Genetic Analysis of Bull Trout in the Kootenai River Basin

FINAL REPORT

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By

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Background

The Kootenai River is the second largest Columbia River tributary. The Kootenai River Sub-basin is an international watershed that encompasses parts of British Columbia (B.C), Montana, and Idaho. The headwaters of the Kootenai River originate in Kootenay National Park, B.C. The river flows south within the Rocky Mountain Trench into Koocanusa Reservoir created by Libby Dam at river km (Rkm) 365.7, located near Libby, Montana. Libby Dam was constructed primarily for flood control and electricity production. Construction of Libby Dam was completed in 1972, and inundates water for 145 km at full pool. Upstream fish passage structures do not exist at Libby Dam. However, Skaar et al. (1996) documented downstream bull trout passage through the turbines at Libby Dam.

Kootenai Falls, a 61 m high waterfall and a natural impediment to fish migrations, is located 18 km downstream of Libby, Montana at Rkm 311. It is not known if Kootenai Falls was an upstream migration barrier for bull trout prior to the construction of Libby Dam. Currently, Libby Dam truncates spring time flows that may have allowed seasonal bull trout upstream passage. A recent bull trout telemetry research project (Dunnigan et al. 2003) documented upstream migration of an adult bull trout over Kootenai Falls. Nevertheless, Kootenai falls currently represents a substantial upstream migration barrier to bull trout during most periods.

The U.S. Fish and Wildlife Service issued a final rule listing the Columbia River population of bull trout as threatened on June 10, 1998 (63 FR 31637). The Kootenai River Bull Trout Recovery Unit forms part of the range of the Columbia River bull trout population segment. The USFWS recognized five subpopulations of bull trout within the Kootenai River basin (USFWS 1998). These included three portions of the mainstem system: (1) Upper, upstream of Libby Dam, (2) Middle, from Libby Dam downstream to Kootenai Falls, and (3) Lower, downstream of Kootenai Falls through Idaho to the United States/Canada border. The two disconnected subpopulations (referred to as disjunct by the Montana Bull Trout Scientific Group), in Bull Lake (MBTSG 1996a) and Sophie Lake (MBTSG 1996b), were considered separate subpopulations.

The majority of the bull trout upstream of Libby Dam spawn in British Columbia in the Wigwam River, Gold Creek, Middle and North Forks of the White River, Skookumchuck and Redding creeks. Bull trout also spawn in Grave Creek, a tributary to the Tobacco River, located north east of Eureka, Montana (Figure 1). Bull trout redds have been counted in most of these tributaries for the past several years, and have generally exhibited increasing trends in abundance (Table 1). Montana Fish, Wildlife & Parks (FWP) recently conducted a mark-recapture bull trout population estimate below Libby Dam and estimated 978 adult bull trout (95% confidence interval 553 – 1,399) in the 3 miles below Libby Dam, and has reason to believe most of these fish may have been entrained through Libby Dam (Dunnigan et al. 2005).

Bull trout are generally less abundant in the mainstem Kootenai River below Libby Dam compared to upstream of Libby Dam. In the Middle Section of the Kootenai River, located between Libby Dam and Kootenai Falls, bull trout are known to spawn in West Fisher, Libby, Bear, Pipe, and Quartz creeks (Figure 1). Redds have also been counted in these spawning tributaries for several years, with varying trends in abundance (Table 1). The Lower Section of the Kootenai River is located downstream of Kootenai Falls, with bull trout spawning located in O'Brien and Callahan creeks. Bull Lake is considered a disconnected bull trout subpopulation, with fish from this population spawning in Keeler Creek, a tributary to Lake Creek, which flows into the Kootenai River at Rkm 301, near Troy, Montana. Bull trout from the Bull Lake subpopulation can migrate downstream to the Kootenai River, but waterfalls and a small hydroelectric facility prevent upstream migration.

Montana FWP initiated a study in the summer of 2005 to investigate the genetic structure of bull trout within the Kootenai Basin using genetic analysis. Montana FWP collected approximately 30 juvenile bull trout tissue samples from 15 tributaries located in British Columbia and Montana for this analysis (Table 2) to evaluate the efficacy of using noninvasive genetic techniques to determine the geographic or genetic origin of bull trout located below Libby Dam and Kootenai Falls.

There were three primary objectives of this study. Our first objective was to examine how genetic diversity was distributed both within and among bull trout populations in the Kootenai River Basin. Secondly we wanted to generate genetic data on the Kootenai River Basin to enter in to a range wide genetic database for bull trout. Our final objective was to assess our ability to use genetic markers to assign fish of unknown origin captured within the Kootenai River Basin to their population of origin. This would most likely include fish that were captured at the base of Libby Dam to determine if they originated in populations upstream of the dam.

Materials and Methods

Sample collection

During the summer of 2005 personnel from Montana FWP collected approximately 30 juvenile bull trout from 15 tributaries within the Kootenai River Basin in British Columbia and Montana (Figure 1, Table 2). Additionally Montana FWP personnel collected 25 fish identified as bull trout x brook trout hybrids for species ID and 1 fish identified as a brook trout. During the spring of 2006, Montana FWP collected 62 adult bull trout in the Kootenai River below Libby Dam for purposes of population assignment.

Laboratory analysis

DNA was extracted from all samples in a *Chelex 100* (Sigma Chemical Co.) resin solution as described by Miller and Kapuscinski (1996). All individuals were then genotyped at a core set of 12 microsatellite loci that were recently identified as a standard set of loci for population structure analyses. The loci used include: *Sco102, Sco105, Sco109* (Washington Dept. of Fish and Wildlife, *unpublished*), *Sco200, Sco202, Sco212, Sco215, Sco216*, *Sco220* (DeHaan and Ardren 2005), *Smm22* (Crane et al. 2004), *Omm1128* (Rexroad et al. 2001) and *Sfo18* (Angers et al. 1995). PCR reactions were conducted in 15 μl reactions containing 1X polymerase buffer (10 mM Tris-HCL, 50 mM KCL, 1% Triton X-100), 1.5 to 2mM $MgCl_2$, 0.2mM of each dNTP, 0.5μM of each primer and 0.5 units of Taq DNA polymerase (Promega Corporation).

Following PCR, reactions were pooled for electrophoresis on an *ABI 3100* Genetic Analyzer (Applied Biosystems, Inc., Foster City California). Automated electrophoresis was carried out using the G5 filter set following the manufacturer's protocols. *Genescan* and *Genotyper* software (Applied Biosystems, Inc., Foster City California) were used to identify alleles at each locus and to determine the multi-locus genotype of each fish at those loci.

Statistical analysis

We used the program GENEPOP v3.4 (Raymond and Rousset 1995) to perform exact tests for Hardy-Weinberg equilibrium. Hardy-Weinberg tests were adjusted for multiple comparisons using a sequential Bonferroni adjustement (Rice 1989). Measures of genetic diversity including numbers of alleles and observed and expected heterozygosity were calculated using the program GDA (Lewis and Zaykin 2001). We used GDA to estimate levels of genetic diversity among populations (F-statistics, Weir and Cockerham 1984) and the associated confidence levels. Pairwise estimates of *Fst* among all population pairs were also calculated and tested for statistical significance using the program F-Stat v2.9.3.2 (Goudet 2001). We used the program PHYLIP v3.5 (Felsenstein 1993) to generate a neighbor joining tree based on Cavalli-Sforza and Edwards chord distance. The resulting tree was visualized using the program TREEVIEW (Page 1996).

In order to assess our ability to correctly assign unknown fish to their population of origin we performed a jackknife of our baseline dataset for the Kootenai River Basin using the program WhichRun v4.1 (Banks and Eichert 2000). With this procedure fish are removed from the baseline dataset one at a time and treated as unknowns and then assigned to their most likely population of origin based on a maximum likelihood algorithm. The number of individuals that are assigned to their true population of origin provides a means of estimating the statistical power of the baseline dataset to assign unknown individuals. For our analysis we pooled populations from above and below Libby Dam to determine our ability to correctly determine whether fish originated from above or below the dam. Once we had assessed the power of our dataset, we used WhichRun to assign the 62 unknown adults to their first and second most likely population of origin within the Kootenai River system.

Results and Discussion

All 26 samples that were identified in the field as bull trout x brook trout hybrids were genetically identified as hybrids. In addition to these individuals, we identified eight more samples that had hybrid ancestry; KCCS07, KCCS25, PCSS01, PCSS14, PCSS16, OBCS02, OBCS05 and WFCS16 (Table 3). All of the fish identified as hybrids appeared to be F1 hybrids with the exception of 3 individuals, 2 from Pipe Creek and 1 from West Fisher Creek that appeared to be post F1 hybrids. Genetic analyses also confirmed that the individual from O’Brien Creek that was identified in the field as a brook trout was indeed a brook trout. All of these individuals were removed from subsequent statistical analyses.

Of the 15 populations that we surveyed, eight of them showed at least one deviation from Hardy Weinberg Equilibrium (HWE). Bear Creek, Keeler Creek, North Fork White, Middle Fork White and O’Brien Creek all deviated at a single locus, Grave Creek deviated at 2 loci and Bloom and West Fork Quartz Creeks deviated at three loci. Mean number of alleles per locus ranged from 2.083 in Libby Creek to 7.417 in Wigwam Creek (Table 3). Observed heterozygosity ranged from 0.184 in Libby Creek to 0.661 in West Fisher Creek (Table 3). Levels of genetic diversity we observed in this study were similar to those we have observed for bull trout in the Lake Pend Oreille/Clark Fork River system in Idaho and Montana (Ardren et al. 2005). However, levels of genetic diversity that we observed in this study were higher than those observed by Costello et al. (2003) in a study of bull trout that included the majority of the Canadian populations used in this study (Skookumchuck, Wigwam, Bloom, Redding, Grave, Middle Fork White). The greater levels of genetic diversity observed in this study were most likely due to the fact that we utilized microsatellite loci developed primarily from a bull trout DNA library (DeHaan and Ardren 2005) which have greater levels of polymorphism than markers used in previous studies (Costello et al. 2003, Spruell et al. 2003). Levels of genetic diversity were substantially lower in Libby and Keeler Creeks (Table 3). These two populations are both isolated above waterfalls and a small hydropower facility also blocks migration into Keeler Creek. Reductions in genetic diversity have previously been observed for populations isolated above barriers (Wofford et al. 2005) and this appears to be the most likely explanation for the reduction in genetic diversity we observed in these two populations.

Our overall estimate of F_{st} (genetic variance among populations) was 0.197. This value was found to be statistically significant ($P < 0.05$). Pairwise estimates of F_{st} ranged from 0.028 for West Fisher and O'Brien to 0.634 for Libby and Keeler creeks (Table 4). All pairwise estimates were found to be statistically significant ($P < 0.05$) following Bonferroni correction (Rice 1989). The neighbor-joining tree showed 4 clusters of populations (Figure 2) with populations found above Libby Dam grouping separately from populations found below Libby Dam. These data suggest that there is a high degree of genetic variation among different bull trout populations within the Kootenai River basin. Costello et al. (2003) also observed relatively high levels of variation among populations in a study that included many of these same bull trout populations. Levels of genetic variation among populations (F_{st}) that we observed in this study were comparable to those we have observed in other bull trout populations as well. In a similar study of bull trout in the Payette and Deadwood River systems in southwest Idaho, we found that the overall level of genetic variation was 0.270 and pairwise levels of F_{st} ranged from 0.070 to 0.440 (DeHaan et al. 2006). Although Libby and Keeler Creek lie in relatively close geographic proximity, the greatest level of pairwise variation was observed among these two populations

(Table 4). These populations are both isolated by barriers. Costello et al. (2003) found that bull trout populations isolated above barriers tended to show greater differentiation than populations below barriers.

Of the three populations that were below Kootenai Falls (O'Brien, Callahan and Keeler) Callahan and Keeler grouped together on the neighbor-joining tree whereas O'Brien grouped with populations found between the falls and Libby Dam. These data support the hypothesis that there is restricted gene flow between populations above and below Kootenai Falls, however the fact that O'Brien Creek groups with populations above the falls suggests that there may have been or there is currently some level of gene flow among populations above and below the falls. We observed some of the highest levels of pairwise F_{st} for the comparisons between Keeler Creek and the other populations in the study. The neighbor-joining tree also showed Keeler Creek to be highly differentiated from the other populations. These results are likely explained by the fact that Keeler Creek is isolated from the rest of the populations in this study by waterfalls and a hydroelectric facility.

We used the Jackknife procedure in the program WHICHRUN v4.1 to assess our ability to assign unknown individuals to their population of origin. Our jackknife analysis for the Kootenai River Basin assessed our ability to assign fish as originating from populations above or below Libby Dam. Our analysis of the population dataset indicated that we had a high degree of power to correctly assign unknown fish captured in the Kootenai River as originating either upstream or downstream of Libby Dam (Table 5). Ten of the fish (3%) that were sampled above Libby Dam were mis-classified as below dam origin. Of those 10, 2 fish were sampled in Grave Creek and 8 were sampled in Wigwam Creek. Eight fish (5%) that were sampled below Libby Dam were mis-classified as above dam origin. Of those 8, 4 were sampled in W. Fisher Creek, 1 in Pipe Creek, 1 in Bear Creek and 2 in O'Brien Creek.

Of the 62 unknown adults that we assigned to most likely population of origin, 31 were assigned to populations above Libby Dam and 31 were assigned to populations below Libby Dam (Table 6). This data indicates that although there is no upstream passage for bull trout at Libby Dam, bull trout can move downstream through the dam. Two studies of burbot (*Lota lota*) in the Kootenai River also demonstrated downstream movement of fish through Libby Dam (Paragamian et al. 1999, Skaar et al. 1996). The majority of the adults assigned to populations above the dam (17 of 31) were assigned to Wigwam River. This population has had the greatest number of redds observed since 1994 and geographically is closer to Libby Dam than other above dam populations (i.e. MF White and NF White). Of the remaining 14 individuals assigned above Libby Dam, the majority were assigned to Grave Creek (n=6) and Bloom Creek (n=4). While these two populations are smaller than Wigwam Creek, they also lie in close geographic proximity to Libby Dam. Of the 31 unknown adults assigned to populations below Libby Dam, all but 6 of them were assigned to populations above Kootenai Falls (Table 6). The six individuals assigned to populations downstream of the falls were all assigned to O'Brien Creek. The fact that the majority of the fish assigned to populations below the dam were assigned to populations above the falls provides further evidence that Kootenai Falls acts as a partial barrier to bull trout migration within the Kootenai River system.

Our final objective was to incorporate the data generated as a part of this project into a larger range wide bull trout genetic data set. The loci utilized for this project are currently being used by multiple labs conducting bull trout genetics studies. The use of this set of markers will facilitate combining data sets generated by different labs to address bull trout conservation issues on a larger scale.

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Figure 1. Diagram of the Kootenai River basin, including those tributaries where Montana FWP collected juvenile bull trout tissue samples for genetic analysis. Approximate sampling locations are identified with a black dots on Bear, Bloom, Callahan, Grave, Keeler, Libby, O'Brien, Pipe, Redding, Skookumchuck, West Fisher, and West Fork Quartz creeks, Middle Fork White, North Fork White, and Wigwam rivers.

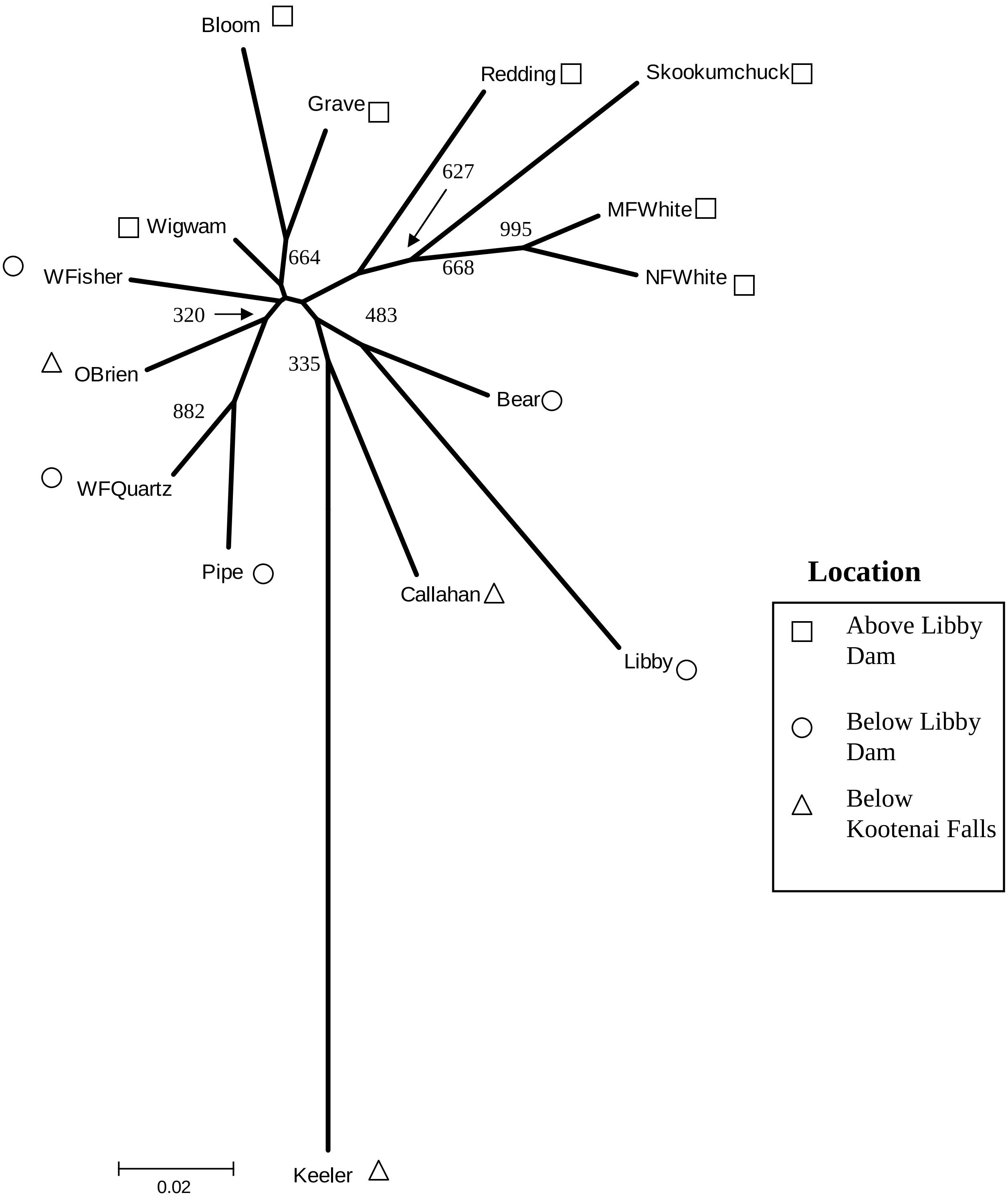

Figure 2. Neighbor-joining based on Cavalli-Sforza and Edwards Chord Distance showing the relationships among 15 bull trout populations in the Kootenai River Basin. Values on the nodes represent the number of bootstrap replicated out of 1000 that showed that structure.

Table 1. Summary of Kootenai Drainage bull trout redd counts from 1993 - 2005 in the stream sections monitored annually.

Stream	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005
Grave Creek [a]	36	71	15	35	49	66	134	97	173	199	245	141	194
Quartz Creek [b]	89	64	66	47	69	105	102	91	154	62	55	49	71
Pipe Creek	6	7	5	17	26	34	36	30	6	11	10	8	2
Bear Creek			6	10	13	22	36	23	4	17	14	6	3
West Fisher Creek	2	0	3	4	0	8	18	23	1	1	1	13	27
O'Brien Creek	6	7	22	12	36	47	37	34	47	45	46	51	81
Keeler Creek [c]				74	59	92	99	90	13	102	87	126	186
Wigwam River (U.S. &B.C.)[d]		104	247	512	598	679	868	1204	1496	1916	2053	2133	649[e]
Skookumchuck River (B.C.)					66	105	161	189	132	143	134	140	111
White River (B.C.) [f]										261	239	184	239
Callahan Creek (IDFG)[g]										19	40	25	21
Total				711	916	1158	1491	1781	1919	2776	2922	2876	1584
Total other than Wigwam				199	318	479	623	577	423	860	869	743	935

[a] Includes mainstem Grave Creek, Clarence Creek, Blue Sky Creek

[b] Includes mainstem Quartz Creek and West Fork Quartz Creek

[c] Includes mainstem Keeler Creek, North Fork Keeler Creek, South Fork Keeler Creek.

[d] Includes mainstem Wigwam River, Ram Creek, Lodgepole Creek, Desolation Creek.

[e] Massive slide downstream of traditional count area caused a partial barrier that likely inhibited migration

[f] Includes mainstem White River and Blackfoot Creek beginning 2002

[g] Includes North and South Callahan Creeks

Table 2. Summary of the bull trout spawning tributaries and the number of juvenile bull trout tissue samples that Montana FWP collected in 2005.

Sample Collection Location	**Number of Samples**	**Storage Media**
Bear Creek, MT	30	EtOH
Bloom Creek, B.C.	30	EtOH
Callahan Creek, MT	30	EtOH
Grave Creek, MT	30	EtOH
Keeler Creek, MT	32	EtOH
Libby Creek, MT	30	EtOH
Middle Fork White River, B.C.	30	EtOH
North Fork White River, B.C.	30	EtOH
O’Brien Creek, MT	46	EtOH
Pipe Creek, MT	28	EtOH
Redding Creek, B.C.	31	EtOH
Skookumchuck Creek, B.C.	30	EtOH
West Fisher River, MT	21	EtOH
West Fork Quartz Creek, MT	30	EtOH
Wigwam River, B.C.	30	EtOH
Total	**458**	

Table 3. Measures of genetic diversity for 15 bull trout populations in the Kootenai River basin in British Columbia and Montana.

Population	A	He	Ho	Number Hybrids
Bear	4.500	0.522	0.489	0
Bloom	4.833	0.484	0.468	0
Callahan	6.000	0.642	0.594	0
Grave	6.167	0.619	0.570	0
Keeler	3.417	0.347	0.308	4
Libby	2.083	0.231	0.184	0
Middle Fork White	6.833	0.614	0.543	0
North Fork White	5.583	0.561	0.531	0
O'Brien	6.583	0.610	0.649	18
Pipe	4.417	0.548	0.575	8
Redding	6.917	0.584	0.538	0
Skookumchuck	5.500	0.604	0.611	0
West Fork Quartz	5.250	0.547	0.563	1
West Fisher	6.167	0.645	0.661	2
Wigwam	7.417	0.632	0.631	0
Mean	**5.444**	**0.546**	**0.528**	

A = Mean number alleles per locus
He = Expected heterozygosity
Ho = Observed heterozygosity

Table 4. Pairwise estimates of Fst based on 12 microsatellite loci for 15 bull trout populations in the Kootenai River Basin. All values were found to be statistically significant following a Bonferroni correction ($P < 0.05$).

	Bear	Bloom	Callahan	Grave	Keeler	Libby	Middle Fork White	North Fork White	O'Brien	Pipe	Redding	Skookumchuck	West Fork Quartz	West Fisher	Wigwam
Bear	-														
Bloom	0.151	-													
Callahan	0.171	0.213	-												
Grave	0.104	0.116	0.115	-											
Keeler	0.438	0.485	0.407	0.392	-										
Libby	0.294	0.391	0.318	0.276	0.634	-									
M. Fork White	0.163	0.168	0.127	0.126	0.415	0.325	-								
N. Fork White	0.184	0.199	0.184	0.150	0.459	0.356	0.034	-							
O'Brien	0.088	0.157	0.119	0.064	0.404	0.273	0.106	0.118	-						
Pipe	0.151	0.217	0.174	0.121	0.394	0.421	0.197	0.235	0.137	-					
Redding	0.134	0.131	0.166	0.098	0.427	0.286	0.078	0.103	0.093	0.194	-				
Skookumchuck	0.182	0.191	0.136	0.116	0.429	0.401	0.125	0.148	0.112	0.186	0.140	-			
W. Fork Quartz	0.130	0.194	0.169	0.105	0.407	0.360	0.171	0.191	0.075	0.077	0.167	0.152	-		
West Fisher	0.094	0.139	0.098	0.063	0.403	0.300	0.092	0.118	0.028	0.123	0.090	0.128	0.098	-	
Wigwam	0.079	0.093	0.110	0.042	0.386	0.268	0.093	0.103	0.030	0.113	0.069	0.111	0.091	0.033	-

Table 5. Results of WHICHRUN jackknife analysis to examine the power of the baseline dataset to correctly assign unknown individuals to populations above and below Libby Dam. Numbers in bold represent the proportion of individuals correctly assigned to their area of origin.

	Proportion of Individuals Assigned	
Area of Origin	Above Libby Dam	Below Libby Dam
Above Libby Dam	**0.97**	0.03
Below Libby Dam	0.05	**0.95**

Table 6. Genetic assignments based on 12 microsatellite loci of 62 adult bull trout captured in the Kootenai River below Libby Dam.

ID	Capture Location	Most Likely Population	Above/Below Dam?	2nd Most Likely Population	Above/Below Dam?	Confidence*
BT-001	Alexander tailout to Fisher River	Libby Cr (above falls)	Below	West Fisher R	Below	16.045
BT-002	Alexander tailout to Fisher River	Bear Creek	Below	WF Quartz Creek	Below	1.36E+03
BT-003	Alexander tailout to Fisher River	O'Brien Creek	Below	WF Quartz Creek	Below	6.69453
BT-004	Alexander tailout to Fisher River	WF Quartz Creek	Below	Wigwam Drainage	Above	2.20409
BT-005	Alexander tailout to Fisher River	Grave Creek	Above	Wigwam Drainage	Above	1.68205
BT-006	Alexander tailout to Fisher River	O'Brien Creek	Below	West Fisher R	Below	2.12286
BT-007	Alexander tailout to Fisher River	West Fisher R	Below	Grave Creek	Above	1.49802
BT-008	Alexander tailout to Fisher River	West Fisher R	Below	Callahan Creek	Below	6.26963
BT-009	Alexander tailout to Fisher River	Libby Cr (above falls)	Below	Wigwam Drainage	Above	2.47E+03
BT-010	Alexander tailout to Fisher River	Grave Creek	Above	West Fisher R	Below	18.822
BT-011	Alexander tailout to Fisher River	Wigwam Drainage	Above	West Fisher R	Below	24.376
BT-012	Libby Dam to Alexander tailout	West Fisher R	Below	Wigwam Drainage	Above	1.304
BT-013	Libby Dam to Alexander tailout	O'Brien Creek	Below	Wigwam Drainage	Above	1.76628
BT-014	Libby Dam to Alexander tailout	Grave Creek	Above	Bloom Creek	Above	4.08227
BT-015	Libby Dam to Alexander tailout	O'Brien Creek	Below	Grave Creek	Above	16.381
BT-016	Libby Dam to Alexander tailout	O'Brien Creek	Below	West Fisher R	Below	2.5351
BT-017	Libby Dam to Alexander tailout	Pipe Creek	Below	Wigwam Drainage	Above	5.42984
BT-018	Libby Dam to Alexander tailout	Wigwam Drainage	Above	Grave Creek	Above	250.3
BT-019	Libby Dam to Alexander tailout	Wigwam Drainage	Above	MF White R	Above	2.40619
BT-020	Libby Dam to Alexander tailout	Redding Creek	Above	Callahan Creek	Below	3.35474
BT-021	Libby Dam to Alexander tailout	Wigwam Drainage	Above	West Fisher R	Below	6.02511
BT-022	Libby Dam to Alexander tailout	West Fisher R	Below	Wigwam Drainage	Above	12.734
BT-023	Libby Dam to Alexander tailout	Wigwam Drainage	Above	Grave Creek	Above	5.87802
BT-024	Libby Dam to Alexander tailout	Wigwam Drainage	Above	Libby Cr (above falls)	Below	1.79464
BT-025	Libby Dam to Alexander tailout	Bloom Creek	Above	Bear Creek	Below	9.01442
BT-026	Libby Dam to Alexander tailout	Libby Cr (above falls)	Below	O'Brien Creek	Below	7.05875
BT-027	Libby Dam to Alexander tailout	Bear Creek	Below	Wigwam Drainage	Above	1.17538
BT-028	Libby Dam to Alexander tailout	West Fisher R	Below	Wigwam Drainage	Above	3.69629
BT-029	Libby Dam to Alexander tailout	Bloom Creek	Above	WF Quartz Creek	Below	11.724
BT-030	Libby Dam to Alexander tailout	West Fisher R	Below	Bear Creek	Below	13.03
BT-031	Libby Dam to Alexander tailout	Bear Creek	Below	Grave Creek	Above	2.04635

ID	Capture Location	Most Likely Population	Above/Below Dam?	2nd Most Likely Population	Above/Below Dam?	Confidence*
BT-032	Libby Dam to Alexander tailout	West Fisher R	Below	Wigwam Drainage	Above	299.6
BT-033	Libby Dam to Alexander tailout	WF Quartz Creek	Below	Grave Creek	Above	2.53415
BT-034	Libby Dam to Alexander tailout	WF Quartz Creek	Below	Pipe Creek	Below	1.92995
BT-035	Libby Dam to Alexander tailout	WF Quartz Creek	Below	Wigwam Drainage	Above	3.03462
BT-036	Libby Dam to Alexander tailout	Wigwam Drainage	Above	West Fisher R	Below	24.376
BT-037	Libby Dam to Alexander tailout	Wigwam Drainage	Above	West Fisher R	Below	1.19952
BT-038	Libby Dam to Alexander tailout	Wigwam Drainage	Above	Grave Creek	Above	1.48688
BT-039	Alexander Tailout to Fisher River	Wigwam Drainage	Above	NF White R	Above	1.77029
BT-040	Alexander Tailout to Fisher River	Wigwam Drainage	Above	O'Brien Creek	Below	8.81112
BT-041	Alexander Tailout to Fisher River	West Fisher R	Below	Pipe Creek	Below	3.47233
BT-042	Alexander Tailout to Fisher River	WF Quartz Creek	Below	Wigwam Drainage	Above	1.26832
BT-043	Alexander Tailout to Fisher River	NF White R	Above	MF White R	Above	1.86854
BT-044	Alexander Tailout to Fisher River	Grave Creek	Above	Bear Creek	Below	1.47273
BT-045	Alexander Tailout to Fisher River	O'Brien Creek	Below	West Fisher R	Below	11.034
BT-046	Alexander Tailout to Fisher River	Wigwam Drainage	Above	WF Quartz Creek	Below	50.894
BT-047	Alexander Tailout to Fisher River	WF Quartz Creek	Below	Grave Creek	Above	55.469
BT-048	Alexander Tailout to Fisher River	Pipe Creek	Below	WF Quartz Creek	Below	377.6
BT-049	Alexander Tailout to Fisher River	Bloom Creek	Above	Grave Creek	Above	3.27691
BT-050	Alexander Tailout to Fisher River	Bloom Creek	Above	Wigwam Drainage	Above	1.94052
BT-051	Alexander Tailout to Fisher River	Bear Creek	Below	Wigwam Drainage	Above	9.97645
BT-052	Alexander Tailout to Fisher River	Wigwam Drainage	Above	Bear Creek	Below	4.23236
BT-053	Alexander Tailout to Fisher River	Wigwam Drainage	Above	West Fisher R	Below	1.60528
BT-054	Alexander Tailout to Fisher River	Grave Creek	Above	Bloom Creek	Above	3.02265
BT-055	Alexander Tailout to Fisher River	WF Quartz Creek	Below	Wigwam Drainage	Above	1.81216
BT-056	Alexander Tailout to Fisher River	MF White R	Above	NF White R	Above	8.8475
BT-057	Alexander Tailout to Fisher River	Wigwam Drainage	Above	NF White R	Above	2.65875
BT-058	Alexander Tailout to Fisher River	Grave Creek	Above	Wigwam Drainage	Above	1.68205
BT-059	Alexander Tailout to Fisher River	West Fisher R	Below	Pipe Creek	Below	1.57374
BT-060	Alexander Tailout to Fisher River	Wigwam Drainage	Above	Bear Creek	Below	2.88185
BT-061	Alexander Tailout to Fisher River	Redding Creek	Above	MF White R	Above	27.959
BT-062	Alexander Tailout to Fisher River	Wigwam Drainage	Above	WF Quartz Creek	Below	2.59886

* **CONFIDENCE (X times more confident Most Likely (ML) vs 2nd Most Likely (SML)) i.e., P(ML/SML)**