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**Spawning Demographics of Bull Trout
in the Upper Red Deer River Drainage,
2009 – 2011**



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Spawning Demographics of Bull Trout in the Upper Red Deer River Drainage, 2009 – 2011

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EXECUTIVE SUMMARY

Insufficient information on the abundance, life history strategy and spawning demographics of bull trout (*Salvelinus confluentus*) in the upper Red Deer River drainage complicates management of this species. Coupled with the lack of information, are impacts on bull trout from increased land use and recreational angling in the drainage. We conducted a three-year study of the abundance, life history strategy and spawning demographics of bull trout in the upper Red Deer River drainage. In the first program year (2009), we investigated the abundance of juvenile/resident bull trout and spawning use in Pinto Creek, in our second year (2010), we assessed the magnitude and timing of bull trout spawning in Pinto Creek and also assessed spawning use in other prioritized streams in the upper Red Deer River drainage, and in our third year (2011), we assessed the magnitude and timing of bull trout spawning in Sheep Creek.

In 2009, we captured 85 bull trout in Pinto Creek with backpack electrofishing gear. Estimated total bull trout abundance was 4,714 (95%CI = 1,644–14,916), and the adult resident bull trout (fish \geq 250 mm fork length) abundance was 413 (95%CI = 146–1,024). We documented 56 bull trout redds in 13 km of Pinto Creek, indicating its importance as a spawning stream.

In 2010, we captured 43 adult bull trout in Pinto Creek using a fish trap, 8 moving upstream from North Burnt Timber Creek into Pinto Creek and 35 migrating downstream out of Pinto Creek. We also documented 17 bull trout redds in 8 km of Sheep Creek, indicating its importance as a spawning location.

In 2011, we captured 41 bull trout in Sheep Creek using backpack electrofishing gear. Estimated total bull trout abundance was 1,097 (95%CI = 384–3,648), and the adult resident bull trout abundance was 198 (95%CI = 72–489). We captured 7 bull trout moving upstream through our fish trap on Sheep Creek and 17 bull trout moving downstream. We documented 68 redds in Pinto Creek and 44 redds in Sheep Creek, confirming their importance as bull trout spawning streams.

At nine microsatellite DNA loci studied, brook trout (*S. fontinalis*) alleles were found in 3.4% of bull trout. This is evidence of low-level hybridization and this introgression of brook trout genes into bull trout populations should be monitored.

Microsatellite DNA analysis supports three bull trout populations in the upper Red Deer River drainage, consisting of; 1) fish from the upper Red Deer River and Scalp Creek, 2) fish from Sheep Creek, and 3) fish from Pinto Creek and North Burnt Timber Creek. Genetic assignment estimated that 11% of sampled bull trout were migrants from another population. In some instances migrants were from geographically close populations, in other instances they were from geographically distant populations. This finding reinforces the importance of stream connectivity for bull trout in the upper Red Deer River drainage. Data collected through this project will aid in making informed management decisions regarding the bull trout populations in the upper Red Deer River drainage.

Key words: Red Deer River, bull trout, redd survey, life history strategy, microsatellite DNA.

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1.0 INTRODUCTION

Insufficient information on the abundance, life history strategy and spawning demographics of bull trout (*Salvelinus confluentus*) in the upper Red Deer River drainage complicates management of this species. The current status of the upper Red Deer River bull trout population is “At risk” (of extirpation), with the short-term trend indicating a population in decline (Alberta Sustainable Resource Development and Alberta Conservation Association 2009). Impacts on bull trout from timber harvest, oil and gas development, off-highway vehicle use, and from increased angling pressure are concerns in this drainage. For example, Ripley et al. (2005) indicated bull trout abundance to be negatively affected by timber harvest and road density. Furthermore, delayed maturity and greater catchability of bull trout may result in high hooking mortality that can prevent population recovery, or lead to population decline despite protection by provincial catch-and-release fishing regulations (Paul et al. 2003; Post et al. 2003).

The objectives of this study were to:

- 1) inventory and estimate the abundance and spatial distribution of juvenile and resident bull trout in two streams in the upper Red Deer River drainage that are believed to be major spawning locations (Pinto and Sheep creeks),
- 2) evaluate the magnitude and timing of fluvial bull trout out-migrations from Pinto and Sheep creeks (streams believed to contain both resident and fluvial life forms of bull trout),
- 3) assess bull trout spawning activity in prioritized streams in the upper Red Deer River drainage, and
- 4) through molecular techniques, describe the genetic structure of the bull trout population in the upper Red Deer River drainage.

Describing bull trout abundance, life history strategy, and identifying spawning habitat in the upper Red Deer River drainage is fundamental to the management and conservation of the species. Data collected through this project will aid in the informed management of bull trout in the upper Red Deer River drainage.

2.0 STUDY AREA

We defined our study area as the upper Red Deer River and its major tributaries, downstream of Banff National Park to the confluence with Burnt Timber Creek (Figure 1). The downstream limit of our study area was selected based on elevation (elevation strongly influences summer water temperature) and stream gradient criteria, both of which have been demonstrated to influence bull trout occupancy in the region (Post and Paul 2001). The boundary of Banff National Park was the upstream limit of our study area, as beyond this point bull trout are managed by Parks Canada. Located within the Upper Foothills, Montane, and Subalpine Natural Subregions (Natural Regions Committee 2006), resource exploration and extraction, and motorized and non-motorized recreational activities are the major land uses in the area.

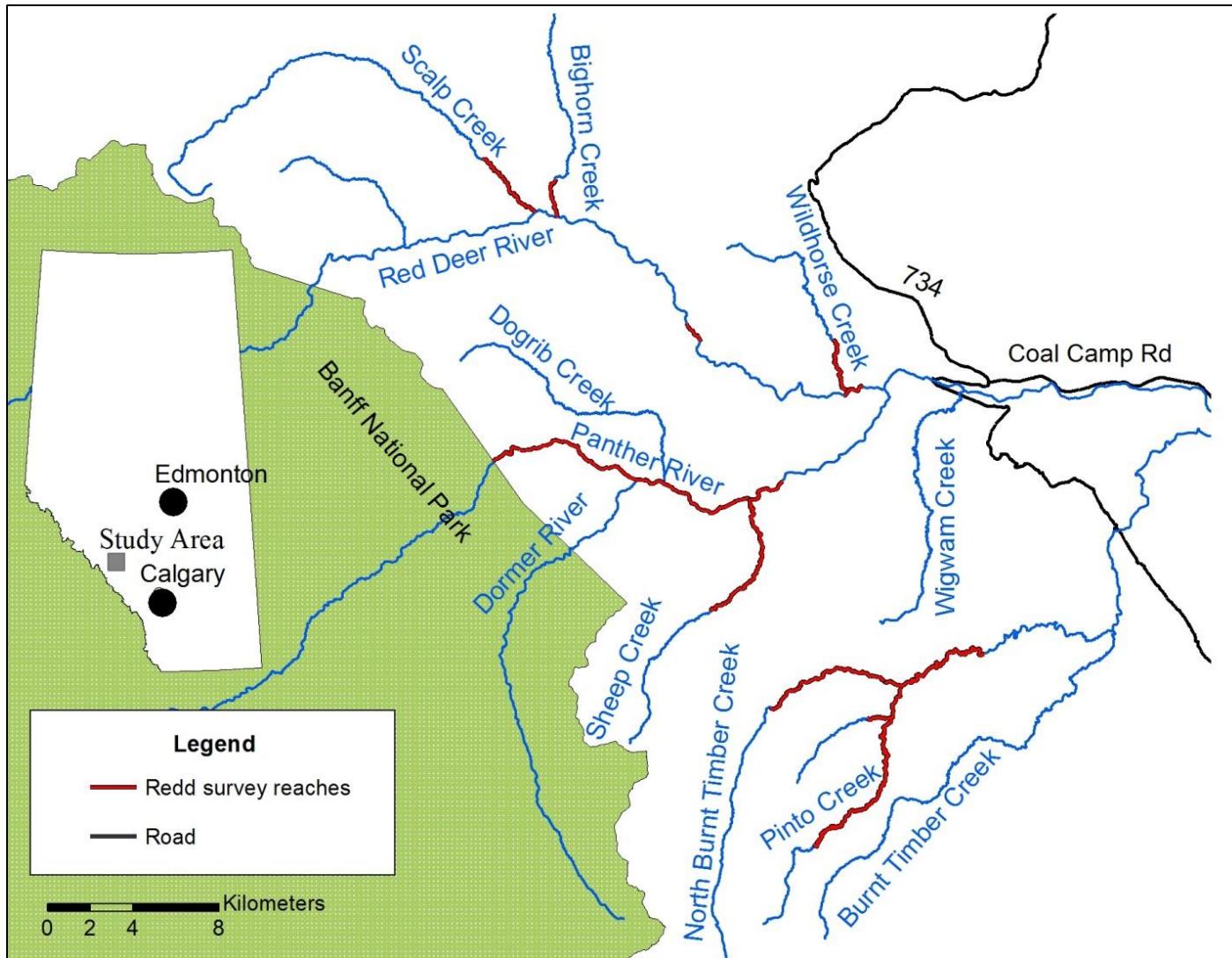


Figure 1. Location of study streams and redd survey reaches in the upper Red Deer River drainage.

3.0 MATERIALS AND METHODS

3.1 Abundance and spatial distribution of bull trout in Pinto and Sheep creeks

We used single-pass backpack electrofishing, in an upstream direction, to capture fish at five locations along Pinto Creek from 28 – 30 July 2009 and from eight locations along Sheep Creek from 5 – 7 July 2011 (Figure 2). Sampling sites were 250 m long except for Sites 2 and 5 on Sheep Creek, where electrofishing was stopped at 50 m and 236 m, respectively, due to personal protective equipment malfunctions. We electrofished with a Smith-Root model LR-20 backpack electrofisher outputting a pulsed direct current (voltage 250–350 V, frequency 35–40 Hz). At all sites we recorded the geographic location using a GPS unit (UTM, NAD 83, Zone 11), measured stream wetted width in 50-m intervals, and enumerated all fish captured by species. Fish were measured (fork length, FL, mm), and a small piece of their adipose fin was clipped for DNA analysis and then fish were returned to the creek.

Our electrofishing capture data from Pinto and Sheep creeks, along with previously acquired capture efficiencies (q) from Canyon Creek, an unnamed tributary to Canyon Creek (Fitzsimmons 2008a), and an unnamed tributary to Waiparous Creek (Fitzsimmons 2008b), were used to estimate bull trout abundance. These data were input into spatial models following the methods of Paul and Dormer (2005) to estimate the total bull trout abundance (juvenile and resident adult) and the abundance of resident adult bull trout (≥ 250 mm FL) in Pinto and Sheep creeks. In this process we modelled uncertainty in q with the beta distribution. The beta distribution ranges in values from 0 to 1, appropriate for describing q , and its parameters (α and β) are defined by the mean and the standard deviation of the values of q derived from mark-recapture estimates. The parameters of the beta distribution are defined as:

$$\alpha = \bar{x} \left(\frac{\bar{x}(1 - \bar{x})}{v} \right) - 1$$

$$\beta = (1 - \bar{x}) \left(\frac{\bar{x}(1 - \bar{x})}{v} - 1 \right)$$

where \bar{x} and v are the mean and variance, respectively, of the estimates of q .

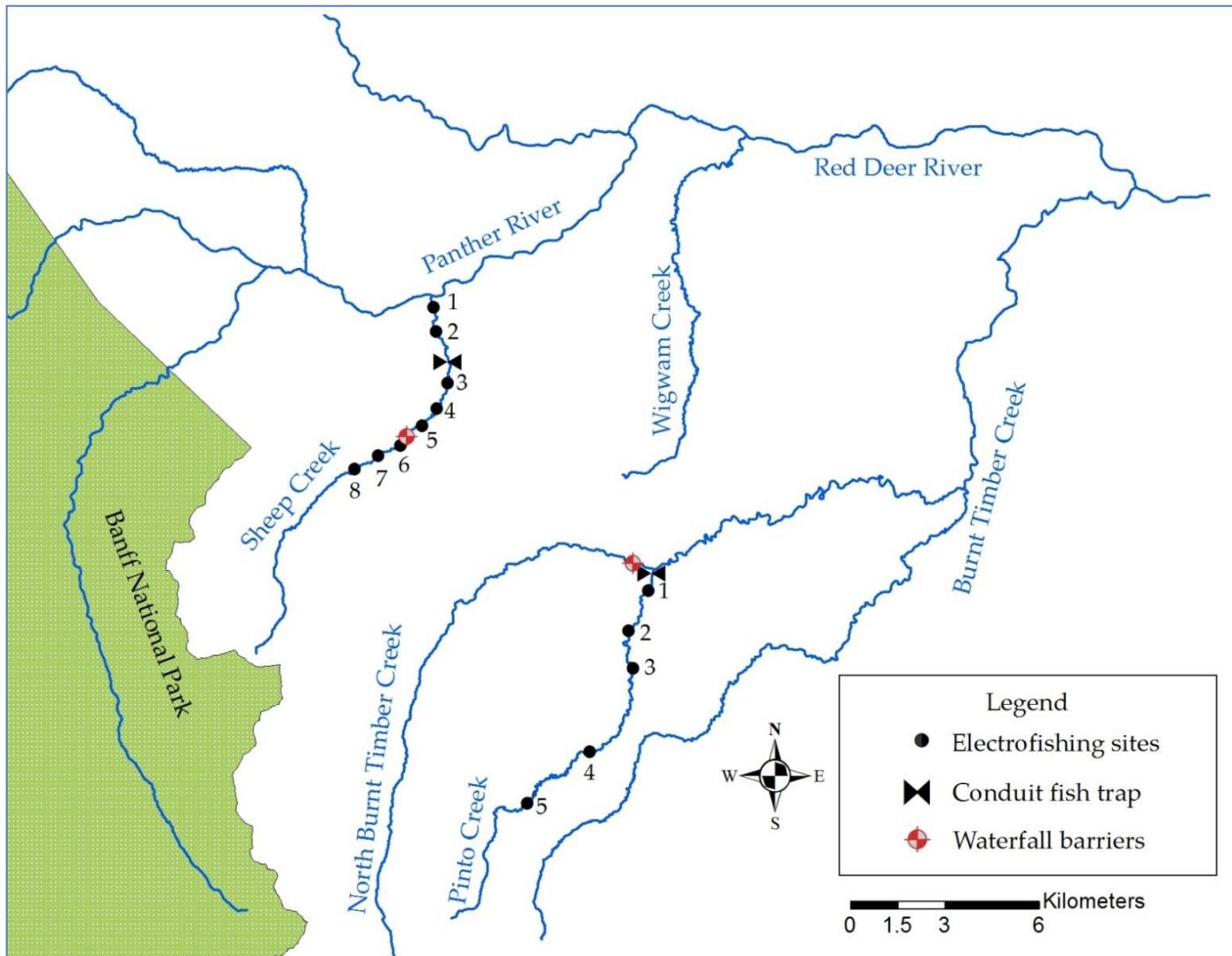


Figure 2. Location of backpack electrofishing sites and conduit fish traps in Pinto and Sheep creeks.

Bull trout abundance at each electrofishing site was estimated using the observed catch at each site, a value of q drawn at random from the modeled distribution of q and the negative binomial distribution. In this step we estimated the number of fish expected to have been missed at each site while electrofishing with a fixed q , and total fish abundance was expressed as the observed catch plus the number of fish expected to have been missed. Finally, bull trout abundance over the entire length of a study stream was estimated using a nonparametric generalized additive model with the estimated fish abundance at each site and each site's distance upstream from its mouth as model input data. The model estimated fish abundance in 1 km increments along study streams and when summed provides an estimate of fish abundance in the stream. To obtain a mean population estimate and 95% confidence intervals (CI), 10,000 replicates were performed. Electrofishing capture efficiencies were estimated using the program MARK (Cooch and White 2008) and abundance modelling was performed using the R software program (R Development Core Team 2011).

3.2 Magnitude and timing of fluvial bull trout migrations

We used a conduit weir and box type fish trap, similar to that described by Hvenegaard and Thera (2001), to assess the magnitude and timing of post-spawn bull trout migrations out of Pinto and Sheep creeks. In 2011, we attached a mesh cone to the inside of the fish trap opening, to reduce escaping fish. To minimize any influence on spawning fish health and behaviour, we installed the trap once the majority of migratory bull trout were suspected to be upstream of the trap location. Our trap was deployed to allow upstream migrating fish to enter it, while acting as a barrier to downstream migration.

In 2010 the trap was installed on Pinto Creek, near the confluence with North Burnt Timber Creek. In 2011 we installed the trap on Sheep Creek, approximately 3 km upstream of the confluence with Panther River (Figure 2). We operated the trap in Pinto Creek, from 2 September to 5 October 2010 and in Sheep Creek, from 6 to 27 September 2011. The trap was checked daily (except for Pinto Creek where 9, 14, and 15 September were missed due to not having staff available) and any debris accumulated on the upstream side of the trap was removed. Downstream migrating fish were captured by dip netting, seine netting or electrofishing at either the trap face or in the pools immediately upstream of the trap where fish were congregating. Captured fish were

measured for FL (mm) and weight (g), scanned for a previously implanted passive integrated transponder (PIT) tag, and a small piece of their adipose fin was clipped for DNA analysis. Untagged fish were implanted with a PIT tag in their dorsal sinus. Fish were moved upstream or downstream of the trap based on their original direction of travel. We removed the fish trap in 2010 after our catch diminished to three fish in 10 days, and in 2011 the trap was removed once we failed to capture a bull trout for four consecutive days.

3.3 Bull trout redd surveys

We identified bull trout spawning habitat in the upper Red Deer River drainage by conducting redd surveys between mid-September and early October in 2009, 2010, and 2011. Surveys were conducted on Pinto, an unnamed tributary to Pinto, Bighorn, Sheep, Scalp, North Burnt Timber, and Wildhorse creeks, and the Panther River (Figure 1). Survey reaches in 2010 were selected from an aerial reconnaissance in the winter of 2010, which identified areas influenced by groundwater upwelling that presented as open water areas. Surveys were conducted with observers on the left and right banks of the stream recording the geographic location (UTM, NAD 83, Zone 11), the number of redds in the immediate area, and the category of red:

- 1) Definite redd: a cleaned area with a pit and tailspill area recognizable, not in an area normally cleaned by stream hydraulics, or
- 2) Probable redd: a cleaned area that may be due to stream hydraulics, but a pit and tailspill area are recognizable, or an area that does not appear clean, but has a pit and tailspill area.

3.4 Bull trout microsatellite DNA analysis

A total of 267 bull trout tissue samples were collected, by angling, electrofishing and at fish traps, from the upper Red Deer River and nine of its tributaries. Samples were collected in 2009, 2010, and 2011 and were stored either dry in sample envelopes or in 99% anhydrous ethanol. Tissue samples were sent to Dr. Taylor at the University of British Columbia for microsatellite DNA analyses. Nine microsatellite loci were included in our study; *Sfo18* (Angers et al. 1995), *Sco102*, 105, 106, (S. Young, WA Dept. Fish and Wildlife, Olympia, WA, unpublished data), 215, 216, 220 (DeHaan and Ardren

2006), *Smm22* (Crane et al. 2004), and *Omm1128* (Rexroad et al. 2001). Polymerase chain reactions were completed with dye-labeled primers in 10 μ l volumes of 10mM Tris-HCl (pH 8.3), 1.5mM MgCl₂, 0.8mM dNTPs, and 0.1 units of Taq polymerase in MJ PTC 100 and 200 thermocyclers using cycling parameters outlined in Warnock et al. (2010), and visualized using a Beckman-Coulter CEQ 8000 automated genotyper.

Sample size, mean number of alleles, and observed and expected heterozygosity were summarized for each sample site using FSTAT 2.9 (Goudet 2001). At 7 of the 13 sites we had sample sizes sufficient for further population level analysis (> 20). For these analyses, GENEPOP 3.3 (Raymond and Rousset 2001) was used to assess if a significant difference between one or more populations existed. Subsequent to finding a significant inter-population result, all pairwise combinations of populations were tested to detect where significant differences occurred. Population structure, or the number of distinct genetic groupings, was assessed with the program STRUCTURE (Pritchard et al. 2000) using a Bayesian clustering analysis, with the prior sample location knowledge option, to model population structure from 1 to 9 theoretical populations. An information theoretic approach was then used to score candidate models relative to each other and to select the most supported model of population structure given our data. Migration was assessed using the program GENECLASS (Piry et al. 2004) to test whether individuals sampled within a location belonged to the population (were born into it) or were migrants. Lastly, the program COLONY (Jones and Wang 2009), which implements methods based on sibship frequencies and linkage disequilibrium, was used to estimate the effective number of breeding individuals (N_B) in each population. For further details of microsatellite DNA analysis see Taylor (2012).

4.0 RESULTS

4.1 Abundance and spatial distribution of bull trout in Pinto and Sheep creeks

During mid-summer electrofishing surveys in Pinto Creek, we captured 85 bull trout ranging in size from 72 to 338 mm FL (Figure 3, Appendix 1). In addition to bull trout, we captured mountain whitefish (*Prosopium williamsoni*; n = 4) at Sites 1, 2, and 3 (Figure 2). Estimated total bull trout abundance in Pinto Creek was 4,714 (95%CI = 1,644–14,916) and adult resident bull trout abundance was 413 (95%CI = 146–1,024). Our spatial models indicated that estimated bull trout abundance increased upstream from the mouth, peaking approximately 9 km upstream (527 bull trout per kilometer), and then decreased to the uppermost electrofishing site (Figure 4).

During mid-summer electrofishing in Sheep Creek, we captured 41 bull trout ranging in size from 66 to 338 mm FL (Figure 3; Appendix 1). Estimated total bull trout abundance in Sheep Creek was 1,097 (95%CI = 384–3,648) and adult resident bull trout abundance was 198 (95%CI = 72–489). Bull trout abundance in Sheep Creek decreased from the mouth upstream to an impassable waterfall barrier, approximately 7 km upstream (Figure 4). No fish were captured or observed at Sites 6, 7, and 8 above the waterfall barrier (Figure 2).

4.2 Magnitude and timing of fluvial bull trout migrations

From 2 September to 5 October 2010, our fish trap captured 8 bull trout moving upstream from North Burnt Timber Creek into Pinto Creek and 35 bull trout moving downstream from Pinto Creek into North Burnt Timber Creek (Figure 5). Peak bull trout movement (58% of migrating fish) out of Pinto Creek was from 13 to 17 September 2010. The 43 bull trout we captured ranged in size from 262 to 630 mm FL (Figure 6) and included 17 males, 13 females, and 13 of undetermined sex.

From 6 to 27 September 2011, we captured 7 bull trout moving upstream through our trap on Sheep Creek and 17 moving downstream (Figure 5). Peak bull trout movement (63% of migrating fish) out of Sheep Creek was from 12 to 16 September 2011. The 24 bull trout we captured ranged in size from 256 to 575 mm FL (Figure 6); and included 9 males, 5 females, and 10 of undetermined sex.

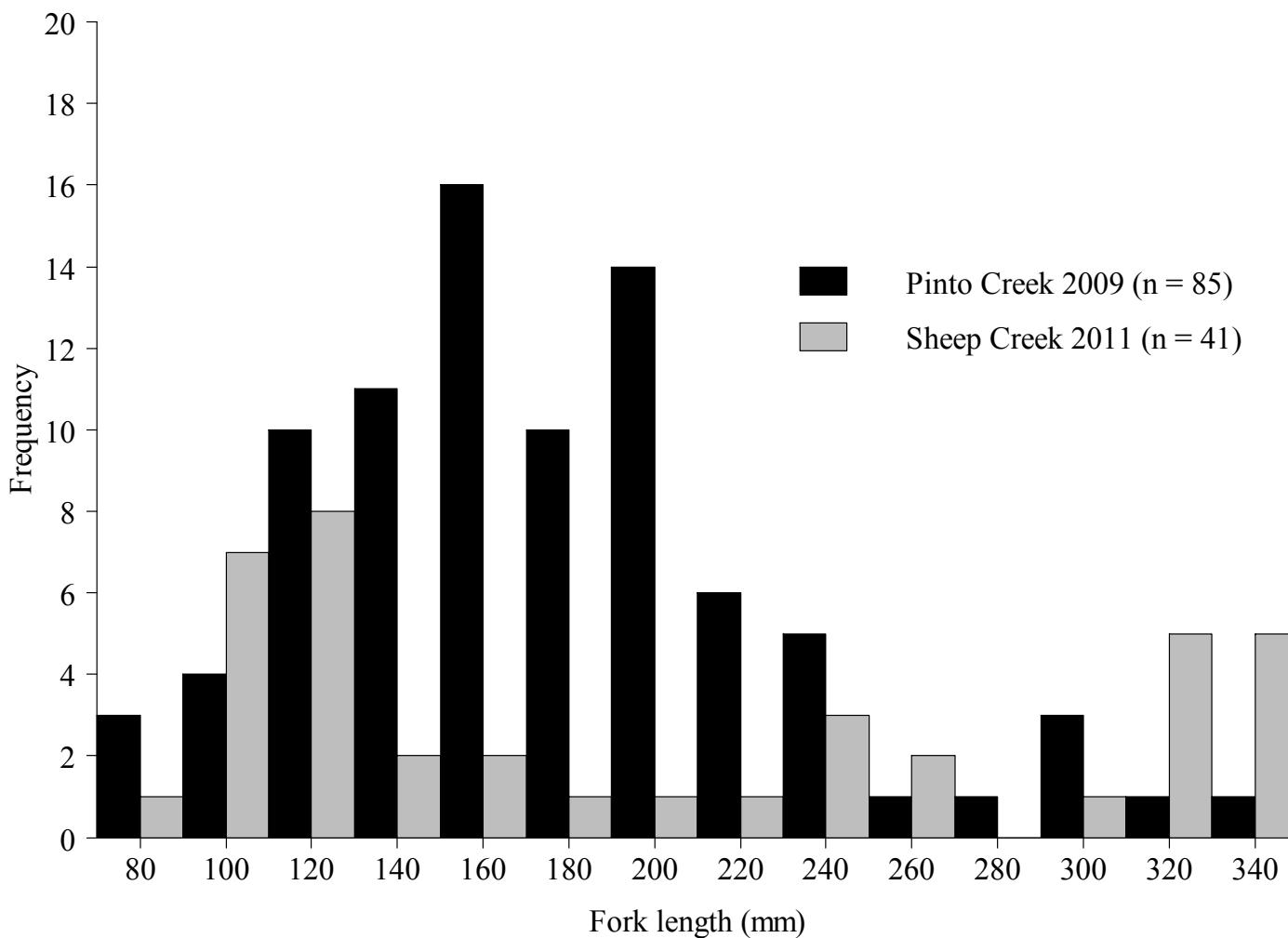


Figure 3. Length-frequency distribution of juvenile/resident bull trout captured during mid-summer backpack electrofishing in Pinto Creek (2009) and Sheep Creek (2011).

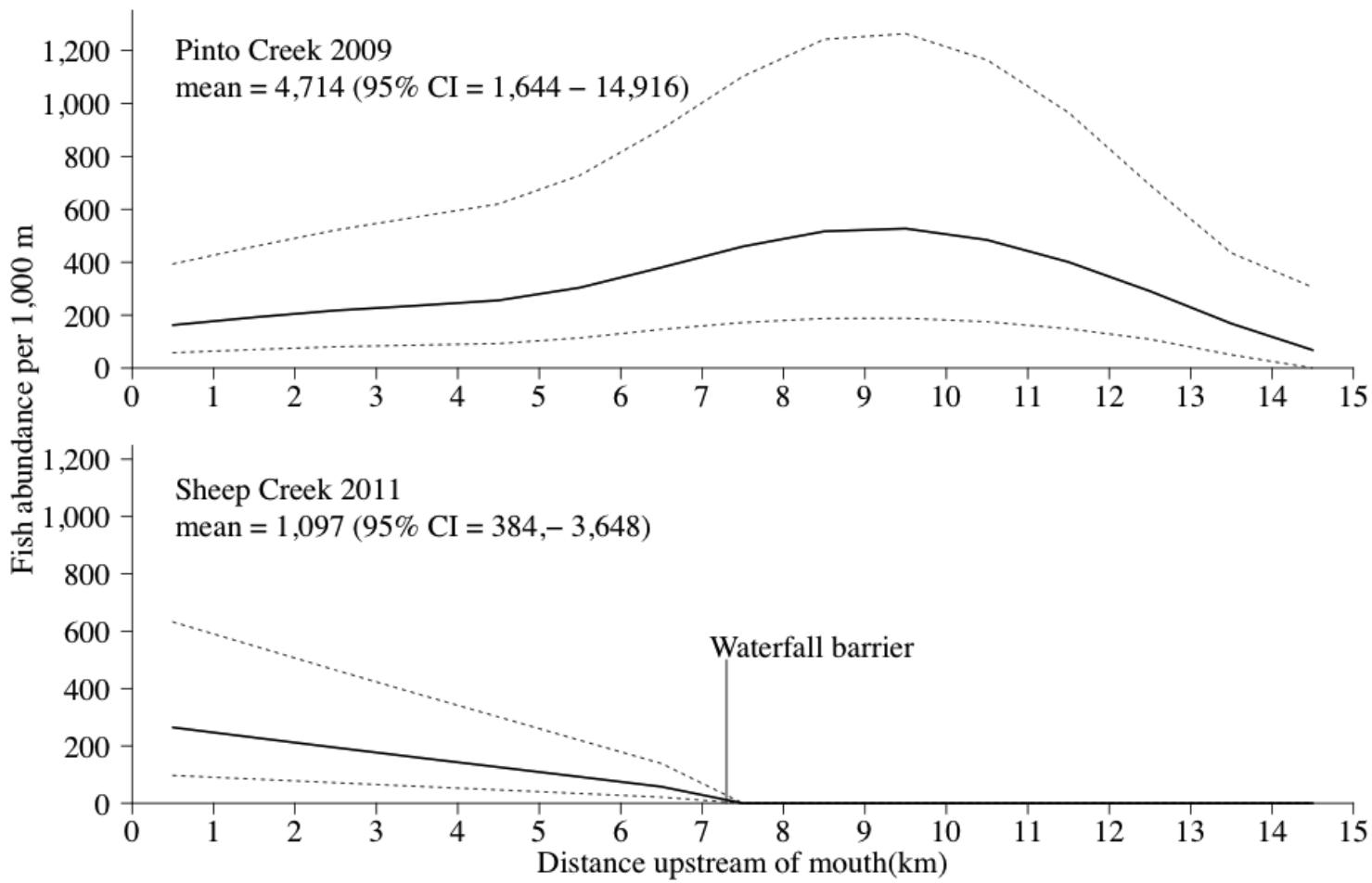


Figure 4. Estimated total abundance and spatial distribution of bull trout in Pinto Creek (2009) and Sheep Creek (2011) in mid-summer. Shown is the mean of all estimates (solid line) and the 95% confidence intervals (dotted lines).

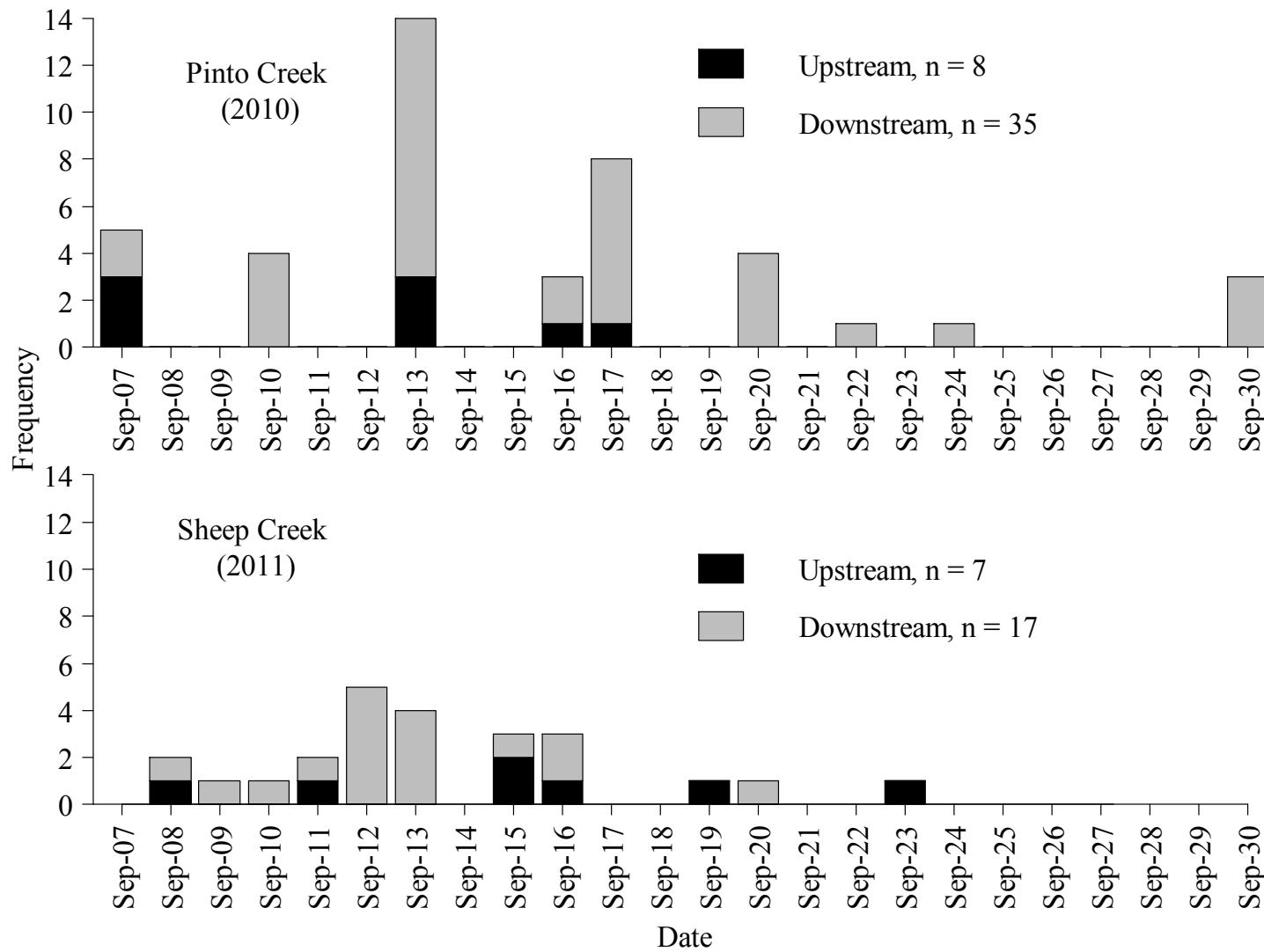


Figure 5. Upstream and downstream movement of new bull trout captures at the conduit fish traps in Pinto Creek (2010) and Sheep Creek (2011). For comparison, the x-axis has been standardized to September 30. The Pinto Creek fish trap was removed on 5 October 2010 and the Sheep Creek trap was removed on 27 September 2011.

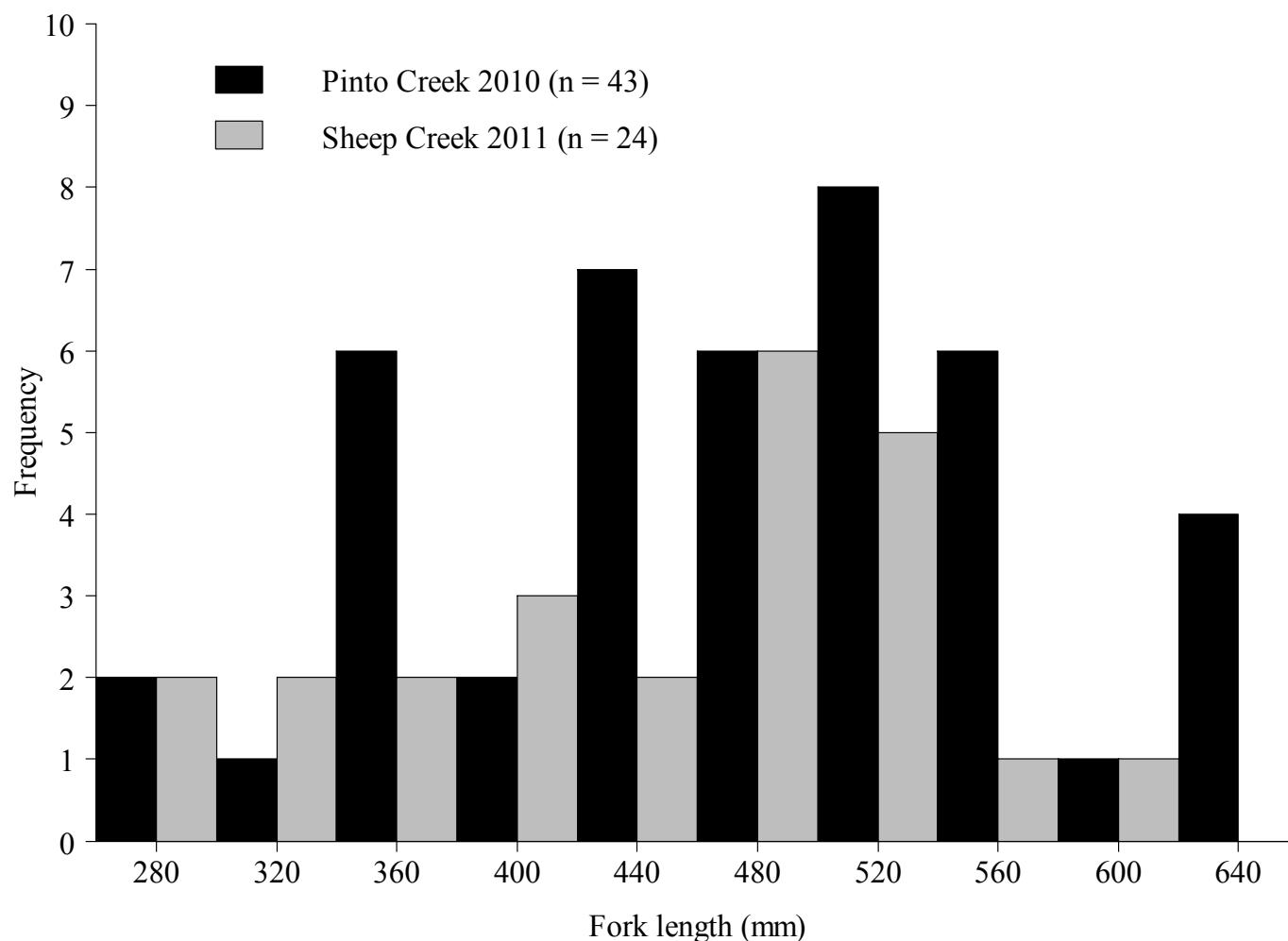


Figure 6. Length-frequency distribution of bull trout captured in the conduit fish traps in Pinto Creek (2010) and Sheep Creek (2011).

4.3 Bull trout redd surveys

In 2009, 2010, and 2011 we completed redd surveys on 100 stream kilometers throughout the upper Red Deer River drainage and we observed 237 definite bull trout redds (Figure 7; Table 1). High densities of bull trout redds were found in Sheep Creek (2011, 5.7 redds/km), Pinto Creek (2011, 5.2 redds/km; 2009, 4.3 redds/km) and an unnamed tributary to Pinto Creek (2009, 3.8 redds/km).

In Sheep Creek, in 2011, the relationship between observed redd count and fluvial bull trout count (assumed to be spawning adults) was 1.83 redds per adult fish. This is contrasted by the ratio of 0.5 redds per adult (one redd per spawning female) found by Mushens et al. (2003) in Smith-Dorrien Creek, and generally expected of most fluvial bull trout populations. The greater ratio of redds to spawning fish is likely explained by resident bull trout spawning in Sheep Creek. This is supported by observations of resident sized (300 mm FL) fish digging a redd immediately upstream of the fish trap on Sheep Creek in September 2011. The relationship between redd count and fluvial bull trout count was not estimated for Pinto Creek, as redd surveys on Pinto Creek in 2010 were incomplete.

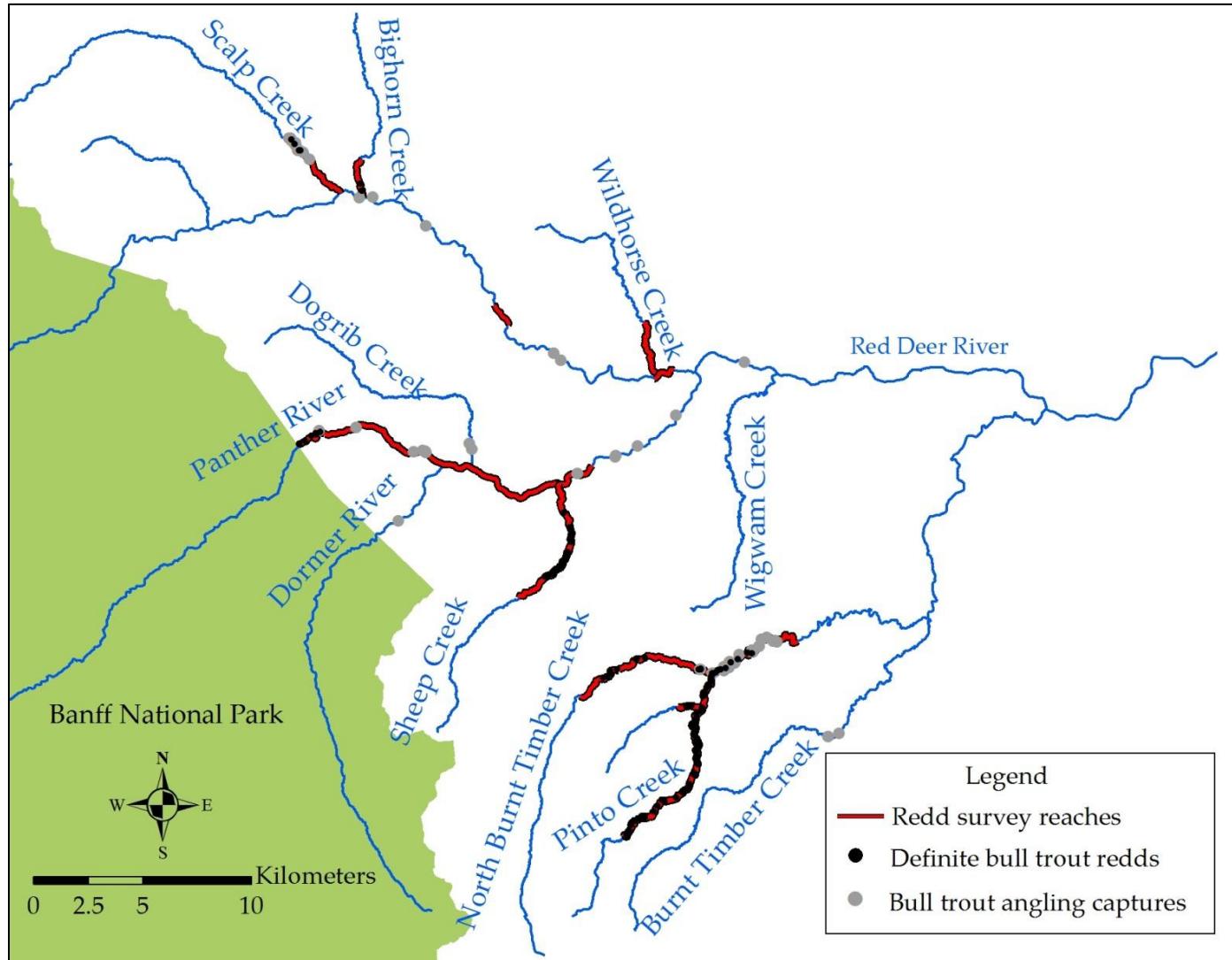


Figure 7. Location of definite bull trout redds and bull trout angling sites in the upper Red Deer River drainage.

Table 1. Summary of redd surveys completed in the upper Red Deer River drainage (2009, 2010, 2011).

Date	Waterbody	Survey start		Survey end		Redd count ^a		Length of survey reach (km)	Definite redds per km
		Easting	Northing	Easting	Northing	D	P		
28 Sep 2010	Bighorn Creek	600989	5731872	600915	5733664	0	0	2.0	0.0
22,29,30 Sep 2010	North Burnt Timber Creek	618864	5710932	611835	5709777	3	6	9.3	0.3
23,24,25 Sep 2011	North Burnt Timber Creek	620861	5711499	613964	5710814	18	0	14.4	1.3
14 Sep 2010	Panther River	611402	5719416	597999	5720482	11	0	16.5	0.7
22 Sep 2009	Pinto Creek	617057	5710019	613016	5702552	56	7	13.1	4.3
22 Sep 2010	Pinto Creek	617037	5710029	616260	5707562	9	1	3.4	2.6
15,16,17 Sep 2011	Pinto Creek	617057	5710019	613016	5702552	68	4	13.1	5.2
22 Sep 2010	Scalp Creek	599928	5732132	599928	5732132	2	0	4.1	0.5
22 Sep 2011	Scalp Creek	599928	5732132	599928	5732132	4	0	4.1	1.0
22 Sep 2010	Sheep Creek	609744	5714691	608246	5713483	17	0	7.7	2.2
20,26 Sep 2011	Sheep Creek	609744	5714691	608246	5713483	44	8	7.7	5.7
22 Sep 2009	Unnamed Creek	616563	5708491	615559	5708453	5	1	1.3	3.8
06 Oct 2010	Wildhorse Creek	614564	5723804	613986	5726071	0	0	3.2	0.0

^a D= definite redd, P = probable redd.

4.4 Bull trout microsatellite DNA analysis

A total of 267 bull trout tissue samples, collected from 13 locations in the upper Red Deer River drainage, were included in our microsatellite DNA analysis (Table 2). At the nine microsatellite loci analyzed, allele frequency ranged from 2 to 33. Within sample locations, the average number of alleles and the expected heterozygosity (two measures of genetic diversity) were comparable throughout the drainage (Table 2). The highest diversity occurred in samples collected from the upper Red Deer River and Burnt Timber Creek below the barrier and the lowest diversity occurred in the Sheep Creek resident/juvenile fish (Table 2). Brook trout (*S. fontinalis*) alleles occurred in eight fish (3.4% of the sample; found in upper Red Deer River n=2, Panther River n=1, Scalp Creek n=3, and North Burnt Timber Creek below barrier n=2), however, only at one locus and these fish were heterozygous (one bull trout allele and one brook trout allele at the locus).

Estimated genetic variance among locations in the upper Red Deer River drainage, F_{st} (θ) = 0.026, indicate a significant difference between one or more of the seven locations where sample sizes were large enough (> 20) for population level analysis (n=233). Genetic variance differed significantly, (Pairwise comparison, $P \leq 0.0137$) among all locations except between; Scalp Creek and upper Red Deer River; Pinto Creek resident/juvenile and Pinto Creek fluvial; North Burnt Timber Creek below barrier and Pinto Creek resident/juvenile; North Burnt Timber Creek below barrier and Pinto Creek fluvial, and Sheep Creek resident/juvenile and Sheep Creek fluvial (Table 3). The greatest intra-location differences were between Sheep Creek resident/juvenile and Pinto Creek resident/juvenile, as well as North Burnt Timber Creek below barrier and Sheep Creek resident/juvenile. The lack of significant differences between fluvial and resident/juvenile fish in both Pinto and Sheep creeks is likely indicative of their occupation of the same spawning area, while the greater significant difference between Sheep Creek and Pinto Creek and North Burnt Timber Creek below barrier is indicative of the geographic separation of the streams (Figure 1).

Table 2. Sample size (N), mean number of alleles (N_a), observed (H_o) and expected (H_e) heterozygosity for 13 locations in the upper Red Deer River drainage.

Sample location ^a	N	N_a	H_o	H_e
URD	39	9.1	0.623	0.626
PFL	41	7.1	0.601	0.593
PRJ	30	6.9	0.593	0.616
SFL	21	7.3	0.487	0.551
SRJ	37	6.7	0.583	0.565
SCL	30	8.7	0.585	0.626
NBTB	35	9.1	0.603	0.644
DOG	1	1.6	0.556	0.556
BGH	1	1.6	0.750	0.750
DOR	2	2.6	0.444	0.685
PAN	15	6.4	0.593	0.602
NBTA	12	5.4	0.593	0.622
BTC	3	2.7	0.481	0.526

^a URD = upper Red Deer, PFL = Pinto Creek fluvial, PRJ = Pinto Creek resident/juvenile, SFL = Sheep Creek fluvial, SRJ = Sheep Creek resident/juvenile, SCL = Scalp Creek, NBTB = North Burnt Timber Creek below barrier, DOG = Dogrib Creek, BGH = Bighorn Creek, DOR = Dormer River, PAN = Panther River, NBTA = North Burnt Timber Creek above barrier, BTC = Burnt Timber Creek.

Table 3. Pairwise comparisons of bull trout genetic variance, F_{st} (θ), from sample locations in the upper Red Deer River drainage. Significant differences, with $P \leq 0.0137$, are corrected for multiple pairwise comparisons. Underlined comparisons are not significant.

Sample location ^a	URD	PRJ	SFL	SCL	PFL	NBTB	SRJ
URD	-	0.0348	0.0289	<u>0.0064</u>	0.0205	0.0289	0.0346
PRJ		-	0.0413	0.0320	<u>0.0052</u>	<u>0.0109</u>	0.0444
SFL			-	0.0281	0.0280	0.0361	<u>0.0171</u>
SCL				-	0.0208	0.0352	0.0375
PFL					-	<u>0.00151</u>	0.0389
NBTB						-	0.0415

^a URD = upper Red Deer, PRJ = Pinto Creek resident/juvenile, SFL = Sheep Creek fluvial, , SCL = Scalp Creek, PFL = Pinto Creek fluvial, NBTB = North Burnt Timber Creek below barrier, SRJ = Sheep Creek resident/juvenile.

Population structure analysis run on the seven locations with sufficient sample sizes indicates support for three genetic populations in the upper Red Deer River drainage with the following groupings:

- 1) Upper Red Deer River and Scalp Creek,
- 2) Sheep Creek (resident/juvenile and fluvial), and
- 3) Pinto Creek (resident/juvenile and fluvial) and North Burnt Timber Creek below barrier.

A *post-hoc* analysis in the program STRUCTURE, with populations fixed to three and including all 267 fish samples, was run to assign fish from the locations with low sample sizes to one of the three population groupings. Results indicate that bull trout from Panther and Dormer rivers and Dogrib Creek were most similar to the Sheep Creek (resident/juvenile and fluvial) population grouping. Bull trout from Burnt Timber Creek and North Burnt Timber Creek above the barrier were most similar to the Pinto Creek (resident/juvenile and fluvial) and North Burnt Timber Creek below the barrier grouping.

Of the 233 bull trout samples included in the population level analysis (Table 2), 11.1% (26 fish) had less than a 0.05 probability of belonging to the population from which they were sampled, suggesting they were migrants from another population. This finding emphasizes the importance of connectivity between streams in the upper Red Deer River drainage for the persistence of bull trout. Variation in microsatellite DNA allowed for the assignment of migrants to their most likely population of origin. These results indicate that while some individuals were migrants from local geographic population sources, others were from geographically distant population sources (Table 4). In particular, four individuals sampled in Scalp Creek and two sampled in Sheep Creek were genetically assigned to the Pinto Creek population, representing a minimum distance (from stream mouth to steam mouth) of 65 km and 78 km, respectively, between these populations. At all sample locations, with the exception of Sheep Creek, at least one migrant was from an unknown population source. This indicates a possible unidentified population in the area or a population with too small of a sample size to characterize the population.

Sibship frequency methods of estimating the effective number of breeding individuals (N_B) in each population consistently produced more conservative estimates with tighter confidence intervals than linkage disequilibrium methods (Table 5). It should, however, be noted that estimates of N_B are more informative when used to track this parameter over time (years) and should not be interpreted as a point estimate. It should also be noted that N_B estimates represent an estimate of the number of breeding fish that produced the samples we collected at each location. This estimate includes parents of fish born into a population at a sampling location, as well as parents of migrants into the location. Therefore, estimates for locations with higher rates of migration would be inflated beyond what would be expected for the individuals that actually breed in that location. For example, Scalp Creek had a high degree of migration, and this likely increased the value of N_B beyond what the stream actually supports as a spawning population.

Table 4. Sample location and source location of bull trout migrants into sampling location.

Sample location ^a	Source location of migrants into sampling location (n)
URD	UKN (1)
PRJ/PFL	NBTB (1), UKN (1)
SRJ/SFL	SCL (2), URD (3), PRJ/PFL (2)
SCL	UKN (2), URD (1), PRJ/PFL (4), SRJ /SFL(2), NBTB (1)
NBTB	SCL (4), UKN (1), PRJ/PFL (1)

^a URD = upper Red Deer, PFL = Pinto Creek fluvial, PRJ = Pinto Creek resident/juvenile, SFL = Sheep Creek fluvial, SRJ = Sheep Creek resident/juvenile, SCL = Scalp Creek, NBTB = North Burnt/Timber Creek below barrier, UKN = unknown.

Table 5. Linkage disequilibrium (LD) and sibship assignment (SA) estimates of the effective number of breeding individuals in seven locations in the upper Red Deer River drainage with sample sizes large enough (>20 individuals, see Table 2) for population level analysis.

Sample location ^a	LD (95%CI)	SA (95%CI)
URD	81 (49 – 186)	41 (27 – 68)
PFL	38 (26 – 62)	32 (21 – 54)
SFL	104 (37 – ∞)	34 (18 – 72)
SCL	111 (48 – ∞)	29 (16 – 53)
PRJ	74 (37 – 445)	29 (17 – 53)
NBTB	36 (24 – 59)	37 (22 – 67)
SRJ	97 (45 – 2184)	30 (18 – 52)

^a URD = upper Red Deer, PFL = Pinto Creek fluvial, SFL = Sheep Creek fluvial, SCL = Scalp Creek PRJ = Pinto Creek resident/juvenile, NBTB = North Burnt Timber Creek below barrier, SRJ = Sheep Creek resident/juvenile

4.5 Summary

In the upper Red Deer River drainage, fluvial bull trout life history forms have been demonstrated in Sheep and Pinto creeks, and a resident life history form is suspected in both streams. Microsatellite DNA analysis supports three population groupings in the upper Red Deer River drainage consisting of; 1) fish from the upper Red Deer River and Scalp Creek, 2) fish from Sheep Creek, and 3) fish from Pinto Creek and North Burnt Timber Creek. Genetic analysis indicates migration between close and distant populations in the upper Red Deer River drainage, emphasizing the importance of stream connectivity in this drainage.

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6.0 APPENDICES

Appendix 1. Site-specific information for back-pack electrofishing sites on Pinto Creek (2009) and Sheep Creek (2011).

Date	Easting	Northing	Waterbody	ID ^a	Mean wetted width (m)	Effort (seconds)	Distance (m)	Species ^b	Count	FL range (mm)
28/07/2009	616988	5709686	Pinto Creek	1	7.2	633	250	BLTR,	10	75 – 303
								MNWH	3	268 – 354
29/07/2009	616232	5708038	Pinto Creek	2	3.4	727	250	BLTR,	17	81 – 289
								MNWH	1	281
29/07/2009	616391	5706853	Pinto Creek	3	5.6	645	250	BLTR,	11	72 – 293
								MNWH	1	201
30/07/2009	613022	5702553	Pinto Creek	4		887	250	BLTR	39	74 – 338
30/07/2009	615007	5704193	Pinto Creek	5	5.1	749	250	BLTR	8	135 – 295
05/07/2011	610040	5718352	Sheep Creek	1	8.5	536	250	BLTR	18	66 – 154
05/07/2011	610119	5717579	Sheep Creek	2	7.1	NA	50	BLTR	2	97 – 108
07/07/2011	610487	5715932	Sheep Creek	3	7.3	418	250	BLTR	6	184 – 316
06/07/2011	610145	5715128	Sheep Creek	4	3.4	495	250	BLTR	11	94 – 338
06/07/2011	609687	5714576	Sheep Creek	5	7.1	303	236	BLTR	4	260 – 334
07/07/2011	608978	5713956	Sheep Creek	6	7.5	233	250	BLTR	0	NA
06/07/2011	608281	5713615	Sheep Creek	7	5.2	363	250	BLTR	0	NA
07/07/2011	607536	5713195	Sheep Creek	8	7.0	262	250	BLTR	0	NA

^a ID on map, Figure 2 .

^b MNWH = Mountain whitefish, BLTR = bull trout.

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