2000a; Randall 2012; Bennett et al. 2014). In contrast, fish maintain high site fidelity (Budy et al. 2007) throughout the watershed and tributaries within the Logan River, which contain primarily resident fish that rarely move >500 m (Randall 2012). These studies have been primarily based on sampling during summer months, following any genetic exchange that may have occurred elsewhere in the watershed during spring spawning. Microsatellite analyses can aid in determining potential spatial structure and the relative degree of genetic exchange between distant sites (Spruell et al. 1999). By combining movement patterns and destinations of individual fish with microsatellite analyses, I can accurately determine the degree of genetic mixing of this important population and promote effective resource management.

In the Logan River, it has long been assumed that cutthroat trout primarily occupying the main-stem river, spawn primarily in the upper watershed. As such, Bonneville cutthroat trout fisheries management is more conservative in the upper 20 km of the Logan River. The goal of my research was to better understand spawning behavior and spatial population structure of Bonneville cutthroat trout within this watershed, to help inform management practices for an important population of an otherwise imperiled species. I hypothesized I would find distinct areas of spawning across the Logan River resulting in population structure, high site fidelity to these areas, and a significant degree of movement out of main-stem sites with low-quality spawning habitat to areas with high quality spawning habitat. Should these hypotheses prove true, I expected to find unique genetic structure among different areas of the river, indicating a spatially-structured metapopulation. My primary objectives were to test these hypotheses by: (1) comparing movement distances and spawning destinations among tributary and main-stem residing cutthroat trout, (2) determining where mobile and sedentary individuals spawn and use this information to identify how these fish are likely affected by current fishing regulations and pressure, (3) determining the proportion of mobile trout to sedentary fish among sites and compare growth, size, survival, and condition among these sites, (4) use objectives (1-3) in combination with a mtDNA genetic analysis to determine whether this population is panmictic or has a spatially-distinct population structure, and lastly (5) determine if the current overall management strategy for these fish fits our current understanding of risk to populations within the basin.

METHODS

Study Area

The Logan River originates in the southeastern corner of Idaho in the Bear River Mountain Range (Budy et al. 2007), flows unobstructed for approximately 64 km (Figure 1), and eventually joins the Bear River, a terminal river of the Great Salt Lake. A series of three hydroelectric/diversion dams in the lower section of this river block historical and present day fish passage in the upstream direction. Stream flow conditions are driven by spring snowmelt floods (15.7 m^3/s) with base flow conditions in the late summer/fall (2.8 m^3/s). Mean summer stream temperatures vary longitudinally from high elevation headwaters (9.3°C) to mid-elevation mainstem sites (12.2°C) with the potential for massive diel fluctuations (9°C; Budy et al. 2007). In winter months, anchor and frazil ice is often observed at high elevations (Meredith 2012; Meredith et al. 2015).

Native fish species present in the Logan River include native Bonneville cutthroat trout, mottled sculpin (*Cottus bairdii*), and mountain whitefish (*Prosopium williamsoni*). Non-native species include brook trout (*Salvelinus fontinalis*), brown trout (*Salmo trutta*), and rainbow trout (*O. mykiss*); however, only brown trout are abundant and widespread. Non-native brown trout increase substantially in the downstream direction (McHugh and Budy 2005; de la Hoz Franco and Budy 2005). The parasite that causes whirling disease, *Myxobolus cerebralis*, was first discovered in 1999, and quickly spread throughout the entire watershed (de la Hoz Franco and Budy 2005). Nearly all trout tested at all sites are positive for *M. cerebalis*; however, little to no population-level effect on the native fish population has been observed to date (Budy et al. 2014).

The population of cutthroat trout residing in the main-stem Logan River is assumed to be partly fluvial and primarily utilize tributaries or the upper portions of the watershed for spawning (Bernard and Israelsen 1982). Primary tributaries for spawning including Temple Fork, Spawn Creek, Beaver Creek, and the Franklin Basin. Each of these streams are perennial, spring fed streams with major contributions from spring runoff from melting snow. Additionally, Little Bear Creek is an occasionally ephemeral tributary where cutthroat trout are known to spawn (Figure 1). The watershed is primarily lotic (e.g., riffles, runs, and to a lesser degree pools) with some lentic reaches in tributaries and headwaters (e.g., extensive beaver ponds). Spawning areas are likely limited in the mainstem below the Logan River and Temple Fork confluence due to lack of sufficient spawning sized gravel and high unit stream power (Meredith 2012; Budy et al. 2012). In contrast, spawning gravel and suitable stream flows are plentiful in some tributaries and in the upper watershed (Meredith 2012; Budy et al. 2012).

Upstream of the dams (Figure 1), habitat quality is considered to be nearly ideal, connectivity is intact with no barriers to fish movement, and there is little direct anthropogenic alteration (Budy et al. 2007) except the presence of a paved, valley bottom road in the lower section and several unpaved roads adjacent to some tributary stream sections. Land management activities such as livestock grazing, road building and logging historically affected stream conditions while livestock grazing and recreational activities such as dispersed camping, hiking trails, and Off Highway Vehicle (OHV) use affect stream communities and riparian conditions at present. Mortality related to angling pressure is presumed low as catch-and-release practices make up the majority of recreational fishing in the upper stream sections (97%, Budy et al. 2003). Upstream of the Red Banks campground (Figure 1), bait fishing is permitted and two fish are allowed to be harvested. Fishing is prohibited from 1 January until the second Saturday in July to avoid harvesting fish prior to and during the spawning season. Conventionally, it was thought most mainstem fish move into this upper area to spawn; therefore, understanding of the number of cutthroat trout moving into this area is of most interest to fishery and land managers. Downstream of this section, fishing is open year-round.

Fish Movement Among River Sections

The research described herein is part of a larger, ongoing long-term research and monitoring program since 2001 (e.g., Budy et al. 2007) within the Logan River consisting of capturing and recapturing fish with electrofishing techniques to measure, weigh, tag, quantify abundance, determine population trends and vital rates, and check for external signs of whirling disease (Budy et al. 2007, 2008b) during July and August low-flow conditions. I collected trout using a three-pass depletion technique at seven 100-200 m sites (Figure 1); site abbreviations used in key figures can be found in Table 1. I used a single pass electrofishing method to sample Spawn Creek and Temple Fork tributaries with the goal of tagging additional fish in these important sections. I determined movement of individual cutthroat trout among sections of the Logan River by the detection of passive integrated transponder (PIT) tags as they moved across passive interrogation array (PIA) systems (e.g., Bottcher et al. 2011), during mobile antenna surveys, and when fish were occasionally caught during targeted angling efforts. I recorded the locations of all captured fish spatially using a handheld global positioning system (GPS; Garmin etrex Legend HCx) with accuracies ranging from 1 to 7 m. I anesthetized, measured, weighed, and tagged smaller numbers of additional fish caught during angling surveys throughout other times of the year

Since 2008, researchers tagged captured cutthroat trout with 12 mm PIT tags using an implanting needle. Prior to this change, all captured fish > 120 mm were tagged with site-specific floy tags, while a subset was tagged with PIT tags, resulting in more than 10,000 individually tagged fish in the system. Of the fish I actively captured, I tagged fish > 150 mm in the dorsal sinus cavity, while fish between 150 mm and 80 mm I tagged ventrally in the body cavity as described in Dieterman and Hoxmeier (2009). I removed adipose fins to visually determine whether or not a fish was previously tagged, to speed recognition of tagged fish in the field, and to determine tag retention rates across sampling years. I only measured trout displaying signs of stress following the electroshocking event. Following tagging, I placed trout in large, shaded revival bins and allowed them to fully recover before release in original capture locations. Myself and previous researchers PIT-tagged fish in Spawn Creek and Temple Fork from 2008-2013 and fish from the main-stem portion of the river in 2009, 2010, 2012, and 2013. In 2011, sampling in the main-stem only took place at the Red Banks site due to high flows. Trout tagging in Beaver Creek began in 2012.

To detect trout after implantation, I first used full-duplex (134.2 kHz) PIT-tag PIA systems at three strategic locations within the basin. Locations of PIAs include the confluence of Spawn Creek and Temple Fork, the confluence of Temple Fork, and the within the Logan River at the Forestry Camp site (Figure 2). The PIA units linked to instream antennas recorded the date, time, and unique identification number each time a tagged fish passes an antenna (e.g., Zydlewski et al. 2006). The PIA at the junction of Temple and Spawn Creek, installed in 2008, could determine detections as well as the direction of movement. The Lower Temple Fork and the Logan River PIA could only detect fish, not movement direction. Within Spawn Creek, five antenna loops monitor fish passage: two antenna loops are several meters upstream of another three antenna loops, and each set spans the width of the stream making inference of directional movement likely. The data recovered from the PIA at the Forestry Camp site (Figure 2) allowed me to partition cutthroat spawning in the Logan River into upper and lower sections, monitor movement into Little Bear Creek (a tributary of the Logan River), as well as movement into or from upstream reaches during primary spawning months (May to July). I also placed a PIA in Little Bear Creek approximately 15 m up the creek just above a small waterfall. Because of the distance and difficulty fish would experience scaling the waterfall, I assumed a detection of a mature PIT-tagged fish on this antenna meant a fish accessed this creek to spawn. All PIA systems operated nearly continuously from installation dates (Figure 2) with the exception of short-term (less than 1 week between March-November, less than one month between December-February) outages associated with common equipment failures. Additionally, I estimated detection efficiency every two weeks by floating PIT tags over each antenna. Antennas detected nearly 100% of PIT tags floated across them; therefore, I made no data corrections for PIA efficiency.

I used mobile antennas combined with synchronized handheld GPS units to determine the locations of tagged fish within reaches that included the site in which fish were originally tagged as well as other intervening reaches. Similar to PIAs, I recorded the unique identification number of tagged fish along with date, time, and location when the fish was in close proximity to the mobile scanner. I focused mobile scanning efforts on seven, 1 rkm reaches that encompassed the 100-200 m reach in which I tagged fish. I scanned four additional reaches, two between sampled reaches and one upstream of both the Franklin Basin and Beaver Creek sections. I randomly scanned these 11 reaches (Figure 2) three times each (33 total scans, 6 May to 1 July), and Little Bear Creek 4 total times during the 2013 spawning season. To determine the relative accuracy of mobile scanning efforts, I also scanned reaches at each tagging location site during summer electrofishing endeavors of 2014. I placed block nets as described above, scanned the reach with mobile antennas and normal electrofishing activities took place. Post-hoc, I compared scanned fish identification numbers with recaptured individuals in each site, and determined a relative efficiency (expressed as a percentage) of individuals detected versus individuals present. I compared these values between mainstem and tributary reaches as stream size was likely to be the primary factor determining efficiency of the mobile antennae (Hill et al. 2006).

Watershed-Scale Population Estimate and Fishing Pressure

To evaluate the proportion of fish in the upper section of the Logan River watershed that are closed to fishing during the spawning season versus those that could be fished year around, I estimated the population abundance of spawning cutthroat trout (fish ≥ 225 mm) throughout the entire watershed. To do this, I used several sources of information including abundance estimates from this study, snorkel data from a previous study (Meredith 2012), and legacy abundance data from previous studies (Budy et al. 2007). To determine population abundance within river sections, I utilized the three-pass, closed-model, generalized maximum likelihood removal estimator (White and Burnham 1999) for the 100-200 m long sample sites (Figure 1). I used snorkeling data to characterize the proportion of cutthroat trout distributed throughout the mainstem and to add legitimacy to sampled section cutthroat numbers. To determine appropriate boundaries over which to apply these estimates, I employed the River Style Framework (Brierley and Fryirs 2008) to determine geomorphic segments for the entire Logan River Watershed (unpublished report from Mohn et al. 2013).

Using a level one River Styles analysis (Brierley and Fryirs 2008), I identified distinct segments of the watershed within the mainstem Logan River and associated major tributaries including Temple Fork and Spawn Creek, Beaver Creek and Right-hand Fork. This classification scheme assists in separating rivers into “styles” based on vegetation, elevation, ecoregions, rock types, landscape units, known fault zones and aerial assessments of river features. I obtained the stream network feature used for the River Styles delineation in ArcGIS from the National Hydrography dataset (NHD+). Similar River Styles within the Logan River contained similar substrate size, slope, level of river confinement, floodplain accessibility, and in some cases beaver activity. I made additional trips to specific sites in the watershed to validate River Style choices made from aerial imagery in the office. I generated a map in ArcGIS using all available information to delineate 7 River Styles in the Logan River watershed (Figure 3).

In addition, I also incorporated finer scale slope data and snorkeling counts for trout species into the watershed scale population abundance estimate. Changes in slope are important to fish in the Logan River, and variations observed by Meredith 2012 aligned with changes in River Styles in the Logan River. I expanded stream length (km) for each River Style in ArcGIS and 100-200 m population estimates from long-term Logan River sites across these “styles”. During years when sampling at specific sites did not take place, I used mean population estimates from years when sampling did take place. Because most study sites coincidently occur within different river styles, I expanded the fish per kilometer estimation from study sites across each geomorphic segment (“style”), for watershed scale population abundance estimate for the Logan River watershed. There are currently no long-term sites upstream of Franklin Basin and Beaver Creek; therefore, I estimated mature trout abundance based on the relative amount of streamflow present. For example, a tributary upstream of the Franklin Basin site contributed 50% of the river’s streamflow; above this stream junction, the population estimate was reduced by 50% to account for the loss in rearing habitat. Although this is a coarse-scale technique, it provides a method of categorizing the Logan River Watershed into relatively homogenous segments and thus, allows me to estimate the fish population for the full, upper 64 rkm of the Logan River. I compared the percentages of fish assumed to be spawning within upstream protected zone or downstream of this section, in order to infer the relative “level of protection” for cutthroat trout within the river as a whole.

I also undertook an analysis of relative stream use (e.g., primarily fishing, but also swimming and wading) in different areas of the Logan River watershed during the summer of 2014 using time-lapse photography (PlantCam®). I set time-lapse cameras to take a photograph every 15 minutes during daylight hours. I placed cameras at each stream site sampled for trout as well as near Card Canyon in the lower Logan River. These are places in riparian areas where long stretches of the river could be visualized. No camera was set on Spawn Creek, as near-daily work within the watershed by USDA Forest Service employees confirmed there are rarely anglers at this site. Unfortunately, cameras malfunctioned at Red Banks and Beaver Creek; therefore, no estimates were possible at these locations. At the 5 remaining sites, cameras operated nearly continuously between approximately 15 June 2014 and 1 September 2014. I determined stream users (generally anglers), from the series of pictures as those within the water or on the stream bank next to the water. I graphed cumulative frequencies of stream users at each site against the time of year to indicate relative use in the studied areas of the watershed.

Assessment of Genetic Structure

Genetic analysis can identify closely related groups of individuals or outliers in a group of samples, based on allelic composition at hypervariable loci. The geographic locations of these groups or outliers can help identify longer-term patterns of spawning or migration that might not be apparent from short-term movement data. I took approximately 20 fin clips (Table 1) from fish > 200 mm at each of the 7 sites in the Logan River watershed for genetic analysis (Figure 1).

Working with the Utah State University Molecular Ecology Lab (Mock et al., personal communication), we extracted genomic DNA from fin clip samples using a salt-chloroform protocol (Müllenbach et al. 1989). We used extracted DNA as a template for PCR amplification of nine polymorphic microsatellite loci (H18, H126, H220, J3, J14, J132, K222, OMM1036, and OMM1034). We performed amplification in 10-µL reactions by employing a 3-primer system that used a CAGTCG Universal primer (5'-CAGTCGGGCGTCATCA; Glenn 2006) attached to the shortest primer (forward or reverse) of each primer pair. We then used this expanded primer in conjunction with a CAGTCG Universal primer fluorescently labeled with 6-FAM, HEX, or TAMN on the 5' end. We used previously developed markers for *Oncorhynchus* spp. and selected for previous success in literature, repeat sequence simplicity, similar PCR and annealing conditions, estimated product and primer length (to optimize multiplexing), and reportedly highly polymorphic characteristics (Rexroad et al. 2002; Pritchard et al. 2007a, 2007b). We used the following reaction mix: 1.5 µL template DNA (~5-10 ng/µL); 0.2 mM each deoxynucleotide triphosphates; 1.5 mM or 2.0 mM $MgCl_2$; 0.25 µM each modified forward or reverse primers, and a CAGTCG modified fluorescently-labeled primer; 0.3 units *Taq* DNA polymerase (NEB); and 1X standard *Taq* reaction buffer (NEB). We conducted PCR using a GeneAmp 2720 Thermal Cycler under the following conditions: initial denaturation 95° C (2 min), followed by 40 cycles of 95° C (15 s), primer specific annealing temperature (90 s), and 72° C (90 s), and terminating with a final extension of 72° C (10 min) followed by a rapid cool down to 4° C. We confirmed successful amplification of microsatellite loci on a 1.4% agarose gel, run for 45 minutes at 95 volts. We multiplexed individually amplified PCR products into sets containing up to 3 loci (OMM1034, H18, and H126; H220 and K222; OMM1036, J14, and J132; and J3). We analyzed samples using an ABI3730 DNA analyzer. We automatically scored peaks using GeneMarker 2.6.2 (Softgenetics). We performed final bin creation and scoring manually and verified in GeneMarker.

Data Analyses

Using initial tagging locations of fish coupled with detections from PIAs and mobile scanning, I determined the destinations of trout and distance traveled during the spring of 2013 based on individual cutthroat trout tagged in previous years. I evaluated the data for four potential reproductive behaviors and in order to test for the potential for a metapopulation structure. The first three relate to existing fishing regulations and imply a metapopulation structure for cutthroat trout in the Logan River Basin; 1) mainstem fish primarily migrate to tributaries to spawn, 2) fish migrate from the lower section of the river to the upper section of the river to spawn, or 3) mainstem fish migrate in a manner that suggests they use both spawning strategies. Because each of these hypotheses are based on the assumption of movement, failure to find strong support for these three models implies: 4) little movement among stream segments and the majority of fish spawn near their original capture reach.

Next, I divided the Logan River watershed into sections based on fishing regulations and the contrast between main-stem and tributaries in order to estimate the relative potential importance of each of these areas to sustaining the overall cutthroat trout population in the watershed. For example, while the lower main-stem, Spawn

Creek, and Temple Fork all have the same fishing regulations, I divided them into separate sections due to potentially important differences in juvenile recruitment, fish size, and condition. Section 1 includes the mainstem Logan River from the Forestry Camp PIA downstream, excluding all tributaries. Section 2 contains the mainstem Logan River above Forestry Camp PIA but excludes Beaver Creek. Section 3 is Temple Fork. Section 4 is Spawn Creek. Section 5 is Beaver Creek from its confluence with the Logan River. Section 6 is Little Bear Creek which holds few resident fish but supports a high number of spawning individuals.

I defined fish as ‘mobile’ if I detected them moving from one river section into another by means of mobile scanning or a PIA. If I detected a tagged trout within the same section in which I tagged them (by mobile scanning or not detected), I assumed they spawned within that section (sedentary behavior) or are deceased. I knew the tagging locations of fish, therefore, on PIAs that could only determine passage and not direction (Temple Fork and Forestry Camp PIAs), a single detection of a fish indicated the fish moved across the antenna to spawn in the next upstream or downstream section (unless detected at another distant PIA). I detected many fish a second time approximately two weeks later on these PIA; I assumed these fish spawned and were in the process of returning to their home range. I assumed tagged trout detected multiple times in the same general locations and never detected at a distant PIA, to be resident trout that did not make spawning movements.

I estimated the number of fish moving and movement rates from each section of river. To begin, I estimated the number of tagged trout alive and spawning in spring of

2013 by using established annual survival estimates (Budy et al. 2007) for the Logan River. I assumed survival during each year was constant, and accrued the number of fish from each batch of tagged fish expected to survive from each tagging year. I calculated a movement rate for fish leaving each site by dividing the observed number leaving by the number expected alive. I generated confidence intervals for the proportion of fish moving using a standard binomial distribution test with a p-value set at 0.05.

To determine the distance moved by each fish, I created a unique record for each encounter for each individual trout for each day it was encountered. I quantified individual fish movement using ArcMap and the ArcToolbox using the linear referencing tools within the ArcGIS 10.0 software. The Logan River watershed is represented as polyline shapefiles. To ensure the highest degree of accuracy, I added an aerial photography layer and manually adjusted the stream layer to properly fit the actual stream route. I created all possible routes fish could have traveled (Linear Referencing tools; create route) starting at the farthest upstream point of Spawn Creek. Routing the streams in this way allows points (in this case fish sightings) to be measured along the stream layer (Linear Referencing Tools; locate feature along route). The difference between the most recent sighting of a fish prior to the spawn (often the previous summer) and the farthest point distance away during spawning defined maximum distance traveled per individual fish (although it is possible on occasion fish could have moved further and not been detected). I combined the maximum observed distance I was able to detect each individual cutthroat trout during spawning months (1 April-30 June) into mainstem or tributary groupings based on where the fish was originally tagged and resided in year-round. I then plotted these groupings as a histogram. In this analysis, I included the maximum distance value for each individual detected at least once during the spawning season. I conducted a two-sample Kolmogorov-Smirnov test ($p < 0.05$) to determine if the distributions of movement distances traveled between mainstem and tributary fish were significantly different.

To determine if fish capture location was related to growth or size of the fish, I fit von Bertalanffy growth curves by means of the Fabens (1965) method as detailed in Guy and Brown (2007) to different Logan River sections. I used recapture data (i.e., length, weight, and time since last sighting) from any fish marked and also recaptured at least once during all years of study (2008-2013). I created growth curves for river sections 1-4, but Section 5 (Beaver Creek) did not have sufficient numbers of recaptured fish. Density-dependent effects on the native trout population were likely; therefore, I calculated the asymptotic lengths from age 7 fish for each site using the above growth curve method. I graphed these maximum lengths against fish densities in each site across study years (2008-2013) and fitted with a linear regression line. To determine if mobile fish were larger (length) than sedentary spawning-sized fish, I used data of all fished captured in 2012 and separated them into mobile or sedentary categories based on their 2013 movements. I used a Mann-Whitney U Test in order to statistically determine if mobile fish are larger than sedentary individuals.

I compared fish condition at tagging between the same four river sections in the Logan River watershed for mobile and sedentary to determine if there was a beneficial (or detrimental) effect to a mobile life strategy in this watershed. I calculated standard weights of tagged and measured Logan River cutthroat trout using established equations for standard weights based on lotic inland cutthroat trout populations (Kruse and Hubert 1997). These ratios allow comparison of the relative condition between these populations and other Bonneville cutthroat trout populations, as well as comparisons between different sections within the Logan River Watershed. I conducted an ANOVA among sections grouped by mobile or sedentary fish, to test for significant differences in relative weight (Wr). I conducted a Tukey HSD (honest significant difference) test to compare means and differences between groups, and graphed the resulting means and their respective groupings.

Based on this tagging data, and re-encounters from 2008-2013, I calculated Cormack-Jolly-Seber (CJS) apparent survival rates (Φ) at each site based on individual capture/recapture histories for each fish. This model uses maximum likelihood estimation procedures found in program MARK (White and Burnham 1999). All capture, tagging, and re-encounters were grouped by year. I considered a set of candidate models based on survival and probability as a function of time and site. I included individual covariates comprising the fish's total length, relative weight (condition), and global covariates including maximum daily air temperature within these models, and ranked the best model according to Akaike's information criteria (AIC; Table 2; Burnham and Anderson 2002). Because my goal was to compare vital rates across sites (including mainstem versus tributary), and based on movement patterns, I calculated survival by site based on the best model from Table 2 that calculated reasonable survival estimates. In a separate analysis, I grouped all data by mobility (sedentary or mobile) and area of the watershed (main-stem or tributary); however, a low number of samples made model estimates for mobile fish classes unavailable.

For estimates of relative fishing pressure, the number of deployed days for each camera differed amongst sections; therefore, I calculated the number of stream users per day. I extrapolated those per day values to a month-long value to standardize amongst cameras with different lengths of time being deployed. I used these standardized monthly observations averaged across all sites as expected values (i.e., expected anglers) for each site. I analyzed the number of users per day using a chi squared test at p=0.05, and analyzed each site individually to examine significant departures from the mean.

I completed all above statistical analyses using R statistical software (version 3.0.2).

For genetic analyses, we performed an assessment of Hardy-Weinberg equilibrium across loci and populations using GenePop software (Raymond and Rousset 1995; Rousset 2008), using Bonferroni-corrected alpha values. We tested the presence of null alleles using ML-Null software (Kalinowski and Taper 2006), with probabilities described using a MonteCarlo randomization (Guo and Thompson 1992) and a U test statistic (Raymond and Rousset 1995). We tested pairwise population differentiation using an exact G test available in GenePop software. More global patterns of population differentiation were described using a principal coordinates analysis (GenAlEx software; Peakall and Smouse 2006, 2012) and construction of a neighbor-joining dendrogram (TreeFit; Kalinowski 2009). We then described population-level allelic richness patterns and performed an analysis of molecular variance using GenAlEx software. An individual-based Bayesian assignment analysis was performed using Structure software (Pritchard et al. 2000), with the number of groups (K) ranging from 1 to 6, with 100,000 Markov Chain Monte Carlo (MCMC) iterations and a burn-in of 10,000 iterations, and a model assuming admixture among model groups.

RESULTS

The numbers of fish tagged over study period (2008-2013) at each site, the likely number of reproducing trout estimated alive during spring 2013, and the estimated percentage of fish moving out of specific river sections are displayed in Table 3. Listed percentages of mobile trout are the proportion of fish detected moving out of each section from 1 April to 30 June 2013 as described above. A total of 2,271 cutthroat trout have been tagged with PIT tags from 2008-2013 (Table 3). Fish lengths at tagging ranged from 86 mm to 436 mm. During this time span, the highest number of fish were tagged within Temple Fork (1210 individuals) and Spawn Creek (534), while the remainder were tagged within Twin Bridges (59), Forestry Camp (108), Red Banks (176), Franklin Basin (107), Beaver Creek (77), and Little Bear Creek (14).

I detected a total of 143 individual cutthroat trout during the spring spawning period using mobile scanning methods (Table 4). Of those 143 cutthroat trout, I detected 10 within main-stem sections. In the main-stem Logan River, I detected trout at Red Banks (5), between Red Banks and Franklin Basin (2), and Franklin Basin (2), while I found only 1 fish at Twin Bridges in the lower main-stem of the Logan River. I detected no fish in the Forestry Camp or within the section between Twin Bridges and Forestry Camp. I detected all remaining trout (133 fish) in tributaries in which lesser flows increased detection probabilities considerably. Relative efficiency (i.e., the expected encounter-percentage of tagged fish) of mobile scanning methods detected tagged trout at an efficiency of 36.3% in tributary reaches and 10.5% in main-stem reaches (Table 5). However, I made efficiency estimations during summer sampling, when stream flows were approximately 1/3 the magnitude of the spring peak flows (18.04 m^3/s). Therefore, these efficiencies are likely overestimated for spring months.

I detected most trout (76.9%) within or near the 100-200 meter section in which they were tagged. I found more mobile fish had moved upstream (16.7%) than downstream (6.3%). Using PIA detections, I detected a total of 201 unique fish during spring 2013 (Table 4). Some fish were detected using both methods; however, I used only one re-encounter per fish (farthest point from most recent detection prior to the spawning period) for estimates of movement degree and travel distance. Combined, I detected 256 unique individual cutthroat trout (221 fish from tributaries, 35 from the mainstem). There was no significant difference between maximum distance traveled of fish tagged in tributaries (median=589 m) and the mainstem-tagged (median=877 m) fish (Kolmogorov-Smirnov, p=0.06).

Based on detections, I determined the destinations of spawning fish throughout the watershed (Table 3.) From fish initially tagged at Twin Bridges and Forestry Camp sites (Section 2, Lower Logan River), 26.3% of fish were mobile. Of those fish that were mobile, 61.5% moved into the upper section (Section 2) of the Logan River with the remainder moving into tributaries. In Section 2 (Upper Logan River), fewer mobile individuals moved with 6.1% of the detected fish moving elsewhere in the watersheds, primarily to Section 1. In Temple Fork (Section 3), 29.8% of fish are defined as mobile and most moved into Spawn Creek (Section 4). Most of the fish considered mobile in Spawn Creek (Section 4, 20.3%) moved to spawn into Temple Fork (Section 3). I found no fish moving into or out Beaver Creek (Section 5). There were a few mobile fish in

Little Bear River (Section 6) from the Lower Logan (Section 2), Temple Fork (Section 3), and the Upper Logan (Section 2). In summary, most fish moved very little in response to spawning (presumably spawning nearby their tagging location) and did not seek out spatially-distinct areas of spawning habitat (Figure 4). Instead, the vast majority of fish spawned very near (at least in the same reach) where they were first captured during the summer. This was particularly true in the upper Logan River and its tributaries, where very few fish moved. The exception was Little Bear Creek where fish from throughout the watershed utilized this stream for spawning (Table 3).

I quantified seven River Styles in the Logan River watershed; only five of those are included in population abundance estimates (Table 6; Figure 3). The Styles listed as “wash” and “steep headwater” did not include fish population estimates, as these Style types were ephemeral streams, often only flowing during high runoff and therefore did not hold fish populations. For the entire Logan River, I estimated a population of 8,499 mature cutthroat trout that were likely to spawn in an average year (Table 6). After accounting for fish movement related to spawning in the watershed (Table 3), a total of 5,165 individuals would likely be spawning in the upper, protected portion of the watershed. Therefore, 61% of spawning cutthroat trout would be not be subject to angling during the spawning season, leaving 34% susceptible to harvest in the lower basin and 5% in several downstream tributaries.

Growth rates and size structure of tagged trout varied among different sections of the Logan River (Figure 5, Figure 6). Large differences were apparent between young individuals, while those differences became less distinguishable at larger sizes. Within tributary reaches, fish grew more slowly and to overall smaller lengths, which equates to lower fecundity (fewer eggs/female). Conversely, fish in the mainstem of the river grew more quickly, to reach larger sizes overall, equating to higher fecundity (more eggs/female); most fish reached a capable spawning size (225 mm) by age 3. Growth rates among mobile and sedentary fish in mainstem and tributary reaches differed only slightly (Appendix A). Mobile fish in the mainstem of the river exhibited high growth rates when these fish were < 250 mm long; however, the difference was non-existent above this size threshold. Overall, mobile trout were not larger or longer (total length mm) than sedentary individuals (Figure 6, Table 7), although mobile trout were on average, slightly larger than sedentary individuals in the upper and Temple Fork sections only. Furthermore, as demonstrated by linear regression, asymptotic lengths of age 7 trout (Figure 5) decreased as a function of the density of fish within a given section (Figure 7, $R^2 = 0.17$, $p = 0.015$).

Fish in the Logan River expressed on average lower condition compared to other lotic interior cutthroat trout populations (Wr < 100, Figure 8). Within sections, mobile fish were generally in lower condition compared to sedentary fish, but these results were for the most part insignificant. Only mobile trout in the upper watershed were in poorer condition compared to their sedentary counterparts. Furthermore, groupings delineated based on the results of a Tukey HSD test demonstrated that fish in the lower section are in generally in lower condition than fish in the rest of the watershed (grouping c, Appendix A).

Survival among sites in the upper river tended to decrease in the upstream direction (Figure 9). The top performing CJS model varied across time and site for both survival and probability of capture, and contained an individual covariate for fish length (Table 2). This top model performed only marginally better than the next 4 models based on the delta AICc. Model selection showed much less support for models including relative weight of individuals and/or air temperature effects at time of tagging. Sites including Temple Fork (64%), Spawn Creek (66%), and Twin Bridges (70%) tended to have higher survival rates than upper most sites, Franklin Basin (43%) and Beaver Creek (24%). Unfortunately, not enough data was available to obtain survival estimates between mobility classes; however, results from sedentary individuals demonstrate mainstem fish are surviving at a lower rate than residential tributary fish (Table 8).

I found a significant difference in the cumulative frequency of recreationists (across the day of year) between five sites on the Logan River. Card Canyon and Temple Fork experienced a higher number of recreationists, while Franklin Basin and Twin Bridges experienced relatively fewer. There was a significant difference in fishing pressure across the five sites evaluated along the Logan River (Figure 10, X-squared = 71.243, p-value = 1.24e-14). Forestry Camp estimates of fishing pressure were not significantly different from average values across all sites (p = 0.80).

The number of fin clips used for the genetic portion of this study ranged from 14-34 clips for the seven sites and abbreviations used for each site can also be found in Table 1. Two sampling locations exhibited departures from Hardy-Weinberg equilibrium, each at two loci; BC (H220, OMM 1034), and FB (H126, OMM 1034). Across loci, these populations did not show evidence of significant heterozygote excesses or deficits. Null alleles were unlikely to contribute to Hardy-Weinberg deviations; in populations FB, RB, and TB, we estimated null allele frequencies to be <15% but found no evidence of null alleles in the remaining populations. We also found no evidence of linkage disequilibrium among pairs of loci.

Four pairs of populations expressed marginally significant genetic differentiation, with a Bonferroni-corrected alpha value 0.005: BC vs TB ($p = 0.0008$), BC v SC ($p = 0.0025$), BC vs TF ($p = 0.0065$), and RB vs TB ($p = 0.0074$). These pairs of populations are separated by the greatest geographic distances, suggesting a gradient of low-level differentiation across the study site. A dendrogram of populations demonstrated low boot-strap support for all other nodes of differentiation (Figure 11).

Individual-based analyses also confirmed a general lack of structure across the study site. No population-level differentiation was apparent using an individual-based PCoA plot (Figure 12). Individual assignment using a Bayesian approach indicated that the most likely level of structure is K=3 groups of individuals. The first group was comprised of 7 individuals from BC(2), FB(3), SC(1), and TF(1), all with little or no evidence of mixed ancestry. The second group was comprised of 9 individuals from FB(4), FC(1), RB(2), TF(1), and TB(1), four of which appeared to have mixed ancestry, and 6 of which had little or no evidence of mixed ancestry. The remaining individuals, representing all populations, appeared as a single group, suggesting pronounced genetic admixture among sites. The AMOVA also indicated very little structuring among populations, with a PhiPT value of 0.005 ($p = 0.069$). The first two groups of individuals each contained unique high-frequency alleles (unique within each group) at H18, H126, and OMM1034 not found in the third group, suggesting that individuals in both the first groups represented immigration from another population. The second group indicated evidence of limited hybridization with the primary (third) group in the Bayesian assignment analysis, but also contained unique, common alleles at H18, H126, and OMM1034.

DISCUSSION

Common contemporary reductions in fish habitat and the oft-resulting inability of those fish to express diverse life-histories normally present in healthy populations can have profound implications for population structure, genetic diversity, angling opportunities, and thus the effective management of the system. I explored the spatial distribution and movement of Bonneville cutthroat trout during the spawning season, to better understand the spatial structure of the population of these fish within the Logan River Watershed. I was able to quantify movement patterns of these potential fish sub-groups throughout the basin by combining extensive but short duration mobile scanning primarily during the spawning season with continuously sampling fixed PIAs. This understanding was further informed by a microsatellite analysis of the genetic structure of these fish. In contrast to my hypotheses and observations elsewhere, I found little evidence of a spatially-distinct metapopulation structure based on low rates of movement system-wide, little evidence of spatially-distinct spawning patches, and little genetic differentiation among individuals from different areas of the watershed.

The degree of movement by spawning PIT-tagged Bonneville cutthroat trout among the main-stem and tributaries within the Logan River Watershed was less than expected and also suggests populations are not strongly spatially-structured. Trout are known to travel long distances in search of spawning gravel, and salmonids in particular (especially anadromous) are known for their ability to return to natal origin spawning gravel (Fullerton et al. 2011). However, herein the vast majority (>70%) of relocated fish remained close to their original tagging location moving a limited distance, < 1000 m during the spring spawning season. Relatively limited spawning gravel exists throughout the system (Budy et al. 2012), therefore, there is little benefit or ecological motivation to move long distances, resulting in most trout utilizing less than ideal stream margin substrates in close proximity to their year-round home range. However, as documented in other watersheds, there were a limited number of fish which moved > 5 km (Schmetterling 2001; Young 2011). Nonetheless, only a small percentage of tagged fish moved out of river sections in which they were tagged to spawn, and those remaining did not move far and were found in close proximity to their tagging location. Therefore, the results from this study suggest most fish are likely “residents” that maintain year-round site fidelity (Budy et al. 2007).

As the limited amount of movement I observed was in the upstream direction in this watershed, some adult spawning cutthroat trout may move upstream out of the lower, brown trout-dominated section of the Logan River in order to increase recruitment success (e.g., more suitable spawning and rearing habitat; lower competition/predation risk). In the lower section of river (Twin Bridges and Forestry Camp combined), 26% of fish moved upstream to spawn. Accordingly, densities of exotic brown trout, which are competitively superior, are extremely high in the lower river (Budy et al. 2008a). Juvenile and age-1 Colorado River cutthroat trout survival increased from 23% to 42% when exotic brook trout densities were reduced (Peterson et al. 2004). Additionally, rearing habitat within the upper watershed is of far better quality than the faster, steeper-sloped streambed found at mid-elevation (Meredith 2012; Meredith et al. 2015). Side channels, backwaters, and more lateral habitat, the density and area of which can be beaver influenced, is known to benefit juvenile cutthroat trout (Moore and Gregory 1988); all of these features are present in higher abundance in the upper river and tributaries. As such, maintaining and/or improving the rearing habitat within tributaries and protecting spawning fish is these upper sections of the river is of upmost importance if maintaining the persistence of this threatened population is a priority.

Based on the ‘isolation by distance’ concept (Wright 1943), trout in the upper watershed, relative to those lower in the watershed, might be expected to demonstrate differing genetic makeup potentially in both in the long term (i.e., 20 years) and short term (i.e., 1-5 years). However, while I observed that most fish stayed within the reach in which they were found, a few migrated long distances throughout the watershed likely resulting in genetic exchange occurs (Spruell et al. 1999). My findings suggest a partial stepping stone model may be in place, where, fish are spawning in a prime, nearby spawning area (Koizumi and Maekawa 2004; Kalinowski 2009) rather than a strict metapopulation model, where populations are balanced between localized extinctions and recolonizations (Harrison 1991). For example, most fish using Temple Fork were from the mainstem, more specifically the Twin Bridges site of the mainstem (just downstream of Temple Fork). Similarly, relatively high percentages of fish moved between Temple Fork and Spawn Creek, indicating those populations are likely well mixed. In this way, there may be some spatial structuring present within the Logan River, but enough genetic mixture to preclude the formation of distinct metapopulations.

Many of these areas are fishable throughout the year, which could pose a problem for spawning cutthroat trout. Promising strides have been made in protecting stream segments of Spawn Creek which are demonstrating benefits to protection, from decreased nutrient levels, increased riparian vegetation and decreased fine sediments (Hansen and Budy 2011; Hough-snee et al. 2013). Observed movement patterns indicate that these streams could be particularly important for production of fish that will inhabit the lower watershed (Bernard and Israelsen 1982). Similarly, fish using Little Bear Creek primarily came from the adjacent Forestry Camp and Red Banks sites. The lack of a traditional metapopulation structure observed here is also supported by the lack of local extinctions or colonization. Over the ~65 years this system has been monitored; the relative proportions, and overall abundance of cutthroat and brown trout have remained largely unchanged (Fleener 1950; Budy et al. 2007, 2008a). While tributaries in this watershed tend to hold slightly more spawning fish in spring months (Bernard and Israelsen 1982), these data indicate the number of mature cutthroat observed in a specific reach at any given time primarily reflects the number of adult fish located in that reach during the summer, and potentially throughout the year.

The genetic microsatellite analysis of fin clips data bolstered my conclusion that fish in this basin reflect the movement patterns (or lack thereof) observed. Based on this analysis, I did not detect population-level genetic differences, indicating this is a panmictic population throughout the watershed. However, I did detect minor genetic differentiation (though not significant) between the most geographically distant sites, indicating subtle genetic differences exist between high and low elevation populations. However, I would have expected higher levels of differentiation (Wright 1943) given the size of the watershed (64 rkm). Despite the low genetic diversity, genetic integrity is likely high within the system, as the number of adults exceeds the minimum of 2,500 individuals needed for long term persistence (Allendorf et al. 1997) and exceeds the stream length requirements of > 18.5 km proposed by Hilderbrand and Kershner 2000b. The two genetically distinct clusters detected in the Bayesian assignment test did not cluster geographically, and may be due to past introgression with rainbow trout, possibly due to past, intense stocking throughout the upper watershed. While current stocking of sterile fish takes place in the dams of the lower watershed and poses little threat at present, an increase in temperature can increase hybridization risk (Muhlfeld et al. 2009). Maintaining the genetic integrity of fish in the watershed as a whole is of the utmost importance given this population’s status; therefore, management actions will be most effective if focused on increasing the size and connectively of the watershed (Isaak et al. 2007) while also maintaining currently observed levels of connectivity.

Although I observed little spatial or meta-population structure, trout distributed across the strong environmental gradient of the Logan River might be predicted to experience different vital rates. Fecundity, for example, is directly related to fish size (growth) and condition (Downs et al. 1997). Fish in mainstem reaches grew more quickly and to comparatively larger sizes, while tributary fish grew slower and to smaller sizes. These generalizations, however, were not without exceptions; Franklin Basin and Temple Fork, for example, both demonstrated higher maximum size estimates than expected given their location within the watershed, as headwater reaches in this watershed typically grow smaller fish (Hilderbrand and Kershner 2004). These anomalies may be a result of the increased extent of beaver activity in these areas, which provide preferred complex habitat, velocity refugia, and warmer temperature habitat (Schrank and Rahel 2006), combined with lower numbers of exotic brown trout (Budy et al. 2008a). Past studies within the watershed demonstrated brown trout lower cutthroat trout performance (McHugh and Budy 2005), an impact presently in the lower portion of the river. Complementary to other studies, mobile fish in my study were, on average, larger in the upper watershed (Hilderbrand and Kershner 2004) and in Spawn Creek (Randall 2012), but smaller, on average, in Temple Fork and the lower watershed. Somewhat unsurprisingly based on my movement results, I observed only minor differences between growth rates of mobile and sedentary fish. Mobile fish in this system are not exhibiting true “fluvial” traits as Bonneville cutthroat trout do in other, larger river systems (Colyer et al. 2005). Condition estimates across the watershed also varied very little (but see Hilderbrand and Kershner 2004). While fish did express minor differences in growth and age characteristics, these were for the most part statistically insignificant and likely biologically unimportant due to the productive and connected high-quality habitat found throughout most of the Upper Logan River.

The fragmented nature of the lower section of the Logan River Watershed, higher harvest rates by anglers, and large abundance of brown trout have dramatically lowered cutthroat abundance and distribution (Budy et al. 2007); this section can therefore serve as a reminder of the potential problems that could arise within the remainder of the watershed. Had my research found strong indications of separate metapopulations within the watershed, management recommendations would focus on maintaining effective population sizes in each metapopulation in order to insure persistence. Due to population panmixia and an abundance of other factors affecting cutthroat trout in this watershed, management may need to focus on mitigating these risks. Natural limitations to anglers, such as spring runoff, can make many systems unwadeable during spring months when cutthroat trout are spawning, resulting in a natural protection to spring-spawning trout. Brown trout however, exert negative effects on adult cutthroat in the form of competition and survival (McHugh and Budy 2005; McHugh et al. 2006; Budy et al. 2007), which would reduce adult fecundity and lower survival of juvenile offspring as well. Brown trout juveniles (spawned several months prior) likely out-compete cutthroat fry due to their larger size and existing establishment of an area (Johnsson et al. 1999), therefore, decreasing the overall brown trout population in this area through angling or other means could prove highly beneficial. The native cutthroat trout population in the Logan River would likely benefit by decreasing limits on native cutthroat trout, increasing limits on non-native trout, and encouraging non-native take (particularly in the lower section), thereby using a precautionary or risk-averse management strategy (Potter et al. 2003) for one of the most important populations of cutthroat trout.

Methods employed for capturing, and re-encountering fish allowed for robust estimates of spawning movements, in part due to the high number of tagged individuals over multiple years. Additionally, detection methods used for this study were a cheap, effective way to judge movement rates of stream dwelling fish, test the potential effectiveness of fishing regulations, and estimate the potential genetic mixture of this stream population. Using a combination of PIAs and mobile scanning methods, I was able to obtain adequate results; using only one of these methods would not have yielded strong results. Mobile antenna methods were difficult to use and detection was unlikely unless a tagged fish is within a foot of the antenna (Cucherousset et al. 2005; Hill et al. 2006). This makes detection difficult in larger rivers, but this can be balanced with the use of PIAs with high detection efficiency (100%) as fish move over the antennae arrays. The combined use of these systems likely alleviated any bias in over or under-estimating movement distances, and provide a strong model for future studies in other watersheds.

Threats to aquatic ecosystems are numerous, but currently the most pressing threats to many salmonid populations, particularly in the West are the presence of non-native fish (brown and brook trout), riparian grazing (Belsky et al. 1999; Peterson et al. 2010; Budy et al. 2012), increasing use by recreationists including dispersed camping on federal lands (Wohl 2005) and climate change (Williams et al. 2009; Wenger et al. 2011). These impacts may become multiplicative in their effect instead of additive, if interactions occur between or among impacts. For example, warming effects of climate change may result in the expansion of the range of brown trout and increase embryo survival (Wood and Budy 2009). Native species may decline in response to warming temperatures at a faster rate than non-native fish (Wenger et al. 2011), and Bonneville cutthroat trout in the Bear River and its tributaries, are particularly susceptible to warming (Williams et al. 2009). The destructive effects of cattle grazing on aquatic ecosystem is well documented; however, direct redd trampling resulting in the mechanical destruction of egg or fry has only recently been studied (Gregory and Gamett 2009). The likelihood that cattle will trample redds in a given area is relatively high, with the percentage of trampled redds likely to increase with rising cattle grazing intensity (i.e., more cows). Further, Peterson et al. 2010 found cattle trampling can increase embryo mortality and decrease population resiliency, particularly in already-stressed watersheds. Although the Logan River is considered relatively pristine, these threats are present throughout the watershed.

Negative effects of sedimentation via bankside erosion from grazing livestock and direct trampling of redds has been documented within the Logan River (Budy et al. 2008b; Seidel 2009). Similarly, in an experimental environment Roberts and White (1992) observed that angler wading significantly reduced survival of in-gravel eggs while in a natural setting, the effects of angler wading did not appear to be significant (Kelly 1993); however, it is the combination of these activities with other threats that may negatively impact cutthroat. Tributary reaches that sustain increased numbers of trout during spawning months, are even more likely to be adversely affected by the combination of all of these factors (Bernard and Israelsen 1982; Hilderbrand and Kershner 2000a; Budy et al. 2008b). In response to these numerous potential threats, I suggest the mitigation of cattle grazing and angling, in particular, and especially during spawning months. Proactive management may also include increased brown trout harvest or removal, and the continued education of anglers regarding the benefits and protection of their local resource.

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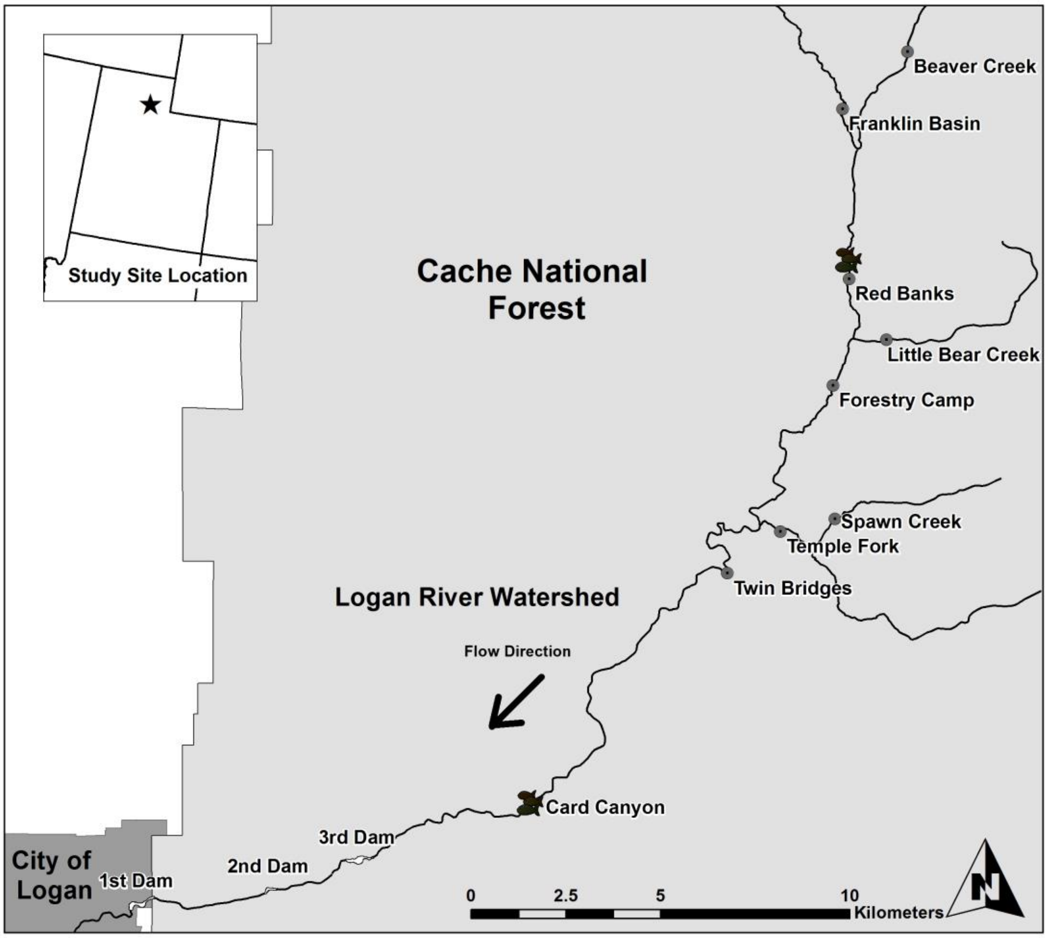

FIGURE 1.—Map of the Logan River drainage in northern Utah in the Cache National Forest. Study sites in which fish were tagged are indicated by the dark grey circles. The City of Logan and the location of impassable (upstream) dams are noted; locations of fishing regulation changes are indicated by a fish symbol.

TABLE 2.—Number of fin-clip samples taken at each site and used for the genetic component of this research. All samples except for Beaver Creek were collected summer 2010, Beaver Creek samples were taken in summer 2014.

Population	Abbreviation	n
Beaver Creek	BC	20
Franklin Basin	FB	33
Forestry Camp	FC	32
Red Banks	RB	27
Spawn Creek	SC	34
Twin Bridges	TB	14
Temple Fork	TF	34

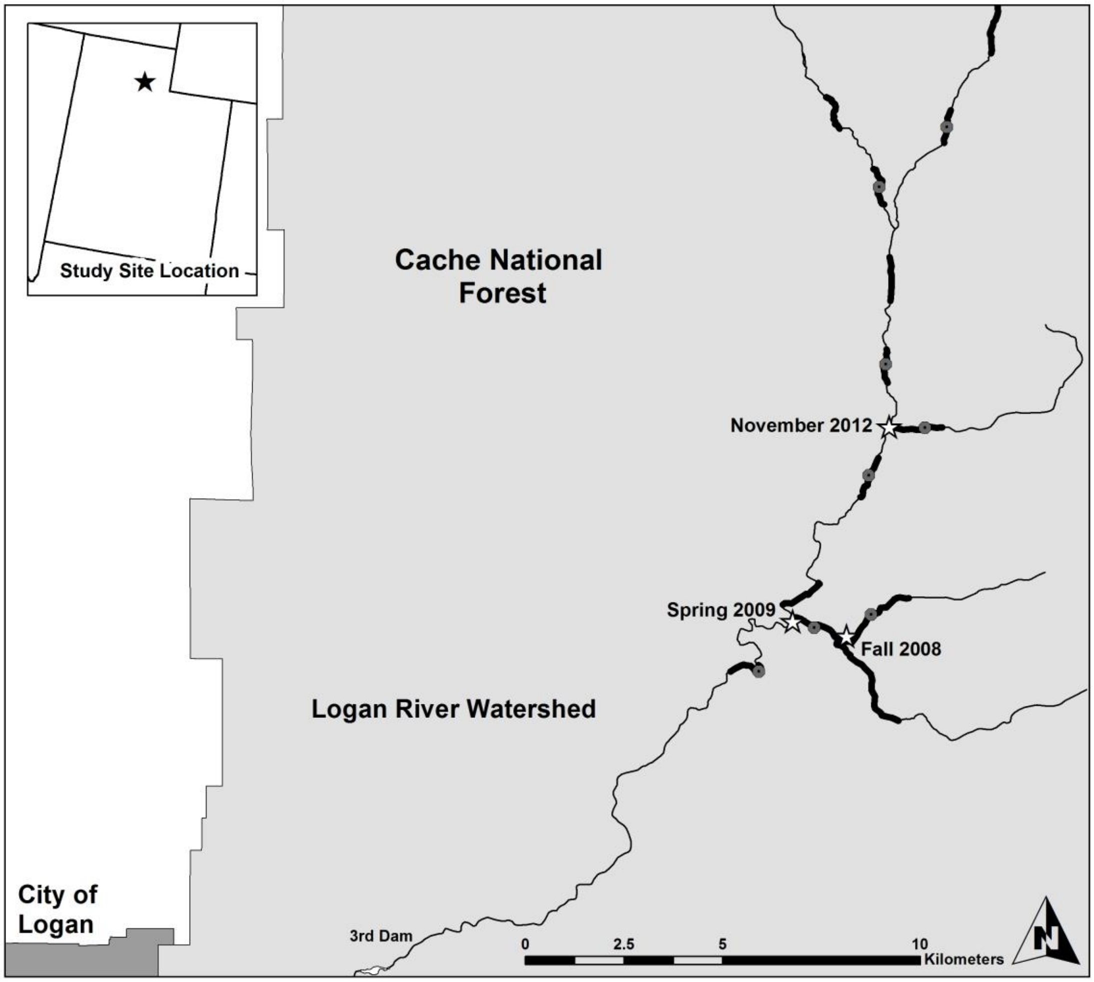

FIGURE 2.—The location and time of placement of PIA systems with the Logan River Watershed are starred, long-term study sites are displayed as dark grey circles, and the black overlay lines describe the reaches scanned by mobile antenna surveys.

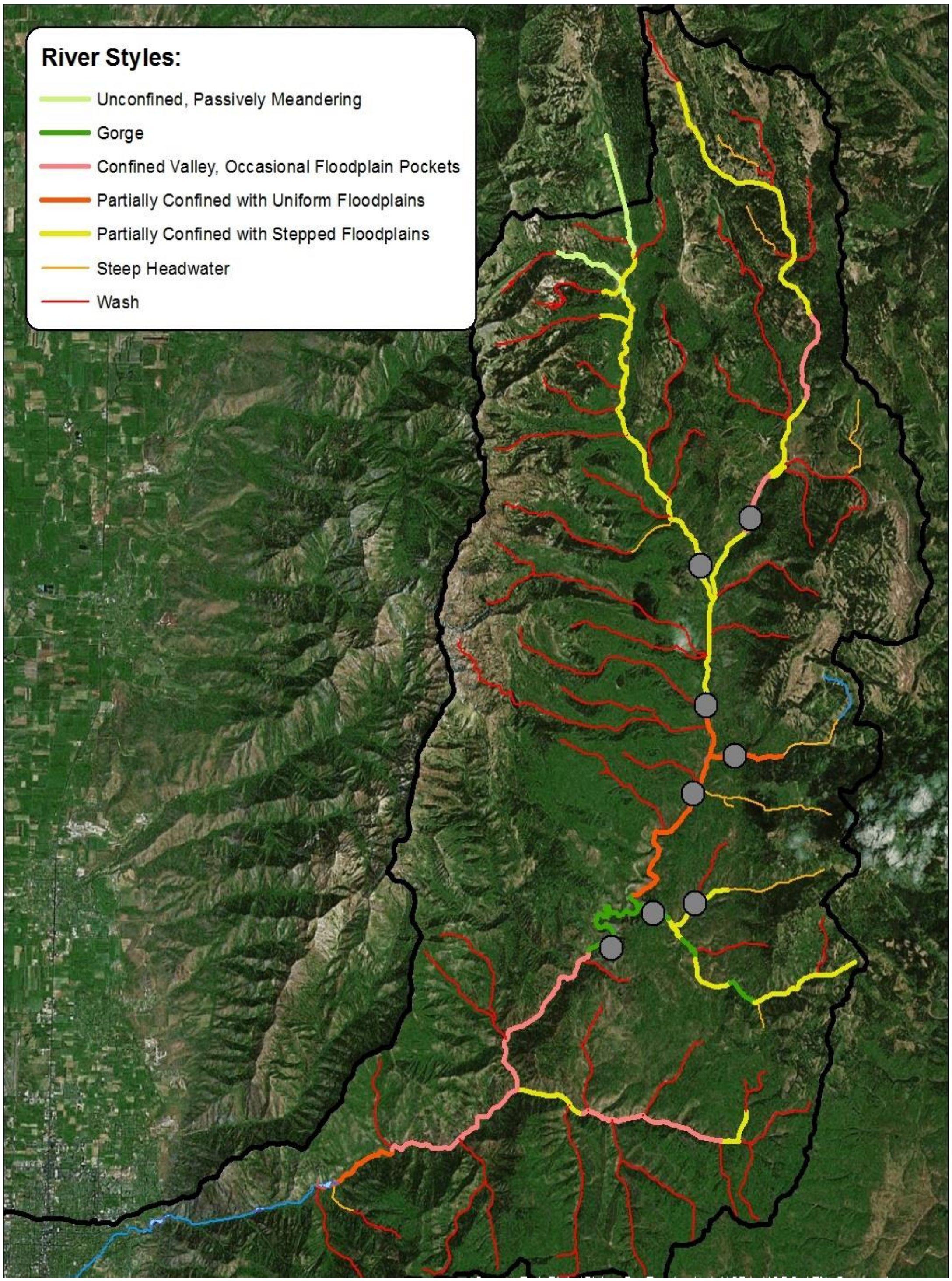

FIGURE 3.—River Style geomorphic reaches for the Logan River above Third Dam. Seven River Styles were identified in this watershed, five (orange, pink, green, yellow, and light green) were reaches that contained fish populations. Gray dots represent long-term sampling and tagging sites.

TABLE 2.—The top-16 most parsimonious models of Cormack-Jolly-Seber survival (**Φ**) for Logan River Bonneville cutthroat trout, based on program MARK output (completed through RMARK) and information theoretic selection criteria. Site and time; condition (relative weight), total length, and air temperature during tagging day (NP =number of parameters; AIC_c = corrected Akaike's information criterion; (.) = constant parameter).

Model	AIC_c	ΔAIC_c	AIC_c Weight	NP	Deviance
Φ (site, time, total length), *p* (site, time)	2067.88	0.00	5.80E-01	23	2021.44
Φ (time, total length), *p* (site, time)	2068.97	1.09	3.37E-01	17	2034.72
Φ (site, time, relative weight), *p* (site, time)	2073.15	5.27	4.15E-02	23	2026.72
Φ (time, relative weight), *p* (site, time)	2073.63	5.75	3.28E-02	17	2039.38
Φ (site, time), *p* (site, time)	2076.89	9.01	6.43E-03	22	87.56
Φ (time), *p* (site, time)	2079.18	11.30	2.04E-03	16	102.04
Φ (time, air temperature), *p* (site, time)	2085.50	17.62	8.67E-05	17	2051.26
Φ (site:time), *p* (site:time)	2135.89	68.01	0	70	46.96
Φ (site, total length), *p* (site, time)	2771.22	703.34	0	19	2732.92
Φ (site, air temperature), *p* (site, time)	2802.12	734.24	0	19	2763.82
Φ (site, relative weight), *p* (site, time)	2802.59	734.71	0	19	2764.29
Φ (site), *p* (site, time)	2811.16	743.28	0	18	829.97
Φ (.), *p* (site, time)	2855.18	787.30	0	12	886.13
Φ (.), *p* (time)	2951.93	884.05	0	6	994.98
Φ (.), *p* (site)	3185.44	1117.56	0	8	1224.46
Φ (.), *p* (.)	3241.63	1173.75	0	2	1128.73

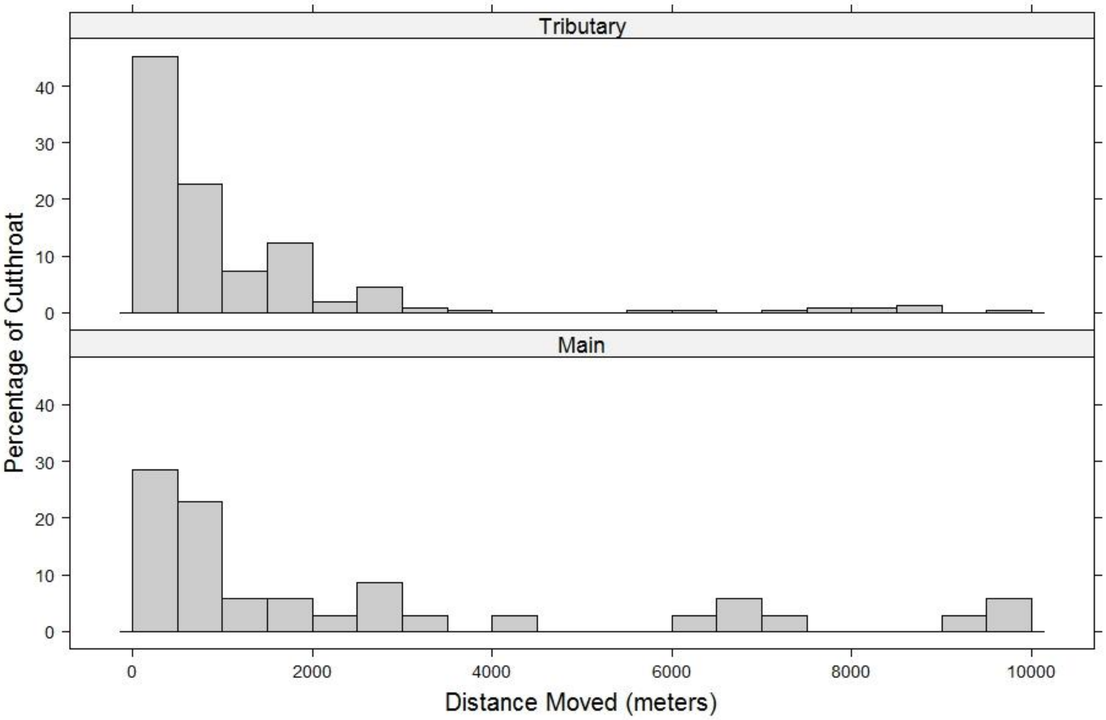

FIGURE 4.—Maximum detected movement distances (meters) traveled by cutthroat trout originating in either tributary or main-stem Logan River sections. Data consists fish tagged during summer sampling during years 2008-2012, and re-sighted during the spawning months of 2013 (Apr-Jun).

TABLE 3.—The number of fish tagged within stream sections or reaches, the number expected to have survived to spawn in spring 2013, and where those fish were recaptured. The “Lower Section” includes both Twin Bridges and Forestry Camp long-term sites while the “Upper Section” includes both Red Banks and Franklin Basin. Site name abbreviations can be found in Table 1. The movement rate was calculated by taking the total number moved from each tagging location against the total number estimated alive and able to spawn. Confidence intervals were generated using a standard binomial distribution test (p=0.05).

		Segment of Origin						
		T.B.	F.C.	R.B.	F.B.	S.C.	T.F.	B.C.
	Total Tagged (Est. alive)	59 (8.9)	108 (40.6)	176 (56.2)	107 (59.3)	534 (78.9)	1210 (238.4)	77 (26.4)
Section of Recapture	Lower Section			4	1	4	12	
	Upper Section	2	6				4	
	Temple Fork	2				12		
	Spawn Creek		1		1		53	
	Little Bear Creek		2	1			2	
	Beaver Creek							
	Movement Rate	44.9%	22.2%	8.9%	3.4%	20.3%	29.8%	0.0%
	95% CI	(13.7-78.8)	(10.8-38.4)	(3.0-19.6)	(0.4-11.7)	(12.0-30.8)	(24.1-36.1)	(0.0-0.0)

TABLE 4.—Number of native Bonneville cutthroat trout encountered via mobile scanning (143 individuals) and PIA detections (201 individuals) at all main-stem and tributary sites in the Logan River, Utah during the spawning season. Data were collected between Apr 1, 2013 and Jul 1, 2013.

	Number of Individuals	
Encounter Location	Mobile Encounters	PIA Encounters
Tributary		
Beaver Creek	22	
Little Bear Creek	4	
Spawn Creek	61	74
Temple Fork	46	52
Lower Temple Fork		42
Main-stem		
Franklin Basin	2	
Red Banks/Franklin Basin	2	
Red Banks	5	
Forestry Camp		33
Twin Bridges	1	

TABLE 5.—Maximum scanning efficiency of mobile scanning use of native Bonneville cutthroat trout, at long-term study sites. Data were collected during summer sampling in 2013.

Site	Individuals Scanned	Individuals Captured	Number of scanners	Estimated Efficiency
Tributary				
Spawn Creek	2	3	1	
Temple Fork	0	2	2	
Beaver Creek	2	6	2	
Combined	4	11	5	36.30%
Main-stem				
Franklin Basin	0	8	3	
Red Banks	2	18	3	
Twin Bridges	2	9	2	
Forestry Camp	0	3	2	
Combined	4	38	10	10.50%

TABLE 6.—Population estimates from long-term study sites within the Logan River, Utah were expanded across similar geomorphic reaches in order to obtain a whole river population estimate. The percentage of mature fish (≥ 225 mm) estimated from yearly capture data was used to calculate the number of mature, spawning individuals within each management section. I combined these to determine the number and percentage of spawning fish within each management section to assess the relative benefit of management regulations.

Site	Total Fish	Percent Mature	Number Mature	Management Section	Number of Spawning Fish	Percent in each Section
Franklin Basin	9,535	33%	3,147	Upper	5,680	66.1%
Beaver Creek	11,354	14%	1,590			
Red Banks	1,691	31%	524			
Forestry Camp	4,361	24%	1,047	Lower	1,949	22.7%
Twin Bridges	2,970	62%	1,841			
Temple Fork/Spawn Creek	847	41%	347	Tributaries	966	11.2%
Little Bear Creek	100	100%	100			

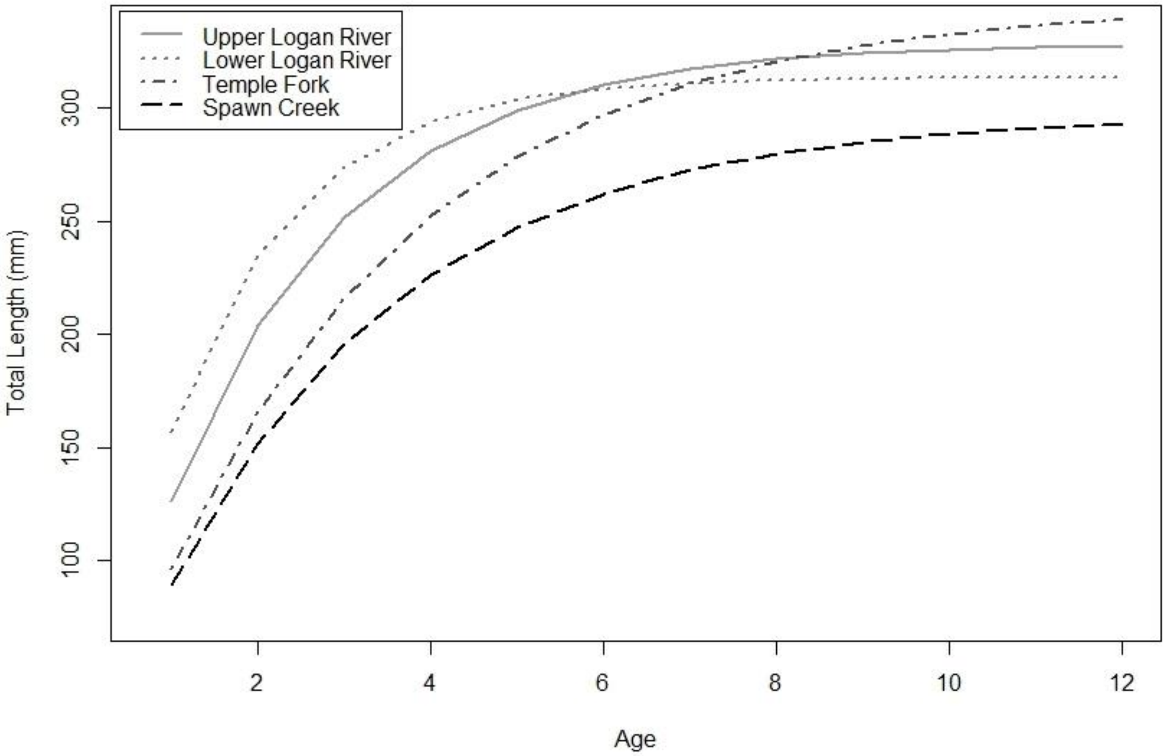

FIGURE 5.—Growth rates based on fish recaptures within two mainstem and two tributary sections of the Logan River watershed. Upper (Twin Bridges and Forestry Camp) and Lower (Red Banks and Franklin Basin) sections were pooled into sections in order to provide sufficient numbers of recaptured fish to generate reliable estimates. Age at length estimates were back-calculated using the Fabens (1965) method.

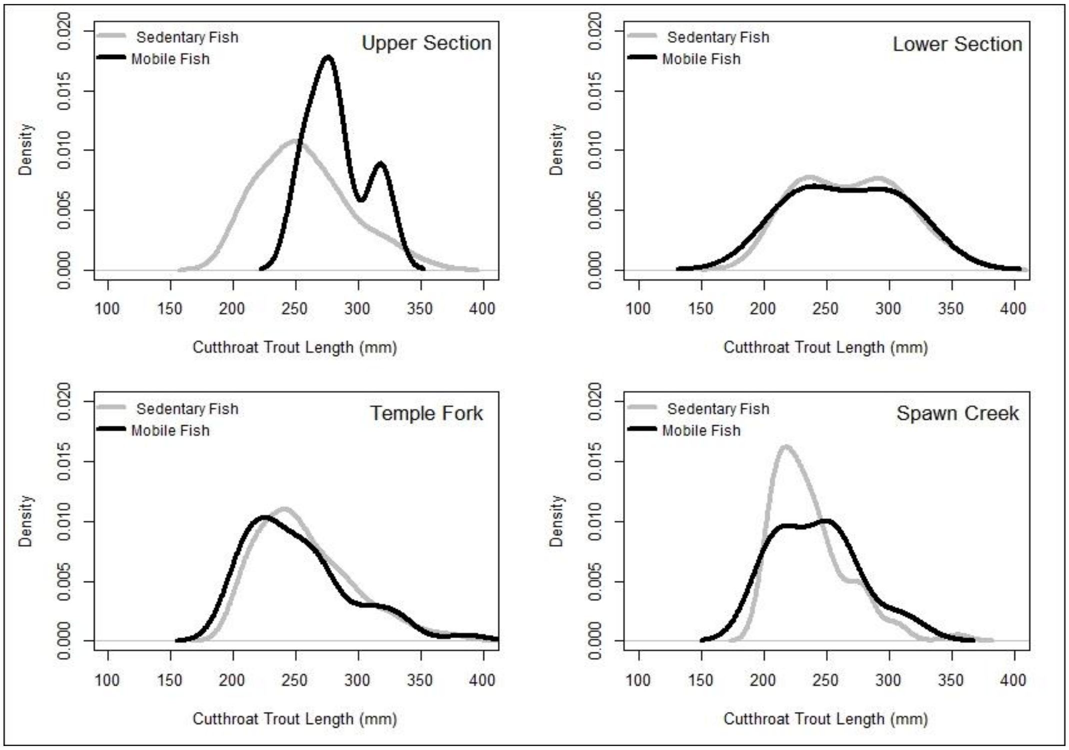

FIGURE 6.—Total length of all fish tagged in 2012 graphed by section and their movement status following the 2013 spawning period (Apr-Jun). Groups were graphed using a kernel density function where the shape of the curve depends on the number of localized data points in a given area. The area under each curve is standardized to equal a value of 1.0.

TABLE 7.—Mann-Whitney U Tests for each section within the Logan River (Figure 3) in order to test whether mobile fish are larger than sedentary fish. This test assesses statistically significant differences between mobile and sedentary groups.

Independent 2-group Mann-Whitney U Test						
Section	Movement Pattern	n	Mean	Standard Deviation	W	p value
Upper	Mobile	4	282	26.0	52	0.1351
	Sedentary	48	256	35.8		
Lower	Mobile	4	266	43.9	32.5	0.8414
	Sedentary	15	269	40.4		
Temple Fork	Mobile	54	252	41.6	9102	0.1605
	Sedentary	301	259	41.1		
Spawn Creek	Mobile	10	241	33.7	380	0.6687
	Sedentary	83	236	29.5		

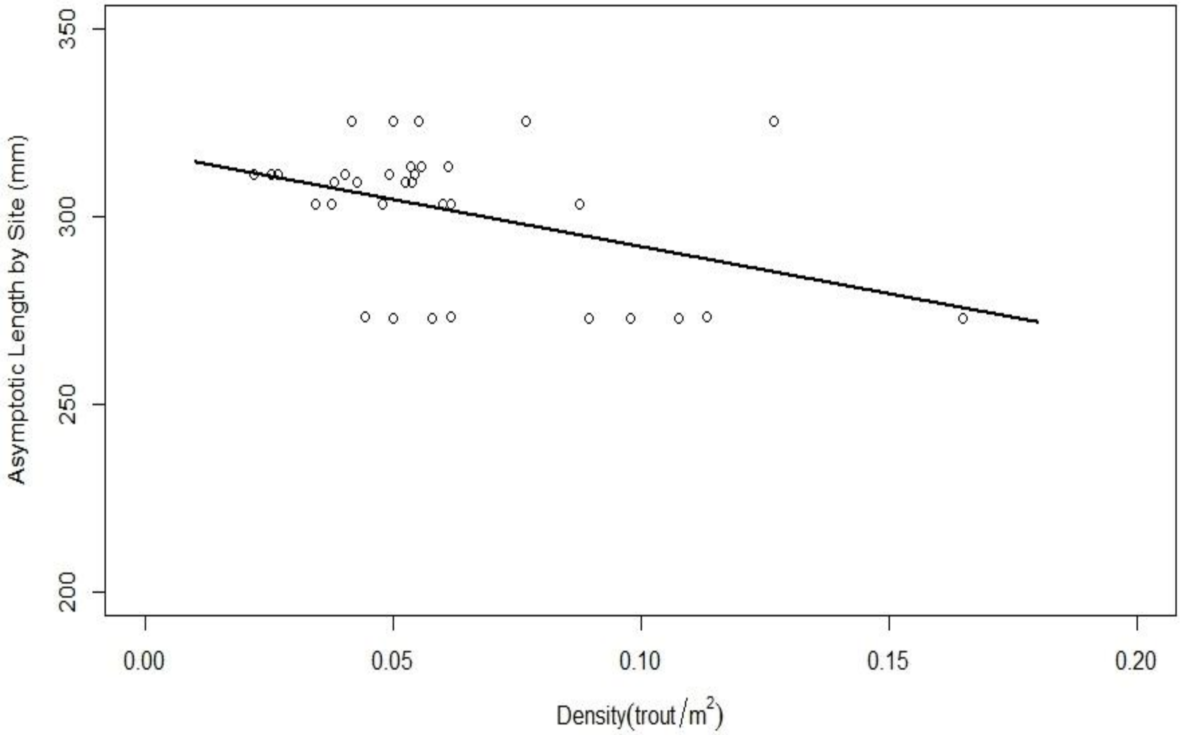

FIGURE 7.—Asymptotic lengths estimated for age 7 individuals (Table 9) versus density of trout at each site for years 2008-2013. Both native cutthroat trout and non-native trout species were included in this density estimate.

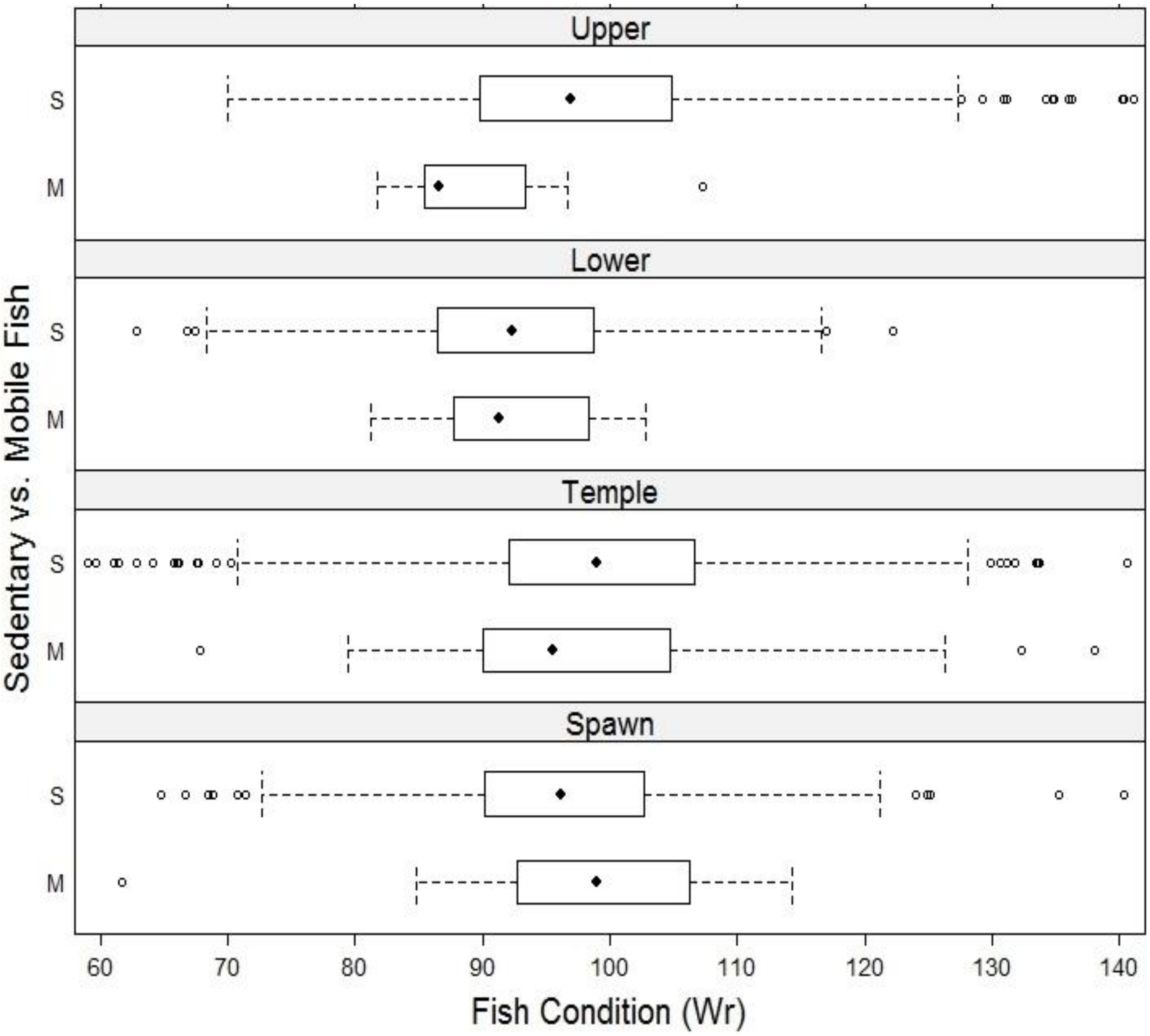

FIGURE 8.—Estimates of condition (Wr, relative weight) of Bonneville cutthroat trout for each section of the Logan River, Utah from fish sampled and tagged from 2008-2012, separated by 2013 movement status. Center circles represent median values, the primary box represent the 25-75% quartile range, whisker ranges represent the minimum and maximum values excluding outliers, and open circles represent outliers for each group.

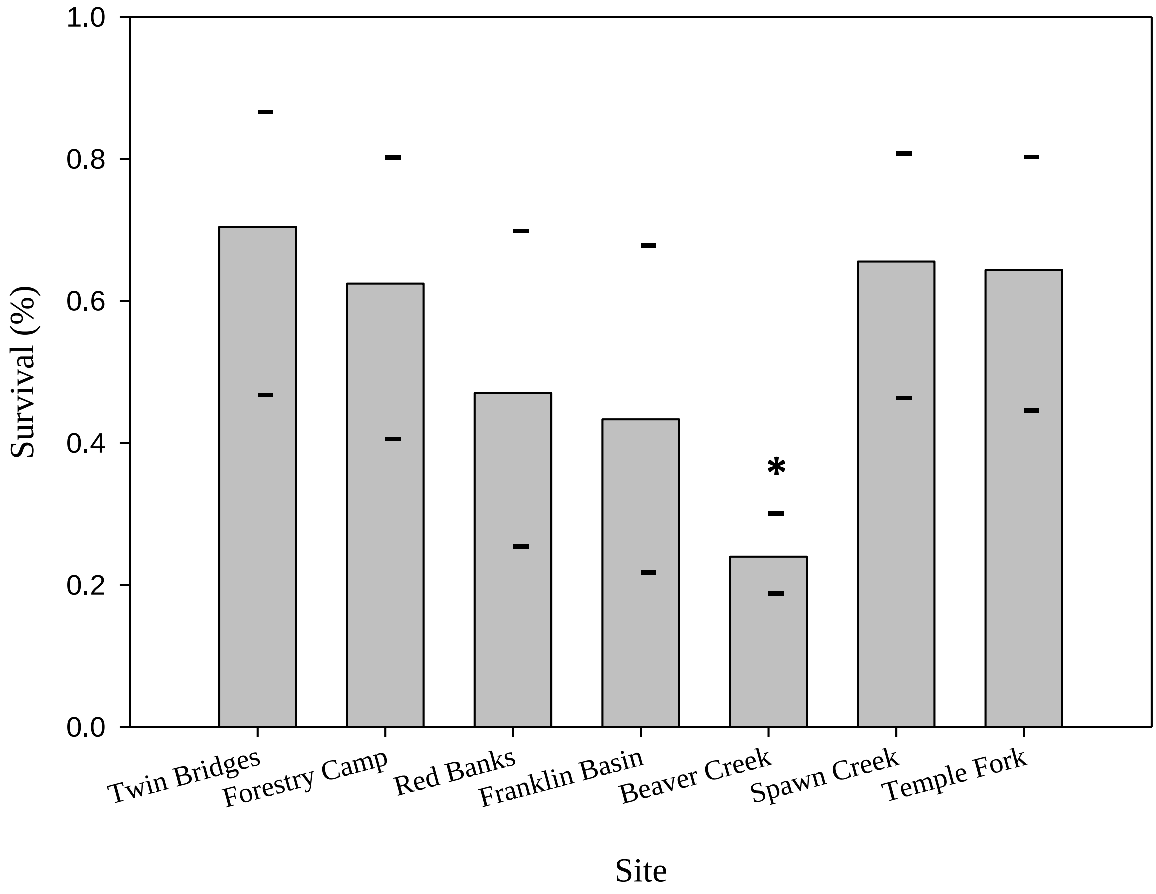

FIGURE 9.—Mean (± 1 SE; across years) Cormack–Jolly–Seber (CJS) survival rates of Bonneville cutthroat trout at seven sites on the Logan River, Utah, 2008–2013. * Tagging at the Beaver Creek site began in 2011, and recaptures were too low to allow a reliable estimate of survival.

TABLE 8.—Mean (with 95% confidence intervals) Cormack-Jolly-Seber (CJS) survival rates between mobile and sedentary groups of native Bonneville cutthroat trout in main-stem or tributary sites (7 total) on the Logan River, Utah, 2008-2013. No reliable estimates were obtained for mobile trout indicating an overall lack of data for those two groups.

Survival (Φ)	Estimate	95% CI
Main-stem mobile	100.0%	(0-100%)
Main-stem sedentary	61.2%	(56.7-65.5%)
Tributary mobile	100.0%	(0-100%)
Tributary sedentary	66.4%	(64.3-68.4%)

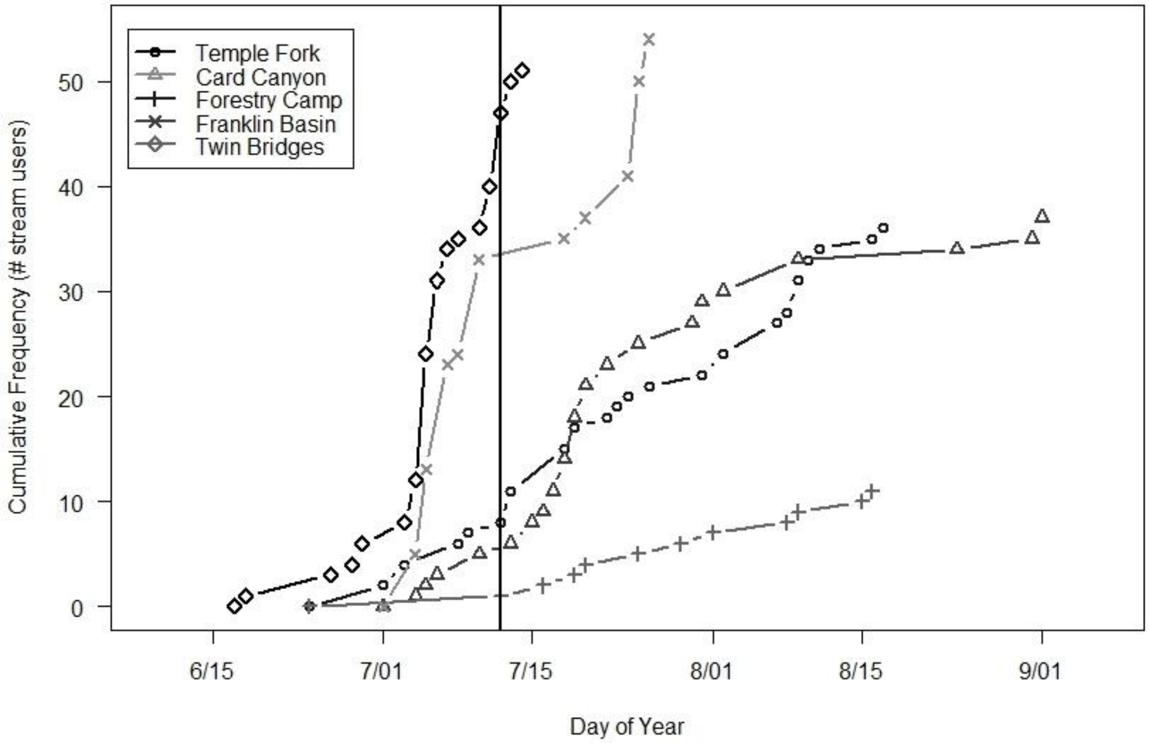

FIGURE 10.—The cumulative frequency of stream users against the day of the year in 2014 by site. Time-lapse cameras were used to determine relative stream use in 5 sites on the Logan River. The vertical black line indicates a temporal regulation change: prior to this fishing is prohibited in the upper basin (Franklin Basin), while after this time fishing is permitted.

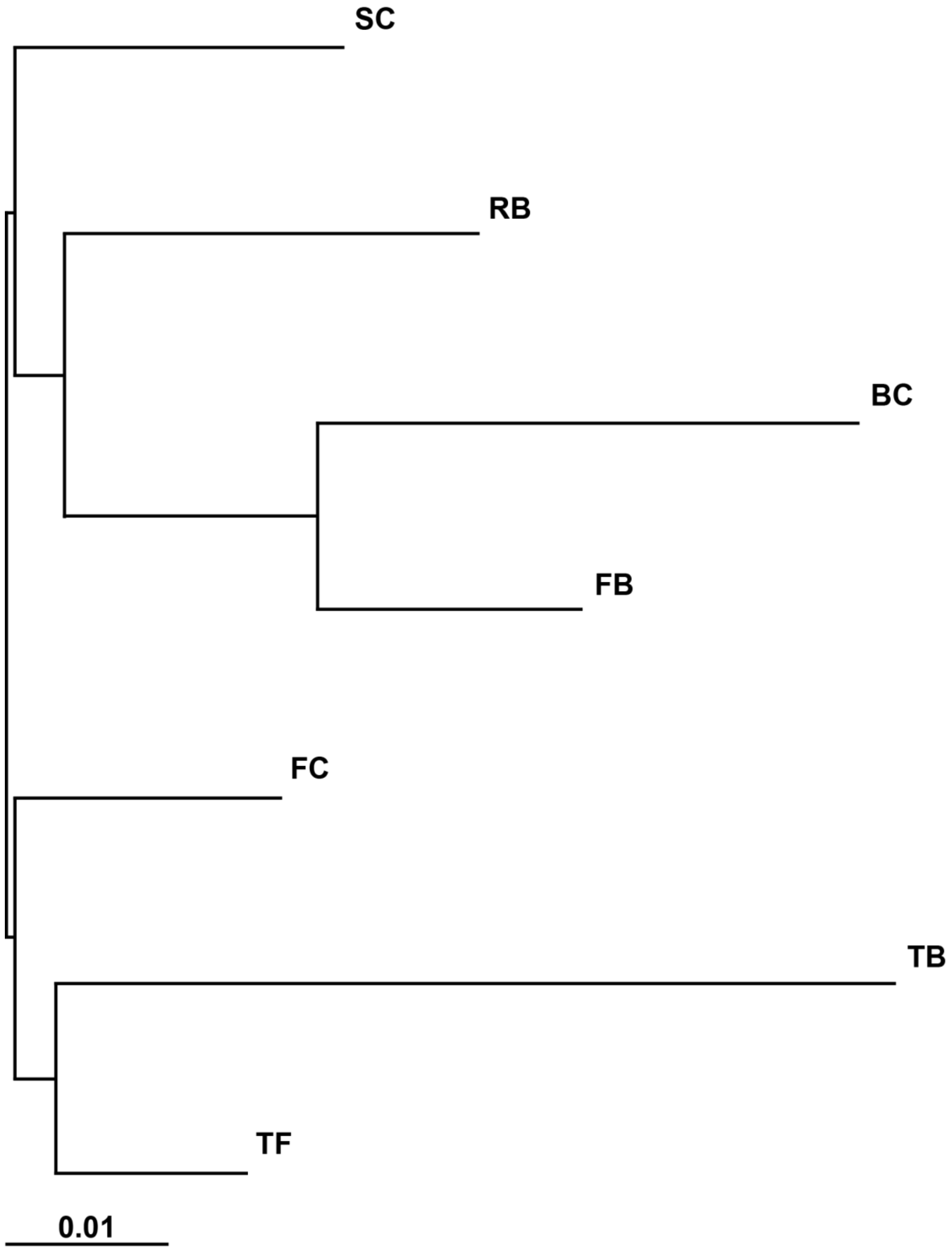

FIGURE 11.—Global patterns of population differentiation were described using a neighbor joining dendrogram in order to describe relative genetic differences between 7 sites on the Logan River, Utah. Site name abbreviations can be found in Table 1. Fin clips for analysis were collected in 2010.

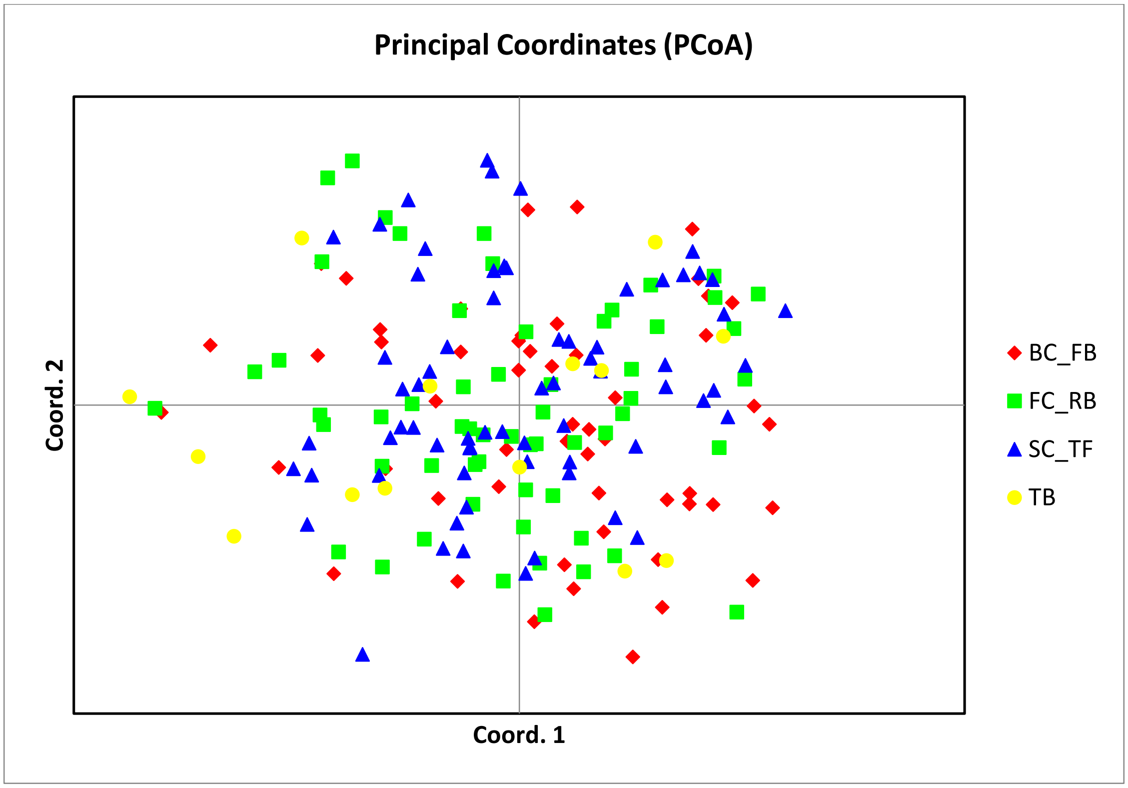

FIGURE 12.—Global patterns of population differentiation were described using a principle coordinate analysis approach in order to describe relative genetic differences between 7 sites on the Logan River, Utah. Site name abbreviations can be found in Table 1. Fin clips for analysis were collected in 2010.

APPENDICES

Appendix A. Supplementary Material

TABLE 9.—Asymptotic length estimations from Von Bertalanffy growth curves (Figure 2.) estimated for each site, asymptotes are for age 7.

Asymptotic Lengths: Von Bertalanffy growth curves		
Section	Site	Asymptotic Length
Upper	Franklin Basin	325
	Red Banks	303
Lower	Forestry Camp	309
	Twin Bridges	313
Tributaries	Beaver Creek	273
	Temple Fork	311
	Spawn Creek	273

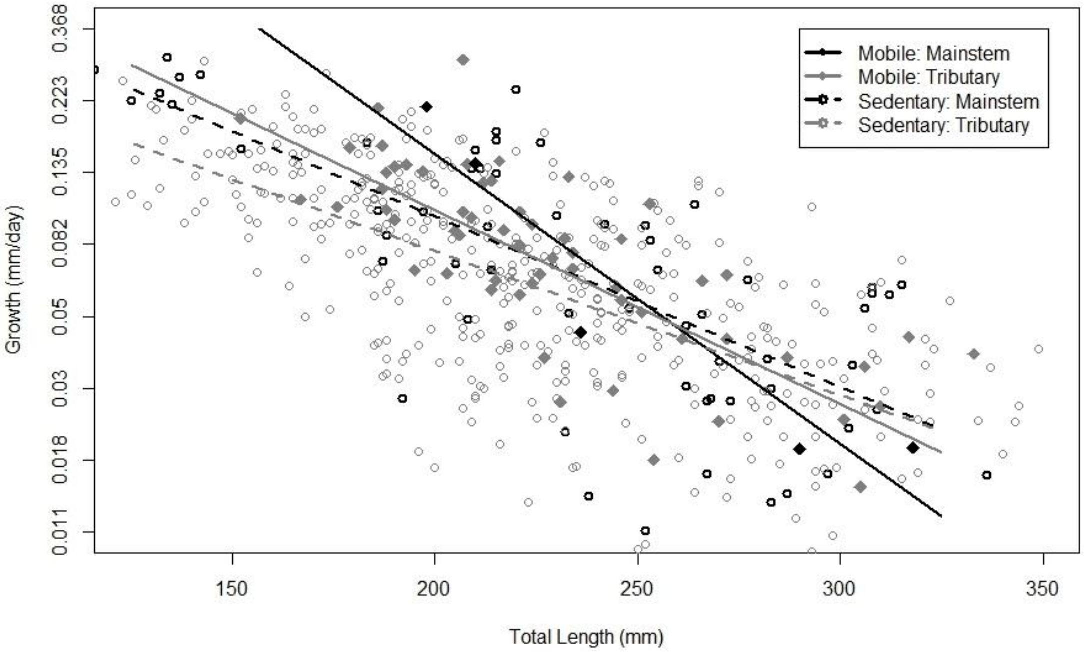

FIGURE 13.—Individual growth rates for mobile and sedentary categories in different areas of the stream, mainstem or tributary reaches. A linear model for each group describing the relationship between individual growth rate and total length at tagging was fit for each mainstem/tributary groups. No significant difference exists between groups (p>0.05).

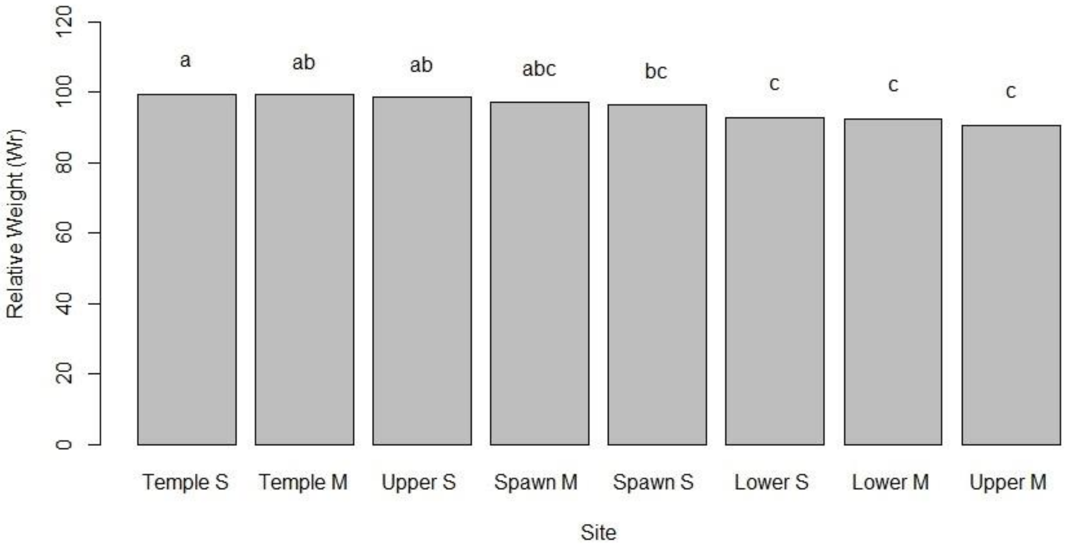

FIGURE 14.—A Tukey HSD test was used to statistically compare means between the relative weight of mobile (M) and sedentary (S) groups by section (Temple, Upper, Spawn, and Lower) in the Logan River. Statistically significant groupings (a-c) are noted above each mean.

TABLE 10.—River Style geomorphic reaches presented in Figure 3 and the total kilometer distance estimate for each reach. The number of fish within each reach was estimated using population estimations from long-term monitoring in 2008-2013.

River Style	Total Stream Length (km)	Estimated Number of Fish
Unconfined, Passively Meandering	7.2	2,343
Gorge	7.4	923
Confined Valley, Occasional Floodplain Pockets	17.2	5,202
Partially Confined with Uniform Floodplains	14.1	4,544
Partially Confined with Stepped Floodplains	39.2	17,846
Steep Headwater	22.0	0
Wash	200.8	0
Total (stream km with trout)	307.8 (85.0)	30,857

TABLE 11.—Pearson’s Chi-squared test was conducted for sections within the Logan River in which time-lapse photography was used to estimate angler use. All sites except for Forestry Camp found significant departures from mean users per month estimates.

Pearson's Chi-squared Test for Count Data

Site	Users Observed	Camera Days Out	Users/day	Users/month	Mean	p values
Forestry Camp	36	54	0.67	20.7	34.2	0.068
Card Canyon	54	25	2.16	67.0	34.2	0.001
Temple Fork	51	27	1.89	58.6	34.2	0.011
Franklin Basin	37	62	0.60	18.5	34.2	0.031
Twin Bridges	11	53	0.21	6.4	34.2	1.33E-05
Overall	X-squared = 83.7735, df = 4, p-value < 2.2e-16					

Appendix B.

Detailed Description of Fishing Regulations in Place 2012-2015 within the Logan River, Utah.

Current angling regulations (Utah Division of Wildlife 2014) break the river into three sections: below Card Canyon Bridge, between Card Canyon Bridge and the Red Banks campground, and upstream of the Red Banks campground. All tributaries flowing into each mainstem sections are subject to the same restrictions as the mainstream section into which they flow. Below Card Canyon, fisherman may harvest up to four fish (any trout species or whitefish). This section harbor high numbers of brown trout, stocked triploid rainbow trout, mountain whitefish, and few cutthroat trout. All standard fishing methods can be used in this section. Card Canyon upstream to the Red Banks area contains a sympatric mix of brown and cutthroat trout occurring in relatively equal numbers. Within this section, a limit of two fish (any species) may be harvested using only artificial lure or fly methods. In both of these lower sections, anglers fish year-round. The third section found upstream of the Red Banks campground, bait fishing is permitted and two fish are allowed to be harvested; however, fishing is prohibited from January 1st until the second Saturday in July. Cutthroat trout exist nearly allopatrically and it is conventionally thought most mainstem fish will move into this upper area to spawn. Therefore an understanding of the number of cutthroat trout moving into this area is of most interest to fishery and land managers.