Movement of resident rainbow trout (*Oncorhynchus mykiss*) transplanted below barriers to anadromy in Freshwater Creek, California.

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Project Summary

Research was conducted to determine if resident rainbow trout (*O. mykiss*) isolated above an upstream barrier to anadromous migration would exhibit migratory behavior when relocated to a stream reach below the barrier. Age 1+ trout above a 5 m high waterfall in Freshwater Creek, California were captured during 2005 - 2006 and individually marked with passive integrated transponder tags. Analysis of otolith microchemistry indicated that above-barrier trout had resident rather than anadromous parents, and genetic analysis indicated that the trout showed some degree of introgression with cutthroat trout. At each of three sampling events, half of the tagged individuals (n = 22 and 43 trout in 2005 and 2006, respectively) were released below the waterfall, approximately 10 km from tidewater, and an equal number of tagged individuals were released above the barrier. Tagged individuals in above- and below- barrier reaches were subsequently relocated and/or recaptured to track their movement. Most transplanted individuals displayed little movement or moved in an upstream direction only, while four individuals were last detected in the tidally influenced lower river. Five tagged, above-barrier individuals were found in below-barrier reaches, presumably washing over the falls. Of seven tagged trout captured in downstream migrant traps, two had smolted and one was a pre-smolt. The smoltification of at least some transplanted individuals, coupled with above-barrier ‘leakage’ of fish downstream, demonstrates the potential for resident trout to exhibit migratory behavior and to enter breeding populations of steelhead.

Introduction

Oncorhynchus mykiss is a polytypic species characterized by populations of resident, adfluvial, and fluvial rainbow trout as well as anadromous steelhead (Behnke 1992). In some cases, resident rainbow trout co-occur with anadromous individuals within the same waterbody, a phenomenon referred to as partial migration (Jonsson and Jonsson 1993). The underlying basis of the migratory polymorphism is poorly understood. Migratory polymorphism may be derived from phenotypic plasticity within a single gene pool or from fixed differences between sympatric but reproductively isolated populations. Reproductive isolation between sympatric life history morphs has been identified in various locations for anadromous and landlocked sockeye salmon (*Oncorhynchus nerka)* (Wood et al. 1999) and for Atlantic salmon (*Salmo salar*) (Vespoor and Cole 1989). However, using rearing experiments of controlled pairings of anadromous and resident parents, Nordeng (1983) demonstrated that resident and migratory Arctic char (*Salvelinus alpinus*) were from the same gene pool and that migration was environmentally controlled.

Whether resident rainbow trout and anadromous steelhead represent a randomly mating gene pool or exhibit reproductive isolation has significant implications for the study and management of steelhead populations in California, which have undergone precipitous decline in recent years. Steelhead are listed under the U.S. Endangered Species Act (ESA) as threatened in the northern California ESU (evolutionary significant unit) and elsewhere (U.S. Office of the Federal Register 1997, 2000). If resident and anadromous populations within a basin share a common gene pool, resident fish could be managed to buffer extinction risks to anadromous populations. Resident fish above barriers could provide a “reserve” gene pool in times of unfavorable ocean conditions and could recolonize recently available habitat (e.g. through dam removal) with anadromous progeny. Currently, resident populations of rainbow trout are not considered to be part of recognized steelhead ESUs. Busby et al. (1996) acknowledged that resident populations that inhabit areas upstream from numerous smaller barriers in California might contain genetic resources similar to those of anadromous fish in the ESU, but they concluded that little information is available on these fish or the role they might play in conserving natural populations of steelhead.

The objectives of this study were to determine if rainbow trout isolated above waterfalls in a northern California stream would exhibit migratory behavior when individuals were relocated to downstream reaches with access to the Pacific Ocean, and to compare growth and movement between above- and below-barrier populations. We also sought to estimate the extent of genetic differentiation between above- and below-barrier populations of the fish, and to determine the anadromous versus resident parentage of above-barrier individuals.

Study Site

This study was conducted in Freshwater Creek, a 4th order coastal stream in northern California (Figure 1). Freshwater Creek was selected for study for several reasons. It offers a barrier to upstream steelhead migration in the form of a waterfall on its upper mainstem, with a small population of resident rainbow trout above the barrier. The origin and history of the above-barrier population is not known, but there are no records that suggest at least recent stocking. Steelhead escapement is tracked by the Humboldt Fish Action Council at a permanent weir. Finally, during the period of this study, the

California Department of Fish and Game (CDFG) monitored all life-cycles of salmonid species occurring within the Freshwater Creek basin. This monitoring effort, which included use of smolt traps and stationary and portable antenna systems for detecting PIT-tagged fish within all major tributaries and in the mainstem, as well as electrofishing and snorkeling surveys, increased the probability of detecting tagged trout that were transplanted below the barrier.

Freshwater Creek empties into Humboldt Bay via a diked estuarine channel 8.8 km in length (Barnard 1992). The watershed is 67.3 km^2 in area, 75% of which is managed for industrial timber production from upslope forests of redwood (*Sequoia sempervirens*) and Douglas fir (*Pseudotsuga menziesii*). The mainstem and five major tributaries provide approximately 30 km of habitat for anadromous salmonids (Ricker 2006). The upstream limit to anadromous migration on the mainstem occurs at the base of a waterfall (40º 44' 18.27"N, 124 º 00' 04.47"W) that is approximately 16 km from the mouth of the creek as it enters estuarine slough. The waterfall is 5 m high at summer baseflow, and does not present noticeable step pools to allow for fish passage. Several smaller waterfalls lie upstream of this barrier. Land upstream from the waterfalls is undeveloped and largely roadless.

The salmonid assemblage in Freshwater Creek includes Chinook salmon (*Oncorhynchus tshawytscha*), coho salmon (*O. kisutch*), coastal rainbow trout/steelhead (*O. mykiss irideus*), and coastal cutthtroat trout (*O. clarki clarki)*. Other fishes present include prickly sculpin (*Cottus asper*), coast range sculpin (*Cottus aleuticus*), Pacific lamprey (*Entosphenus tridentatus*), brook lamprey (*Lampetra pacifica*) and three spine stickleback (*Gasterosteus aculeatus*).

The experiment was conducted from October 2005 to October 2007. During the period of study, mainstem flows averaged 0.71 m^3/s (25 ft^3/s) during summer months, and were highly variable in winter. A peak discharge of 15.9 m^3/s (563 ft^3/s) during the study occurred in December 2005. Based on prorating flow from an adjacent watershed with a 30-y record (Bigelow 2003), the exceedance probability for this event was two percent. Climate in the region is characterized as marine west coast. Annual average precipitation is 100-200 cm, approximately 75% of which falls as rain between November and March.

Methods

Transplantation experiment.—Above-barrier fish were sampled by electrofishing during three sampling events in 2005 and 2006 (October 2005, July 2006, and October 2006) to obtain a total sample of 131 individuals that were greater than or equal to 100 mm fork length. Captured fish that were greater than or equal to 100 mm fork length were anaesthetized with a solution of tricaine methanesulfonate (MS-222) and implanted with a 23mm passive integrated transponder tag. Coding of tag numbers was coordinated with the on-going CDFG program to ensure that duplicate tag numbers were not assigned. Tagged fish were weighed to the nearest 0.01g, and measured to the nearest mm. Fish that were less than 100mm in fork length were quantified and identified as 0+ (less than 60 mm fork length) or 1+ (greater than 60 mm fork length). Scale samples and caudal fin clips were taken from all fish greater than or equal to 100 mm in fork length. Fin clips were air dried and stored in a freezer until the time of analysis. Fin clips were frozen for a maximum of 1 year before being analyzed. Tagged fish were allowed to recover in an oxygenated bucket for approximately 10 minutes, or until recovery was complete.

Approximately half of the set of tagged individuals during any sampling event was released at the location of capture (total n=66). The other half of the sample of tagged individuals was transported in an aerated 5 gallon bucket to a location approximately 0.5 km downstream from the barrier (total n=65). Individuals were randomly assigned to an above- or below-barrier release location. Transplanted fish were released in the mainstem between 86 meters and 179 meters upstream of the South Fork confluence (Figure 1). This location was upstream from all stationary antennas and provided the potential for a maximum amount of data on fish re-sighting. From this location fish had unobstructed access to the Pacific Ocean.

Several methods were used to relocate and/or recapture transplanted individuals. Tagged fish transplanted below the waterfall were detected without capture using portable PIT tag interrogation systems and as they moved through stationary streamwidth antennae systems. Interrogation systems recorded the PIT tag number of the fish as well as the time of detection. Tagged fish were also captured in downstream migrant traps and during juvenile abundance and bi-annual night-dive surveys. Tagged fish above the barrier were recaptured by electrofishing operations in the fall of 2006 and 2007.

Stationary antennae were located in the lower mainstem near Howard Heights Road in the town of Freshwater, in the upper mainstem just upstream of the South Fork confluence (the furthest upstream major tributary confluence), and in the tributary mouths of South Fork, Cloney Gulch, Graham Gulch, and McCready Gulch, immediately upstream from their confluence with the mainstem (Figure 1). The lower mainstem site is 13 km upstream of the mouth of Freshwater Slough, and occasionally experiences tidal influence (Humboldt Bay Watershed Advisory Council 2005). An antenna consisted of a single loop of braided copper electrical wire formed into a rectangle, with the bottom of the rectangle buried in the substrate and the top of the rectangle positioned above the surface of the stream. Size of the antenna varied with stream width, and ranged from 1.3 meters by 3.8 meters to 1 meter by 9.75 meters. Two antennae were located at each site, approximately 2 m apart, to allow direction of tagged fish to be determined and to enable capture efficiency to be evaluated. Antennae detected the presence of 23 or 32 mm PIT tags. Detection data were recorded onto a battery-powered data logger circuit board from Oregon RFID ™, and records were uploaded weekly to a PDA (Palm Pilot M130™). The antennae were operated year-round by CDFG during this study, except during high-flow storm events. When in operation, antenna detection rate was close to 100%.

The mobile PIT tag reader was a battery-powered backpack unit and wand resembling a battery-powered electrofisher. The same hardware used for the stationary antennae was fit onto a backpack frame and enclosed within waterproof housing. The antenna ran from the backpack through a 2 m length of PVC tube and ended in a 61cm diameter circular antenna. PIT tags could be read within approximately 1 meter of the end of the wand, with individual tag numbers and a time stamp, as well as location, recorded directly onto a PDA M130. The mobile PIT tag reader was used during coordinated watershed surveys conducted by CDFG from May-June and again in October during both years of the study.

Tagged fish were also potentially detected in downstream migrant traps. Downstream migrant traps were operated by the CDFG Anadromous Fish Research and Monitoring Program (AFRAMP) throughout the basin from March through June of each year, in locations immediately upstream from stationary antennae. Pipe traps were deployed in each of the five major tributaries as well as on the upper mainstem, while a floating inclined plane trap (a.k.a. scoop trap) was deployed at the lower mainstem. In addition to these 7 traps, a pipe trap for capturing outgoing smolts was also operated at the weir, which is located 4 km below the lower mainstem site (Howard Heights) in the upper estuarine slough (Wallace 2003). Trap descriptions are provided in Ricker (2006). Fish captured in migrant traps were scanned for the presence of PIT tags. Tagged fish were measured (±1 mm fork length), weighed (± 0.1g), and classified as smolt, presmolt, or resident following visual examination of body morphology, spotting, coloration and skin silvering (Viola and Schuck 1995). Smolts were distinguished by their fusiform body shape, light color with silvery sides and a white belly. Both body morphology (Beeman 1995) and skin reflectance (Haner 1995; Ando et al. 2005) have been successfully used to discriminate between fish that are smolting, and those that or are not. Location of capture and PIT tag number were recorded, and a scale sample of the fish were taken for age and growth analysis. After processing, fish were released downstream from the trap.

Basin-wide summer juvenile abundance surveys conducted by the CDFG provided another opportunity for recapture of tagged fish. Surveys were conducted from 1 Aug to 1 October in 2005, 2006, and 2007 using a modified Hankin and Reeves (1988) protocol employing dive counts calibrated with electrofishing. Fish captured by electrofishing were scanned for the presence of tags. Recaptured fish were measured and weighed, scale samples were collected, and the location of recapture was recorded. Finally, fish were potentially recaptured during bi-annual night dives conducted by CDFG. Night dives were conducted in pool habitats on the Upper Mainstem and South Fork of

Freshwater Creek from June 10 to July 10 in 2005, from June 10 to July 1 in 2006, and from October 1 – November 1 in 2006. During these dives, fish that were detected and immobilized with a flashlight were captured with a dip net. Individuals were measured and weighed, and scanned for the presence of a PIT tag.

Otolith Microchemistry.— Otolith samples collected from a small sample of above-barrier trout (n = 5) were analyzed for strontium:calcium (SR:CA) ratios in the otolith primordial and freshwater growth regions to determine whether the above barrier population was derived from resident or anadromous maternal parentage. The ability of this analysis to distinguish parentage is based on: a) the substitution of strontium for calcium in the calcium carbonate matrix of the otolith at levels relative to the SR:CA ratio in the environment; b) higher SR:CA ratios in seawater than in freshwater; and c) yolk precursors, the composition of which is reflected in otolith primordium, develop in the ocean for anadromous forms (Zimmerman and Reeves 2002). Otoliths were cleaned and prepared following methods in Wells et al. (2003), and Sr/Ca ratios were analyzed by the USGS Alaska Science Center. Ratios were measured at 10 points each within the primordial and freshwater growth regions, and we compared with two-tailed paired *t* tests. A higher SR:CA ratio in the primordial than in the freshwater growth region of an otolith suggests an anadromous origin of the maternal parent, while the lack of a difference between the two regions suggests a resident origin.

Genetic Analysis.— Fin clips from 18 above-barrier trout were analyzed, using restriction fragment length polymorphism (RFLP) technologies, to determine probable genotypes. Genotype analysis determined the extent of hybridization between rainbow trout and coastal cutthroat trout occurred in the above barrier population. Genotyping was conducted according to methods developed by Baumsteiger et al. (2005). In addition to the eight markers (7 nuclear DNA and 1 mitochondrial DNA) used by Baumsteiger et al. (2005), we also analyzed Occ-42, OM-47, Occ-35 and Occ-38 loci with forward and reverse primers. These are insertion/deletion loci that do not require cutting with restriction enzymes before genotyping. Differentiation at the p53 locus used by Baumsteiger gave unreliable results and was therefore not used. Nuclear and mitochondrial markers were chosen that were fixed for alternate alleles in coastal cutthroat trout and rainbow trout. Genetic analyses were conducted in the Genetics Laboratory at Humboldt State University.

Growth Analysis.— Length-mass relationships of rainbow trout between above- and below-barrier reaches were compared by covariance analysis to assess whether potential differences in life history expression were associated with differences in growth. Because many of the trout scales lacked a detectable 1st year annulus, we were unable to compare growth through analysis of fish length or mass at age. Smolts and presmolts were excluded from the length-mass dataset, as were transplanted individuals. Transplanted trout were excluded because they may not experience the same growth opportunities as established residents. Length-mass relationships were compared for each of the two years of the study.

Movement Analysis.— We graphically examined direction and distance traveled by transplanted trout, and compared distance traveled between transplanted individuals and below-barrier residents. Distance traveled represented the distance from the location of release (for transplanted individuals) or tagging (for below-barrier residents) to the location of last detection. Individuals greater than 100mm in fork length tagged during fall night dive surveys in the below-barrier population within 100m downstream and 3200 m upstream of the transplant location were used for movement comparisons. Individuals tagged during night dive surveys were used due to their indeterminate life histories and proximity in size to the transplant group. Movement was determined by a combination of detections from stationary and mobile antennae, and captures in downstream migrant traps. In a few instances, moribund individuals were detected, and these were determined to have moved only to the point of their last live capture.

Results

Above-barrier population.— All fish captured above the waterfall were field identified as rainbow trout. Although the population was not sampled with an objective of characterizing population structure, we observed that subyearling fish were sparse and that the population was dominated by yearling and older fish (Figure 2). Gradient of the above-barrier reach was steep, and habitat was characterized as a series of small step-pools within a confined channel. Typically only 1-3 trout inhabited a pool, and many of the pools without trout were occupied by large (>200mm) Pacific giant salamanders (*Dicamptodon tenebrosus*). Individuals selected for release below the waterfall ranged from 100mm - 226mm in fork length.

The age and size structure of the above-barrier population appeared to differ greatly from that of the below-barrier population into which they were transplanted (Figure 3). While the above-barrier population was sparse and consisted primarily of yearling and older resident trout, the below-barrier assemblage was dominated by young- of- year progeny of anadromous *O. mykiss* in assemblages that also included juvenile cutthroat trout and coho salmon.

Above-barrier trout were determined to have maternal parents of freshwater rather than anadromous origin. Differences in SR:CA ratios were not detectable between primordial and freshwater growth regions of the five otoliths that were examined (two-tailed paired *t* tests, df = 9, all $p > 0.05$, Table 1).

Genetic analysis of above-barrier rainbow trout indicated that all individuals within the sample showed some degree of introgession with coastal cutthroat trout, with preferential backcrossing towards *O. mykiss* (Fig. 4). This population structure is indicative of a hybrid swarm consisting of an initial population with a higher proportion of *O. mykiss* individuals. The mitochondrial ND-1 marker indicated that all of the genotyped individuals were progeny of *O. mykiss* females. Rainbow trout-cutthroat trout hybrids have also been found in below-barrier reaches of Freshwater Creek, however the majority (84.6%) of below-barrier hybrids showed preferential backcrossing with cutthroat trout rather than rainbow trout (Hans Voight, draft MS thesis, Humboldt State University).

Growth.— Length-mass relationships did not differ between above- and below-barrier rainbow trout in Freshwater Creek in 2006 or 2007 ($F= 0.43$, $p = 0.51$ in 2006 and $F = 0.85$, $p = 0.36$ for 2006 and 2007, Figures 5 and 6).

Movement.— Movement of transplanted fish varied considerably among individuals (Fig. 7). More than two-thirds of the trout that were transplanted below the barrier to anadromy were re-sighted or recaptured during the two year study ($n = 44$ of 65 transplanted fish). Stationary antennae and portable PIT tag readers were approximately equally effective in detecting tagged fish, with the portable reader providing detections of 30 individuals, and the stationary antennae providing detections of 27 individuals (Appendices A, B, and C). Downstream migrant traps captured seven tagged trout (Appendix D). Tagged trout were not detected in summer juvenile abundance surveys or during fall and summer night dives. Most of the detected individuals (n = 26) remained within 500 m of the release location in all sightings. Upstream movement was observed in 4 of the transplants, with 2 individuals last detected within 300 m of the waterfall, approximately 4.5 km from the release location. Transplanted individuals were never subsequently detected above the waterfall. Eight individuals traveled in a downstream direction while still remaining in freshwater. Of these, only one entered and remained in a tributary. In a 5-d period, a single individual traveled over 6 km downstream, entering three separate tributaries before returning to the mainstem, whereupon it entered tidally influenced water and returned within hours to the non-tidal mainstem. Four individuals traveled downstream from the release location and were last detected in tidally influenced waters. All individuals last detected in tidal water moved there within one year of their release below the waterfall. For three of the individuals, the last detection occurred in spring; for one individual, it occurred immediately preceding a storm event in December 2006. Capture of transplanted trout in downstream migrant traps allowed assessment of smolting status. Of the 5 transplanted trout that were captured, one was determined to have smolted (Fig. 8), and a second was determined to be a pre-smolt.

Distance and direction of movement was not noticeably associated with fish size. Mean length of trout that were last detected in tidally influenced water was 143 mm FL (n = 4, range 125mm-185mm), and mean length of trout that moved less than 5 km from the release location was 146 mm (n = 38, range = 104 – 226).

The percentage of transplanted trout (6%, or 4 of 65 transplants) that moved into tidally influenced water did not appear to be different from the percentage of prior downstream residents (4%, or 9 of 210 individuals greater than 100mm in fork length) that were captured and tagged in the vicinity of the transplant release location and later captured in tidally influenced water.

Five tagged individuals that were released above the barrier were found alive below the barrier in Freshwater Creek. Two of these individuals were recaptured in the downstream migrant trap on the lower mainstem, where it was determined that one had smolted, and one had not. Two tags from moribund individuals that were released above the waterfall were also discovered near the base of the waterfall. All tags from the above-barrier release group that were found below the barrier were from individuals captured within 1000 m upstream of the waterfall.

Discussion

Movement patterns displayed by the transplanted fish in our study may have been biased by the act of transplantation, as the fish were introduced into downstream habitat already colonized with prior residents. Above-barrier residents enjoyed lower than equilibrium density following the removal of transplants. A reciprocal transplant of below-barrier individuals into above-barrier habitat would have completed the experimental design and strengthened the study, but we did not receive permission to undertake the reciprocal transplantation. Similarity of the length-mass relationship of above- and below-barrier trout suggests that the fish in both habitats experienced similar feeding opportunities, despite differing densities.

We have no direct evidence that any transplanted fish went out to sea. Adult returns of fish transplanted in 2005 and 2006 were not observed at the weir in 2007, and given the very low survivorship that characterizes salmonid populations in marine environments (Quinn 2005), it would be remarkable to observe any adult returns of these transplanted trout. The individuals that were last detected moving downstream from the trap and stationary antennae in the lower mainstem of the river were in or close to a saltwater transition area and may have been traveling to the estuary or sea, but this is only supposition. Morphological changes associated with smolting were directly observed in only two individuals, one of which was transplanted below the barrier, while the other was released above the waterfall and presumably washed over the falls. Nonetheless, evidence that even just two individuals smolted demonstrates the potential for resident trout to express migratory behavior and to enter breeding populations of steelhead trout.

Detection of tagged trout below the waterfall that were released above the waterfall also suggests the likelihood of some gene flow from above to below barriers. This is counter to the findings of Deiner et al. (2007), who concluded that trout populations above and below natural barriers on the same tributary were not interacting substantially of the basis of substantial differences they observed in genetic structure at 22 microsatellite loci. We abandoned planned genetic comparisons of above- and below-barrier populations after failing to identify pure strain rainbow trout above the waterfall.

The effect of hybridization on the movement patterns that we observed in the transplanted trout are unknown.

Genetic studies comparing sympatric populations of steelhead and resident trout generally support a conclusion that differences in population structure are associated with geographic proximity and genetic history regardless of life history type (Docker and Heath 2003, Olsen et al. 2006, McPhee et al. 2007), although some studies have reported some level of genetic divergence between the two life history types (e.g., Narum et al. (2004) in one of two Washington rivers; Docker and Heath (2003) in one of five river basins in British Columbia). Behnke (2002) argued that some amount of gene flow between coexisting resident rainbow trout and steelhead is likely in almost all settings, and that unambiguous genetic differentiation and reproductive isolation between the two life history types will be difficult or impossible to establish. Gene flow arises because steelhead populations typically contain a small proportion of residual males that mature sexually without having smolted, and they might then mate as "sneakers" with resident females (e.g., Seamons et al. 2004, McMillan et al. 2007). For this reason, Behnke contended that resolution of the fundamental question of whether 'like gives rise to like' (i.e. steelhead producing only anadromous progeny and resident rainbow trout producing only resident forms) should be addressed with nongenetic studies. We concur, and add that inferences of genetic differentiation between populations are based on extent of overlap of a very small number of loci chosen for examination. Dating back to the development of taxonomic classification by Linnaeus in the 1700s, taxonomic separations have been based on morphological and behavioral differences that are likely to lead to reproductive isolation. Yet the loci selected for use in genetic analyses generally have an unknown and likely minimal correspondence with the loci controlling the morphological characters and behaviors important in reproductive isolation.

A few studies provide nongenetic evidence that anadromous steelhead and resident rainbow trout forms can be derived from one another. Zimmerman and Reeves (2000) analyzed strontium–calcium ratios in otoliths to determine the parentage of individuals in sympatric populations of steelhead and resident rainbow trout. In the Babine River in British Columbia, 1 of 24 steelhead were determined to have a rainbow trout mother and 2 of 9 resident rainbow trout had steelhead mothers, whereas in the Deschutes River in Oregon, all steelhead had steelhead mothers, and all resident rainbow trout had resident mothers. This suggests that reproductive isolation between coexisting steelhead and resident rainbow trout may have to be evaluated on a case by case basis. Pascual et al. (2001) documented the presence of an anadromous run of rainbow trout in a Patagonian river from introduced rainbow trout, although it is not clear whether the anadromous run are descendents of California steelhead or instead derived from resident fish that developed the behavior secondarily. Thrower et al. (2004) crossed wild steelhead and resident, lake-dwelling rainbow trout originally derived from the same anadromous stock 70 years earlier, and studied growth and life history transitions of progeny within and between lines. The lake population was isolated above waterfalls that prevented upstream migration, and thus there was strong selection against smolting in this population. Yet all crossings produced significant numbers of age 2 smolts, even in progeny of lake x lake pairs. They suggested that the genetic potential for smolting can lie dormant or be maintained through a dynamic interaction between smolting and early maturation for decades even in the presence of selection against a migratory phenotype.

Our study adds to this body of evidence of the potential reversibility of life history pathways, and to our knowledge is the first to study behavior of resident rainbow trout experimentally transplanted below a barrier to upstream migration.

In our study, the lengths of (192 and 203 mm FL) of the two tagged fish that smolted were larger than the typical lengths of steelhead smolts in the basin. Ricker (2004) reported that median fork length of steelhead smolts in the basin ranges from 81 – 146 mm. Sexual maturation and smolting are presented as requiring mutually incompatible developmental conversions (Thorpe 1986 and 1987), and generally trout that mature sexually as parr do not smolt and go to sea (Nordeng, 1983; Johnsson 1985; Jonsson and Jonsson1993). However, Shapovalov and Taft (1954) reported evidence of *O. mykiss* maturing in freshwater and spawning prior to their first ocean migration. Busby et al. (1996) mentioned that this life history variant has also been described for cutthroat trout and some male Chinook salmon. Whether the two fish that smolted in this study had previously matured and spawned in freshwater is unknown, as scale analysis was inconclusive.

Our findings have important conservation and management implications. The National Marine Fisheries Service recently ruled that distinct population segments (DPSs) of steelhead subject to protection under the U.S. ESA would be considered separately from resident O. mykiss (National Marine Fisheries Service, NMFS 2005), based on distinct physical, physiological, ecological, and behavioral differences between anadromous and resident forms. The leakage of above barrier resident trout to downstream reaches that we observed, evidence that resident trout can transform into migratory individuals, and similarity of movement between transplanted trout and prior residents of downstream reaches, suggests that exclusion of the resident trout from protection and recovery efforts afforded to steelhead would be misguided, at least in the Freshwater Creek Basin.

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Table 1. Strontium:Calcium (SR:CA) ratios in the primordium and freshwater growth regions in the otoliths of 5 above-barrier rainbow trout in Freshwater Creek. Ratios were determined at 10 points in each of the two regions on each otolith. Standard deviations are given in parentheses. *P* indicates the significance of the difference between the two otolith regions.

Otolith	SR:CA primordium	SR:CA freshwater growth region	*P*
1	0.001257 (6.8E-05)	0.00122 (8.8E-05)	0.76
2	0.001099 (0.00011)	0.00096 (8.2E-05)	0.98
3	0.001098 (7.8E-05)	0.00106 (8.8E-05)	0.67
4	0.001132 (8.7E-05)	0.00125 (0.00013)	0.93
5	0.00127 (8.9E-05)	0.00107 (3.4E-05)	0.99

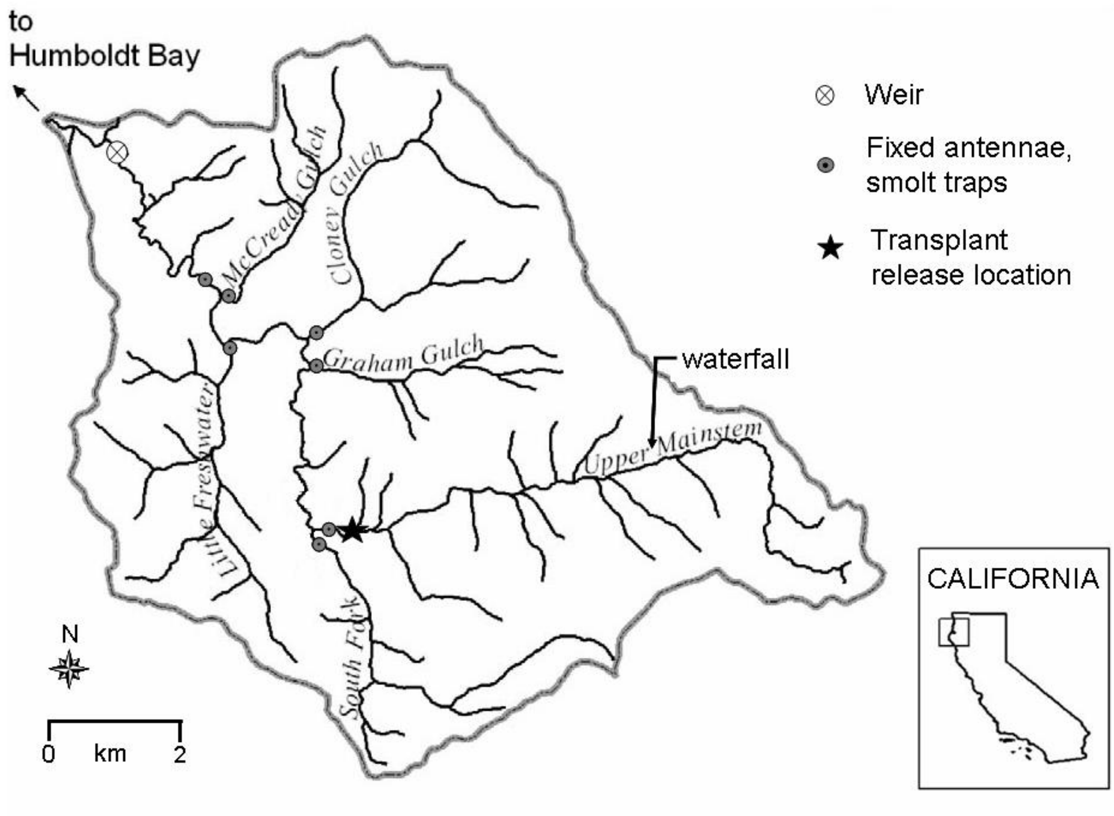

Figure 1. Freshwater Creek watershed, showing locations of the waterfall, smolt traps and stationary antennae, and weir, as well as location where above-barrier trout were were released.

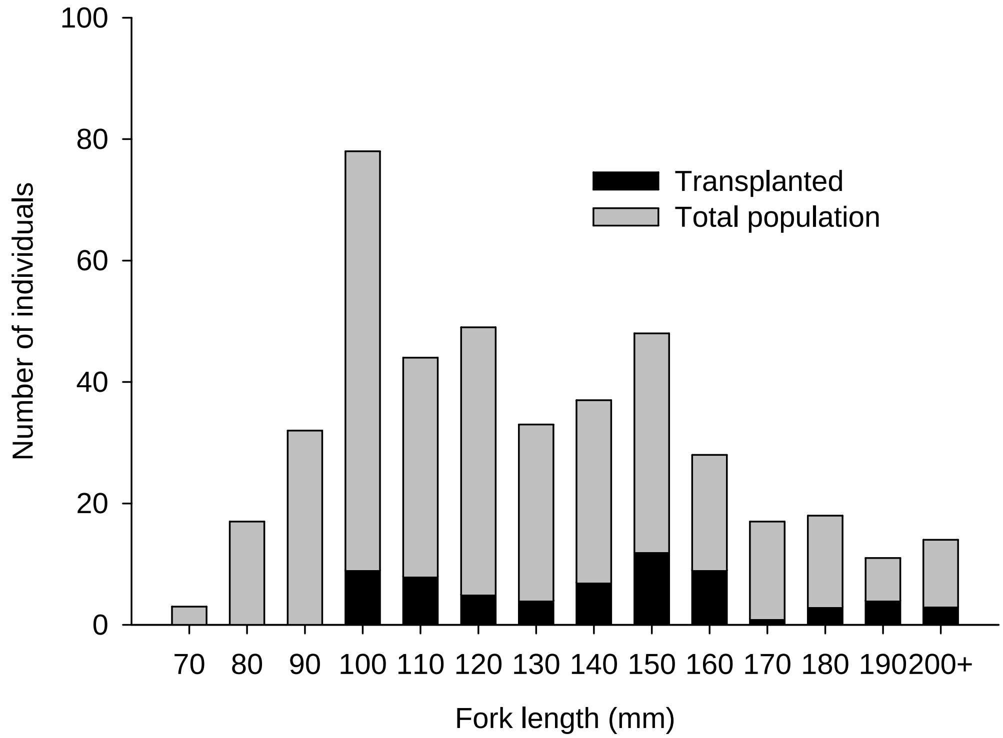

Figure 2. Size frequency relationships for the above-barrier population of rainbow trout in Freshwater Creek, CA, and for the sample of above-barrier individuals (n = 65) that were transplanted below the waterfall. Fish were captured above the waterfall during 4 sampling events over the period of study from October 2005 to July 2007.

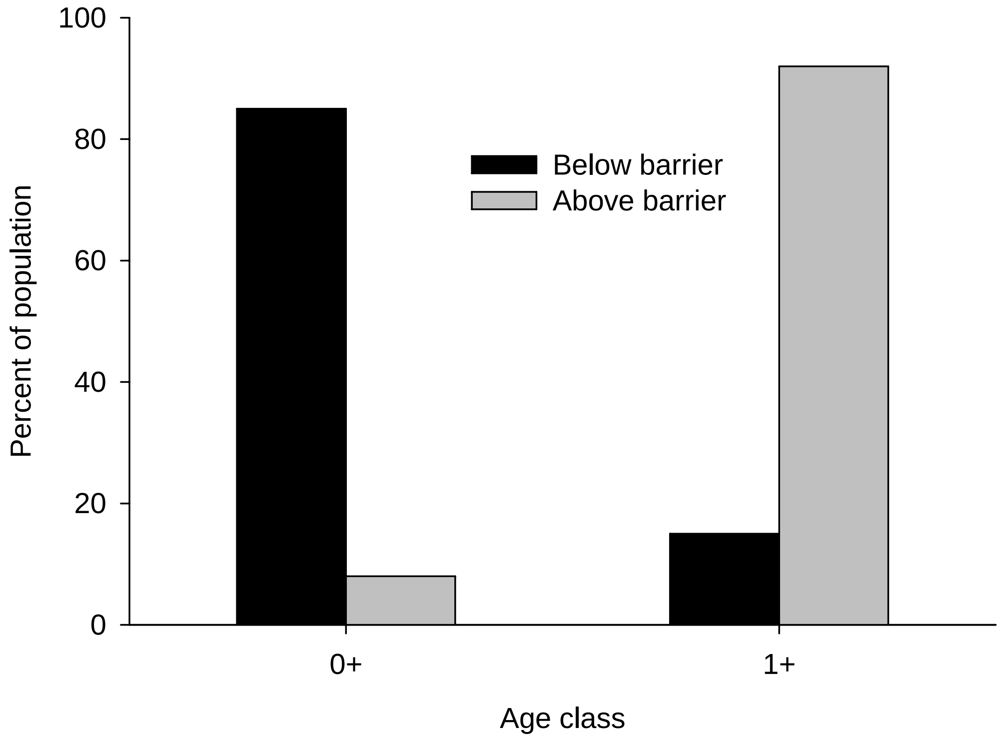

Figure 3. Age class frequency of rainbow trout above the waterfall (n = 364) and below the waterfall (n = 1300) in Freshwater Creek, CA.

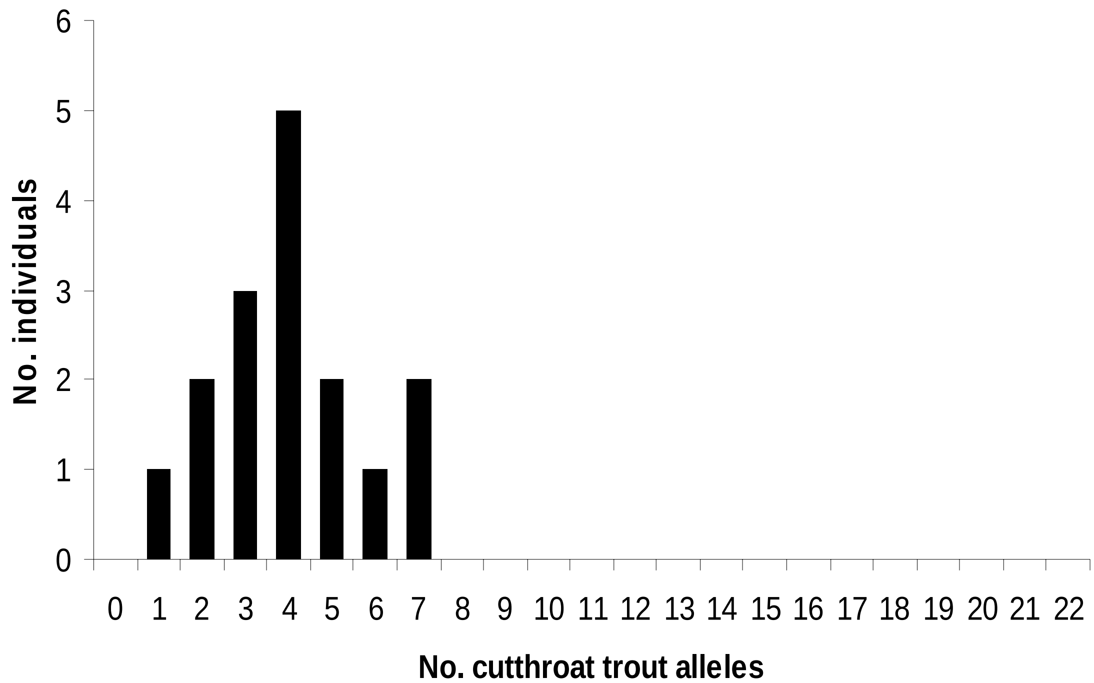

Figure 4. Allelic frequency of 18 above-barrier individuals at 11 differentiating loci, with zero alleles representing pure strain *O. mykiss*, 22 representing a pure strain *O. clarki clarki*, and 11 alleles representing a putative F1 hybrid.

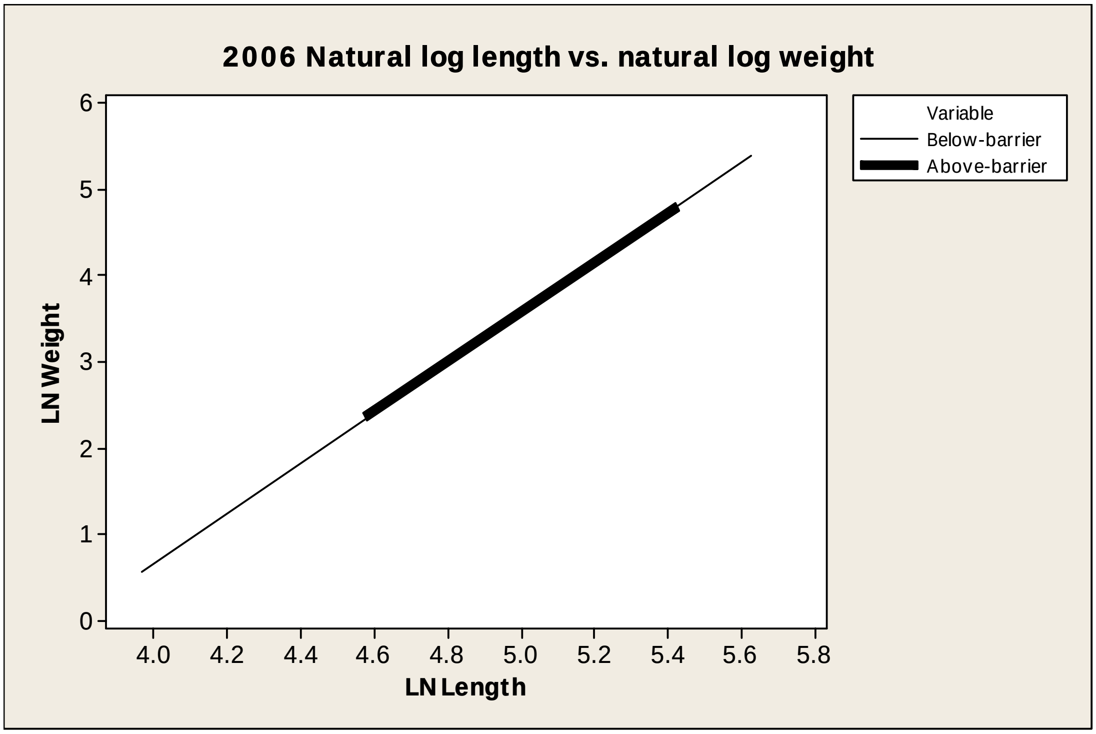

Figure 5. Length-mass relationships of above- and below-barrier rainbow trout in Freshwater Creek, CA in 2006.

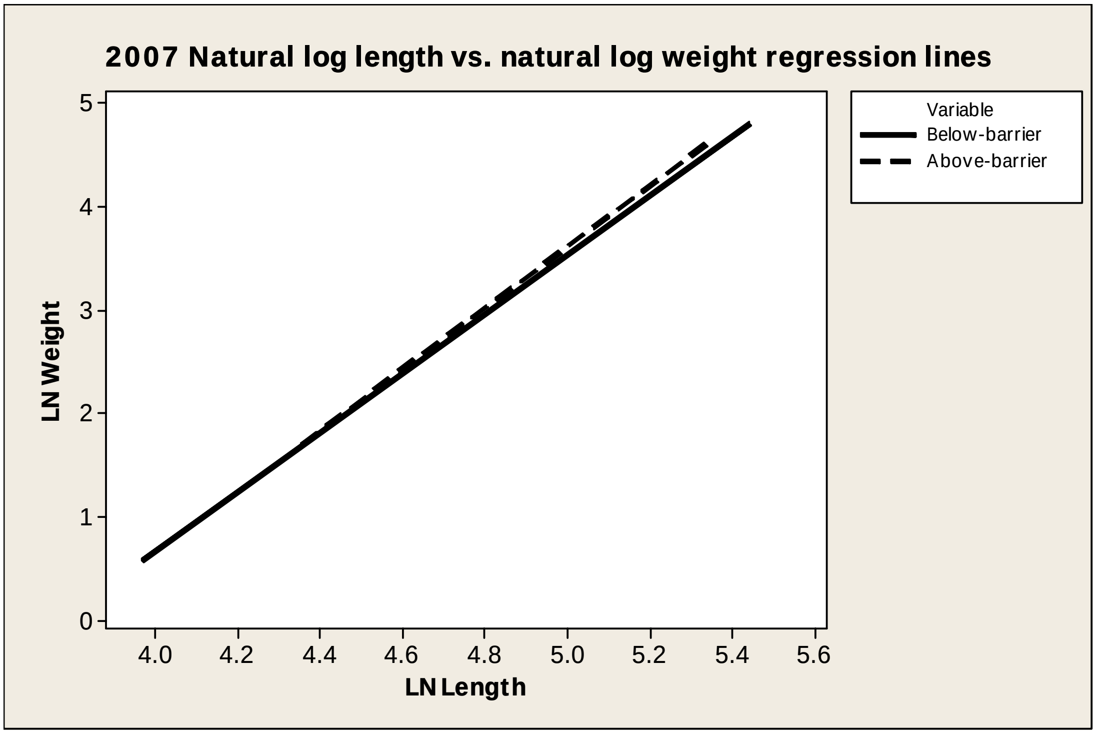

Figure 6. Length-mass relationships of above- and below-barrier rainbow trout in Freshwater Creek, CA in 2007.

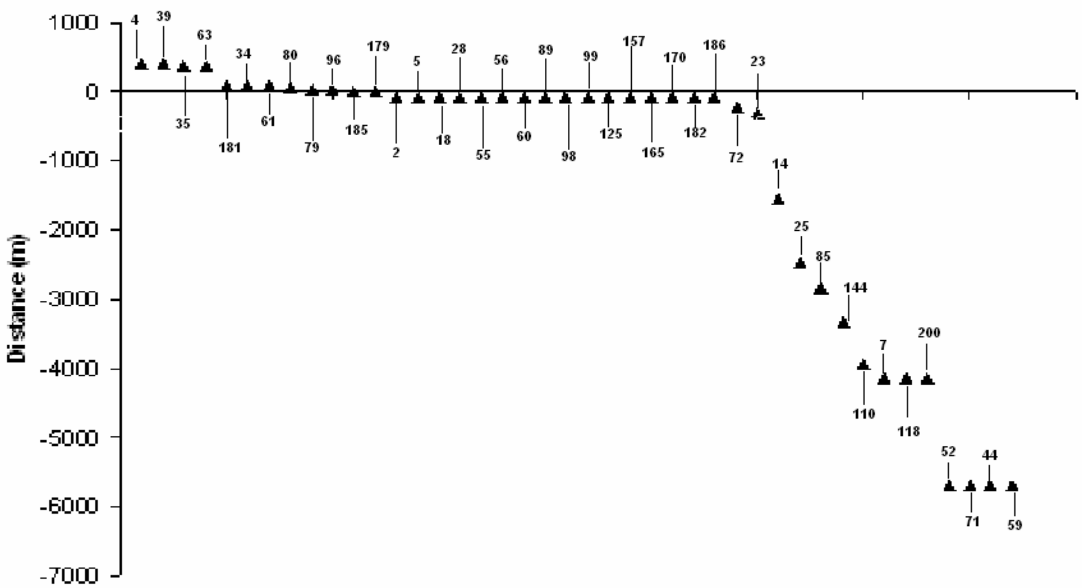

Figure 7. Distance (m) traveled by transplanted trout from release location to last known live location. Negative numbers represent downstream movement while positive numbers represent upstream movement. Each point represents one transplanted individual, identified by the final digit(s) of its PIT tag code (Appendix A). Individuals that passed 5860m downstream from the release point entered tidally influenced water.

Figure 8. Top: Photo of above-barrier trout at time of initial capture above the waterfall on Freshwater Creek, CA; Bottom: Photo of a transplanted trout (# 44, Appendix D) recaptured in a downstream migrant tap 183 days following its release. At release, the fish measured 185 mm FL and weighed 82 g. At recapture, the fish increased 7 mm in length, and lost 12 g.

APPENDIX A. Identity, transplant status (yes or no), and subsequent detection of tagged above-barrier rainbow trout in below-barrier stationary or portable PIT tag interrogation systems or capture in downstream migrant traps during the 2 y study. PIT # gives the final digit(s) of the PIT tag code. Tagged trout that were not transplanted were released in the above-barrier reach. A value of 0 indicates the absence of detection or capture; a value of 1 indicates detection or capture in an interrogation system or trap, but not frequency of detection.

PIT #	Transplanted (Y/N)	Stationary antennae	Mobile PIT tag reader	Downstream migrant trap
1	N	0	0	0
2	Y	1	0	0
3	Y	0	0	0
4	Y	0	1	0
5	Y	1	0	0
6	Y	0	0	1
7	Y	1	0	0
8	N	0	0	0
9	Y	0	0	0
10	N	0	0	0
11	N	0	0	0
12	Y	0	0	0
13	Y	0	0	0
14	Y	1	1	0
15	N	0	0	0

PIT #	Transplanted (Y/N)	Stationary antennae	Mobile PIT tag reader	Downstream migrant trap
16	N	0	0	0
17	Y	0	0	0
18	Y	1	0	0
19	N	0	0	0
20	N	0	0	0
21	N	0	0	0
22	N	0	0	0
23	Y	0	1	1
24	N	0	0	0
25	Y	1	0	0
26	Y	0	0	0
27	N	0	0	0
28	Y	1	1	0
29	N	0	0	0
30	N	0	0	0
31	Y	0	0	0
32	N	0	0	0
34	Y	0	1	0
35	Y	0	1	0
37	N	0	0	0
38	N	0	0	1
39	Y	0	1	0

PIT #	Transplanted (Y/N)	Stationary antennae	Mobile PIT tag reader	Downstream migrant trap
40	N	0	0	0
41	N	0	0	0
42	N	0	0	0
43	N	0	0	0
44	Y	0	0	1
45	N	0	0	0
46	Y	0	0	1
47	Y	0	0	0
48	N	0	0	0
49	N	0	0	0
50	N	0	0	0
51	N	0	0	0
52	Y	1	1	0
53	Y	0	0	0
55	Y	1	0	0
56	Y	1	0	0
57	Y	0	0	0
58	N	0	0	0
59	N	0	0	1
60	Y	1	1	0
61	Y	1	1	0
62	N	0	0	0

PIT #	Transplanted (Y/N)	Stationary antennae	Mobile PIT tag reader	Downstream migrant trap
63	Y	0	1	0
64	Y	0	0	0
65	N	0	0	0
66	N	0	0	0
67	Y	0	0	0
68	N	0	0	0
69	Y	0	0	0
70	N	0	0	0
71	Y	1	1	0
72	Y	1	1	0
73	N	0	0	0
74	N	0	0	0
75	Y	0	0	0
76	N	0	0	0
77	N	0	0	0
78	N	0	0	0
79	Y	0	1	0
80	Y	0	1	0
81	Y	0	0	0
82	N	0	0	0
83	Y	0	0	0
84	N	0	0	0

PIT #	Transplanted (Y/N)	Stationary antennae	Mobile PIT tag reader	Downstream migrant trap
85	Y	0	1	0
86	N	0	0	0
87	N	0	0	0
88	Y	0	0	0
89	Y	1	0	0
90	N	0	0	0
91	N	0	0	0
92	N	0	0	0
93	N	0	0	0
94	N	0	0	0
95	N	0	0	0
96	Y	0	1	0
97	Y	0	0	0
98	Y	1	1	0
99	Y	1	0	0
100	Y	0	0	0
107	N	0	0	0
110	Y	0	1	0
114	N	0	0	0
116	Y	0	0	0
117	N	0	0	0
118	Y	1	1	0

PIT #	Transplanted (Y/N)	Stationary antennae	Mobile PIT tag reader	Downstream migrant trap
119	N	0	0	0
120	N	0	0	0
121	N	0	0	0
123	N	0	0	0
125	Y	1	0	0
130	N	0	0	0
135	N	0	0	0
139	N	0	0	0
144	Y	0	1	0
145	N	0	0	0
157	Y	1	1	0
158	Y	0	0	0
164	N	0	0	0
165	Y	1	0	0
167	N	0	0	0
170	Y	1	1	0
171	N	0	0	0
175	Y	0	0	0
177	Y	0	0	0
179	Y	0	1	0
181	Y	1	1	0
182	Y	1	0	1

PIT #	Transplanted (Y/N)	Stationary antennae	Mobile PIT tag reader	Downstream migrant trap
185	Y	1	1	0
186	Y	1	0	0
187	N	0	0	0
188	N	0	0	0
197	N	0	0	0
200	Y	1	1	0

APPENDIX B. Date, time, direction of movement, and location of tagged, transplanted trout detected in pairs of stationary antennae within the Freshwater Creek basin. PIT # refers to the final digit(s) of the PIT tag code for each individual.

PIT #	Date	Time	Direction of movement	Location
2	12/1/2005	11:35:39	Upstream	Upper mainstem
5	11/15/2006	7:20:53	Downstream	South Fork confluence
	11/15/2006	16:52:23	Downstream	South Fork confluence
	11/15/2006	6:12:19	Upstream	Upper mainstem
7	11/20/2006	23:49:37	Downstream	Upper mainstem
	11/20/2006	19:11:34	Upstream	Upper mainstem
	11/20/2006	23:49:25	Upstream	Upper mainstem
	11/21/2006	8:34:27	Downstream	Upper mainstem
	2/11/2007	11:56:33	Downstream	Little Freshwater confluence
	2/11/2007	11:56:34	Downstream	Little Freshwater confluence
14	11/3/2005	21:25:33	Downstream	Upper mainstem
18	7/21/2006	3:25:11	Downstream	Upper mainstem
	7/21/2006	3:25:14	Downstream	Upper mainstem
	7/21/2006	3:22:41	Upstream	Upper mainstem
	7/21/2006	3:32:40	Upstream	Upper mainstem
25	12/18/2005	21:15:9	Upstream	Cloney Gulch confluence
	12/18/2005	21:50:37	Upstream	Cloney Gulch confluence
28	7/6/2006	6:13:51	Downstream	Upper mainstem

PIT #	Date	Time	Direction of movement	Location
	7/6/2006	21:38:26	Downstream	Upper mainstem
	7/6/2006	22:7:31	Downstream	Upper mainstem
	7/6/2006	6:20:40	Upstream	Upper mainstem
	7/6/2006	21:37:59	Upstream	Upper mainstem
	7/6/2006	22:9:44	Upstream	Upper mainstem
	7/11/2006	23:34:21	Downstream	Upper mainstem
	7/11/2006	23:34:36	Downstream	Upper mainstem
	7/11/2006	22:20:57	Upstream	Upper mainstem
	7/11/2006	23:38:39	Upstream	Upper mainstem
	7/16/2006	0:13:33	Downstream	Upper mainstem
	7/16/2006	0:10:53	Upstream	Upper mainstem
52	7/7/2006	0:18:28	Downstream	Upper mainstem
	7/7/2006	0:16:55	Upstream	Upper mainstem
	7/7/2006	0:16:56	Upstream	Upper mainstem
	11/14/2006	6:48:23	Downstream	Lower mainstem
	11/14/2006	6:48:11	Upstream	Lower mainstem
55	7/10/2006	5:51:42	Upstream	Upper mainstem
	7/10/2006	5:51:43	Upstream	Upper mainstem
	7/13/2006	11:6:19	Downstream	Upper mainstem
	7/13/2006	11:12:25	Upstream	Upper mainstem
	7/22/2006	22:35:5	Upstream	Upper mainstem
	7/23/2006	3:27:40	Downstream	Upper mainstem

PIT #	Date	Time	Direction of movement	Location
	7/23/2006	3:27:41	Downstream	Upper mainstem
56	11/15/2005	6:52:31	Downstream	Upper mainstem
	11/15/2005	6:47:43	Upstream	Upper mainstem
	11/26/2005	17:38:43	Downstream	Upper mainstem
	11/26/2005	17:40:35	Upstream	Upper mainstem
	11/30/2005	7:12:56	Downstream	Upper mainstem
	11/30/2005	6:50:46	Upstream	Upper mainstem
	11/30/2005	7:28:0	Upstream	Upper mainstem
	11/30/2005	7:28:8	Upstream	Upper mainstem
60	11/4/2005	7:19:43	Downstream	Upper mainstem
61	11/15/2006	6:56:38	Downstream	Upper mainstem
	11/15/2006	6:56:59	Downstream	Upper mainstem
	11/15/2006	6:44:32	Upstream	Upper mainstem
71	7/8/2006	0:20:37	Upstream	Upper mainstem
	7/8/2006	1:29:45	Upstream	Upper mainstem
	11/17/2006	9:55:31	Downstream	Lower mainstem
	11/17/2006	9:55:4	Upstream	Lower mainstem
	11/20/2006	11:46:53	Downstream	Lower mainstem
	11/20/2006	20:18:35	Downstream	Lower mainstem
	11/20/2006	11:47:50	Upstream	Lower mainstem
	11/20/2006	20:18:22	Upstream	Lower mainstem
72	7/7/2006	2:39:47	Downstream	Upper mainstem

PIT #	Date	Time	Direction of movement	Location
	7/7/2006	2:39:48	Downstream	Upper mainstem
	7/7/2006	2:38:54	Upstream	Upper mainstem
	7/7/2006	2:38:55	Upstream	Upper mainstem
89	1/23/2006	7:14:5	Downstream	Upper mainstem
	1/23/2006	7:14:6	Downstream	Upper mainstem
	1/23/2006	7:10:30	Upstream	Upper mainstem
	1/23/2006	7:10:31	Upstream	Upper mainstem
98	11/14/2006	13:13:50	Downstream	Upper mainstem
	11/14/2006	14:3:47	Downstream	Upper mainstem
	11/14/2006	13:13:43	Upstream	Upper mainstem
	11/21/2006	7:42:59	Downstream	Upper mainstem
	11/21/2006	8:19:11	Downstream	South Fork confluence
	11/21/2006	7:42:40	Upstream	Upper mainstem
	11/21/2006	8:33:11	Upstream	South Fork confluence
	11/21/2006	19:6:28	Upstream	South Fork confluence
	12/15/2006	7:10:25	Downstream	South Fork confluence
	12/15/2006	7:11:22	Downstream	South Fork confluence
	12/15/2006	7:22:22	Downstream	South Fork confluence
	12/15/2006	13:2:34	Downstream	South Fork confluence
	12/15/2006	17:9:7	Downstream	South Fork confluence
	12/15/2006	23:18:17	Downstream	South Fork confluence
	12/15/2006	23:36:24	Downstream	South Fork confluence

PIT #	Date	Time	Direction of movement	Location
	12/15/2006	7:20:11	Upstream	South Fork confluence
	12/15/2006	13:2:58	Upstream	South Fork confluence
	12/15/2006	17:8:45	Upstream	South Fork confluence
	12/15/2006	23:19:18	Upstream	South Fork confluence
	12/15/2006	23:35:35	Upstream	South Fork confluence
	12/16/2006	6:57:56	Downstream	South Fork confluence
	12/16/2006	16:40:44	Downstream	South Fork confluence
	12/16/2006	7:2:32	Upstream	South Fork confluence
	12/16/2006	8:18:1	Upstream	South Fork confluence
	12/17/2006	7:16:21	Downstream	South Fork confluence
	12/17/2006	7:17:5	Upstream	South Fork confluence
	12/17/2006	16:58:22	Upstream	South Fork confluence
	12/18/2006	5:25:56	Downstream	South Fork confluence
	12/18/2006	5:26:44	Upstream	South Fork confluence
	12/18/2006	5:37:35	Upstream	South Fork confluence
	12/19/2006	7:21:29	Downstream	South Fork confluence
	12/19/2006	16:59:13	Downstream	South Fork confluence
	12/19/2006	19:7:40	Downstream	Upper mainstem
	12/19/2006	21:42:11	Downstream	Upper mainstem
	12/19/2006	7:21:42	Upstream	South Fork confluence
	12/19/2006	16:59:10	Upstream	South Fork confluence
	12/19/2006	19:13:11	Upstream	Upper mainstem

PIT #	Date	Time	Direction of movement	Location
	12/19/2006	21:41:43	Upstream	Upper mainstem
	12/20/2006	5:27:24	Downstream	South Fork confluence
	12/20/2006	5:27:31	Downstream	South Fork confluence
	12/20/2006	17:15:52	Downstream	South Fork confluence
	12/20/2006	19:3:25	Downstream	South Fork confluence
	12/20/2006	5:28:15	Upstream	South Fork confluence
	12/20/2006	17:15:46	Upstream	South Fork confluence
	12/20/2006	19:4:16	Upstream	South Fork confluence
	12/21/2006	6:52:50	Downstream	South Fork confluence
	12/21/2006	9:36:50	Downstream	South Fork confluence
	12/21/2006	9:44:17	Downstream	South Fork confluence
	12/21/2006	13:15:4	Downstream	Upper mainstem
	12/21/2006	6:50:37	Upstream	South Fork confluence
	12/21/2006	9:37:6	Upstream	South Fork confluence
	12/21/2006	9:44:10	Upstream	South Fork confluence
	12/21/2006	13:19:33	Upstream	Upper mainstem
	12/28/2006	11:33:20	Downstream	South Fork confluence
	12/28/2006	13:27:4	Downstream	South Fork confluence
	12/28/2006	14:16:0	Downstream	South Fork confluence
	12/28/2006	15:33:48	Downstream	South Fork confluence
	12/28/2006	15:34:2	Downstream	South Fork confluence
	12/28/2006	16:23:4	Downstream	South Fork confluence

PIT #	Date	Time	Direction of movement	Location
	12/28/2006	23:5:52	Downstream	South Fork confluence
	12/28/2006	23:55:10	Downstream	South Fork confluence
	12/28/2006	11:34:0	Upstream	South Fork confluence
	12/28/2006	13:26:48	Upstream	South Fork confluence
	12/28/2006	14:16:54	Upstream	South Fork confluence
	12/28/2006	15:15:6	Upstream	South Fork confluence
	12/28/2006	15:39:59	Upstream	South Fork confluence
	12/28/2006	16:22:45	Upstream	South Fork confluence
	12/28/2006	23:7:59	Upstream	South Fork confluence
	12/29/2006	6:49:3	Downstream	Upper mainstem
	12/29/2006	6:52:17	Downstream	Upper mainstem
	2/23/2007	11:5:14	Downstream	South Fork confluence
	2/23/2007	12:7:16	Downstream	South Fork confluence
	2/23/2007	13:5:43	Downstream	South Fork confluence
	2/23/2007	13:37:51	Downstream	South Fork confluence
	2/23/2007	13:37:52	Downstream	South Fork confluence
	2/23/2007	11:55:31	Upstream	South Fork confluence
	2/23/2007	12:6:56	Upstream	South Fork confluence
	2/23/2007	13:10:25	Upstream	South Fork confluence
	2/23/2007	13:35:49	Upstream	South Fork confluence
99	12/3/2005	13:24:54	Downstream	Upper mainstem
	12/3/2005	13:42:32	Upstream	Upper mainstem

PIT #	Date	Time	Direction of movement	Location
	7/9/2006	21:44:56	Downstream	Upper mainstem
	7/9/2006	21:45:0	Downstream	Upper mainstem
	7/9/2006	21:43:30	Upstream	Upper mainstem
	7/9/2006	21:43:40	Upstream	Upper mainstem
118	11/18/2006	4:30:56	Upstream	Upper mainstem
	12/23/2006	11:25:57	Downstream	Little Freshwater confluence
	12/23/2006	14:32:7	Downstream	Lower mainstem
	12/23/2006	9:44:2	Upstream	Cloney Gulch confluence
	12/23/2006	11:26:5	Upstream	Little Freshwater confluence
	12/23/2006	13:4:22	Upstream	Lower mainstem
	12/23/2006	14:32:1	Upstream	Lower mainstem
	12/28/2006	9:25:55	Downstream	Little Freshwater confluence
	12/28/2006	9:26:3	Downstream	Little Freshwater confluence
	12/28/2006	9:46:58	Downstream	Little Freshwater confluence
	12/28/2006	9:46:59	Downstream	Little Freshwater confluence
	12/28/2006	9:26:11	Upstream	Little Freshwater confluence
	12/28/2006	9:46:54	Upstream	Little Freshwater confluence
125	7/10/2006	3:19:19	Upstream	Upper mainstem
	7/10/2006	3:20:20	Upstream	Upper mainstem
157	7/18/2006	4:29:0	Upstream	Upper mainstem
	7/18/2006	4:37:36	Upstream	Upper mainstem
165	7/11/2006	1:56:46	Upstream	Upper mainstem

PIT #	Date	Time	Direction of movement	Location
	7/11/2006	1:56:53	Upstream	Upper mainstem
170	11/20/2006	3:51:19	Upstream	Upper mainstem
	11/20/2006	3:51:31	Upstream	Upper mainstem
	12/18/2006	8:10:17	Downstream	South Fork confluence
	12/18/2006	8:10:46	Upstream	South Fork confluence
	12/18/2006	18:23:33	Upstream	South Fork confluence
	12/19/2006	16:59:27	Downstream	South Fork confluence
	12/25/2006	0:44:18	Downstream	Upper mainstem
	12/27/2006	10:23:34	Downstream	South Fork confluence
	12/27/2006	10:26:22	Upstream	South Fork confluence
	2/21/2007	11:28:45	Downstream	South Fork confluence
	2/21/2007	11:29:27	Downstream	South Fork confluence
181	11/16/2006	17:1:37	Downstream	Upper mainstem
	11/16/2006	16:59:31	Upstream	Upper mainstem
	11/17/2006	12:29:5	Downstream	Upper mainstem
	11/17/2006	12:29:34	Upstream	Upper mainstem
182	4/2/2007	13:22:58	Upstream	South Fork confluence
	4/2/2007	13:23:35	Upstream	South Fork confluence
185	7/10/2006	6:21:21	Upstream	Upper mainstem
	7/19/2006	13:4:27	Downstream	Upper mainstem
	7/19/2006	13:4:27	Upstream	Upper mainstem
	7/19/2006	13:4:33	Upstream	Upper mainstem

PIT #	Date	Time	Direction of movement	Location
	7/24/2006	12:44:41	Upstream	Upper mainstem
	4/9/2007	5:23:24	Upstream	Upper mainstem
186	7/12/2006	3:27:41	Downstream	Upper mainstem
	7/12/2006	4:39:54	Downstream	Upper mainstem
	7/12/2006	3:24:38	Upstream	Upper mainstem
	7/12/2006	3:24:47	Upstream	Upper mainstem
	7/12/2006	4:44:25	Upstream	Upper mainstem
	7/15/2006	4:29:39	Downstream	Upper mainstem
	7/15/2006	9:41:0	Downstream	Upper mainstem
	7/16/2006	20:45:54	Upstream	Upper mainstem
	7/16/2006	20:45:56	Upstream	Upper mainstem
200	11/16/2006	6:58:20	Downstream	Upper mainstem
	3/1/2007	18:4:59	Upstream	Lower mainstem
	3/2/2007	9:28:9	Upstream	Lower mainstem
	3/7/2007	8:0:20	Downstream	Little Freshwater confluence
	3/7/2007	8:0:21	Downstream	Little Freshwater confluence
	3/7/2007	8:4:24	Downstream	Little Freshwater confluence
	3/7/2007	8:0:32	Upstream	Little Freshwater confluence
	3/7/2007	8:0:40	Upstream	Little Freshwater confluence

APPENDIX C. Identity (final digit(s) of PIT tag code), date, location, status (alive or dead) and habitat type of tagged trout that were detected in below-waterfall surveys in Freshwater Creek using a portable PIT tag reader. Pit tag numbers with asterisks represent individuals that were released above the waterfall. Duplicate records of detections of the same individual at the same approximate location (± 10 m) on the same date were deleted from the dataset.

Pit #	Date	Basin	Location (m)	Alive?	Habitat type
4	5/22/07	Upper mainstem	486	Y	Shallow pool
14	6/13/07	Middle mainstem	3523	N	Other
23	6/14/07	Middle mainstem	4763	Y	Shallow pool
28	10/10/06	Lower mainstem	8007	N	Shallow pool
34	10/11/06	Upper mainstem	165	Y	Shallow pool
35	10/11/06	Upper mainstem	474	Y	Deep pool
39	10/11/06	Upper mainstem	478	Y	Deep pool
39	5/22/07	Upper mainstem	480	Y	Shallow pool
52	10/10/06	Lower mainstem	8159	Y	Deep pool
52	10/10/06	Lower mainstem	8157	Y	Deep pool
60	10/9/06	Lower mainstem	6202	N	Shallow pool
61	10/11/06	Upper mainstem	168	Y	Shallow pool
63	10/11/06	Upper mainstem	467	Y	Shallow pool
71	10/11/06	Upper mainstem	166	Y	Shallow pool

Pit #	Date	Basin	Location (m)	Alive?	Habitat type
72	10/10/06	Lower mainstem	8215	Y	Deep pool
79	6/20/06	Upper mainstem	119	N	Riffle
79	10/11/06	Upper mainstem	118	N	Shallow pool
80	10/11/06	Upper mainstem	49	Y	Shallow pool
85	10/9/06	Lower mainstem	5626	N	Deep pool
87*	5/30/07	Upper mainstem	3620	Y	Shallow pool
96	6/20/06	Upper mainstem	118	N	Riffle
96	10/11/06	Upper mainstem	118	N	Shallow pool
98	10/11/06	Upper mainstem	268	Y	Shallow pool
107*	6/19/06	Lower mainstem	5147	Y	Shallow pool
110	6/12/07	Middle mainstem	1134	N	Shallow pool
117*	5/30/07	Upper mainstem	4852	Y	Shallow pool
118	10/11/06	Upper mainstem	479	Y	Deep pool
144	6/19/06	Lower mainstem	5147	Y	Shallow pool
157	10/10/06	Lower mainstem	8105	N	Other
170	10/11/06	Upper mainstem	292	Y	Shallow pool
179	10/11/06	Upper mainstem	101	Y	Shallow pool
181	10/11/06	Upper mainstem	200	Y	Shallow pool
185	10/11/06	Upper mainstem	106	Y	Shallow pool
200	10/11/06	Upper mainstem	260	Y	Shallow pool

APPENDIX D. Identity (last digit(s) of Pit tag code), trap location, date of capture, length, mass, and migratory stage of tagged trout captured in downstream migrant traps below the waterfall on Freshwater Creek during 2006-2007. Pit tag numbers marked with an asterisk represent individuals that were released above the waterfall.

Pit #	Trap location	Date	Length (mm)	Mass(g)	Migratory stage
6	Upper mainstem	4/20/2006	172		non-smolting
23	Upper mainstem	5/7/2007	157	51.8	non-smolting
38*	Upper mainstem	5/3/2007	126	25.4	non-smolting
44	Upper mainstem	4/29/2006	192	70.7	smolt
46	Upper mainstem	4/8/2006	121		pre-smolt
59*	Lower mainstem	5/4/2007	203	83.5	smolt
182	Upper mainstem	4/1/2007	132	18	non-smolting