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Genetic Stock Identification and Relative Contribution of Arctic Char (*Salvelinus alpinus*) from the Hornaday and Brock Rivers to Subsistence Fisheries in Darnley Bay, Northwest Territories

Les N. Harris,[1,2] David A. Boguski,[1,3] Colin P. Gallagher[1] and Kimberly L. Howland[1]

APPENDIX 1

TABLE S1. Polymerase chain reaction (PCR)[1] information.

Multiplex	Primer[2]	Dye[3]	Reference	[Primer] (μM)	[$MgCl_2$] (mM)	[dNTPs] (μM)	Taq[4]
mpAC1	Sco200	VIC	DeHaan and Ardren, 2005	0.40	1.50	200	1.00
	Smm22	NED	Crane et al., 2004	0.40			
	Sco220	6-FAM	DeHaan and Ardren, 2005	0.50			
	Sco215	PET	DeHaan and Ardren, 2005	0.30			
mpAC2a[5]	Sco212	6-FAM	DeHaan and Ardren, 2005	0.50	2.00	200	0.50
	Sco218	VIC	DeHaan and Ardren, 2005	0.50			
	Sfo18	NED	Angers et al., 1995	0.20			
mpAC2b[5]	Sco202	PET	DeHaan and Ardren, 2005	0.20	1.50	200	0.50
	Smm21	VIC	Crane et al., 2004	0.16			
mpAC3	OMM1128	VIC	Rexroad et al., 2001	0.16	2.00	200	0.50
	Smm24	NED	Crane et al., 2004	0.20			
	OtsG253b	VIC	Williamson et al., 2002	0.12			
	SSOSL456	6-FAM	Slettan et al., 1995	0.50			
	OMM1105	PET	Rexroad et al., 2002	0.20			
mpAC4	OtsG83b	6-FAM	Williamson et al., 2002	0.50	2.00	200	1.00
	Smm17	NED	Crane et al., 2004	0.16			
	Sco109	VIC	Washington Dept. of Fish and Wildlife unpubl.	0.50			
	Sco216	PET	DeHaan and Ardren, 2005	0.40			

[1] PCR Protocol: 1 × 95˚C for 5 min; 35 × 95˚C for 30 sec, 55˚C for 30 sec, 72˚C for 45 sec; 1 × 72˚C for 30 min.
[2] Reverse primer is custom tailed (a 7 base sequence added onto the 5’ end).
[3] Forward primer is labeled with fluorescent dye.
[4] AmpliTaq Gold® DNA Polymerase with Gold Buffer and $MgCl_2$ solution from Applied Biosystems.
[5] These multiplexes are post-PCR combined before running on the sequencer.

REFERENCES

Angers, B., Bernatchez, L., Angers, A., and Desgroseillers, L. 1995. Specific microsatellite loci for brook charr reveal strong population subdivision on a microgeographic scale. Journal of Fish Biology 47(sA):177–185. http://dx.doi.org/10.1111/j.1095-8649.1995.tb06054.x

Crane, P.A., Lewis, C.J., Kretschmer, E.J., Miller, S.J., Spearman, W.J., DeCicco, A.L., Lisac, M.J., and Wenburg, J.K. 2004. Characterization and inheritance of seven microsatellite loci from Dolly Varden, *Salvelinus malma*, and cross-species amplification in Arctic char, S. *alpinus*. Conservation Genetics 5(5):737–741. http://dx.doi.org/10.1007/s10592-004-1853-1

DeHaan, P.W., and Ardren, W.R. 2005. Characterization of 20 highly variable tetranucleotide microsatellite loci for bull trout (*Salvelinus confluentus*) and cross-amplification in other *Salvelinus* species. Molecular Ecology Notes 5(3):582–585. http://dx.doi.org/10.1111/j.1471-8286.2005.00997.x

Rexroad, C.E., III, Coleman, R.L., Martin, A.M., Hershberger, W.K., and Killefer, J. 2001. Thirty-five polymorphic microsatellite markers for rainbow trout (*Oncorhynchus mykiss*). Animal Genetics 32(5):317–319. http://dx.doi.org/10.1046/j.1365-2052.2001.0730b.x

Rexroad, C.E., III, Coleman, R.L., Hershberger, W.K., and Killefer, J. 2002. Rapid communication: Thirty-eight polymorphic microsatellite markers for mapping in rainbow trout. Journal of Animal Science 80(2):541–542.

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[1] Fisheries and Oceans Canada, 501 University Crescent, Winnipeg, Manitoba R3T 2N6, Canada
[2] Corresponding author: Les.N.Harris@dfo-mpo.gc.ca
[3] Biodive Scientific Inc., 43 Casselman Crescent, Oak Bluff, Manitoba R4G 0A2, Canada

Slettan, A., Olsaker, I., and Lie, Ø. 1995. Atlantic salmon, *Salmo salar*, microsatellites at the SSOSL 25, SSOSL 85, SSOSL 311, SSOSL 417 loci. Animal Genetics 26:281–282.

Williamson, K.S., Cordes, J.F., and May, B. 2002. Characterization of microsatellite loci in chinook salmon (*Oncorhynchus tshawytscha*) and cross species amplification in other salmonids. Molecular Ecology Notes 2(1):17–19. http://dx.doi.org/10.1046/j.1471-8286.2002.00129.x

TABLE S2. Basic descriptive statistics for 14 microsatellite loci for the eight Darnley Bay and Hornaday and Brock River Arctic char sampling locations. Average number of alleles per locus (N_A), expected (H_E) and observed (H_O) heterozygosities, inbreeding coefficient (F_{IS}), allelic richness (A_R), and private allelic richness (PA_R) are shown for each sampling location for each locus and the averages over all loci. For key to sampling location codes, see Table 1 and Figure 1. A_R and PA_R calculated from a sample of 100 genes.

BRK-A	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	16	12	4	14	9	9	2	9	9	12	5	19	4	18	10.14
H_E	0.91	0.73	0.42	0.89	0.79	0.81	0.51	0.76	0.73	0.88	0.41	0.90	0.62	0.93	0.73
H_O	0.83	0.74	0.43	0.92	0.68	0.86	0.46	0.75	0.65	0.85	0.44	0.80	0.65	0.97	0.72
F_{IS}	0.10	-0.01	0.03	-0.03	0.12	-0.07	0.12	0.02	0.12	0.04	-0.11	0.11	-0.04	-0.05	0.03
A_R	16.00	12.00	4.00	14.00	9.00	9.00	2.00	9.00	9.00	12.00	5.00	19.00	4.00	18.00	10.14
PA_R	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.67	1.00	0.82	0.00	0.02	0.18
BRK-B	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	16	10	3	12	8	7	2	7	6	10	2	15	5	11	8.14
H_E	0.86	0.87	0.42	0.88	0.81	0.66	0.19	0.64	0.60	0.83	0.49	0.91	0.71	0.86	0.69
H_O	0.83	0.60	0.43	0.77	0.80	0.43	0.24	0.77	0.43	0.87	0.53	0.97	0.63	0.90	0.66
F_{IS}	0.07	0.31	0.14	0.14	0.06	0.22	-0.10	-0.18	0.20	-0.07	-0.15	-0.06	0.09	-0.07	0.04
A_R	16.00	10.00	3.00	12.00	8.00	7.00	2.00	7.00	6.00	10.00	2.00	15.00	5.00	11.00	8.14
PA_R	0.01	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.45	0.00	0.00	0.00	0.00	0.10
LAKE-A	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	6	8	3	10	7	7	1	9	4	5	3	14	2	7	6.14
H_E	0.65	0.82	0.49	0.72	0.44	0.80	0.00	0.53	0.61	0.80	0.53	0.75	0.36	0.52	0.57
H_O	0.62	0.81	0.55	0.72	0.40	0.48	0.00	0.56	0.71	0.85	0.54	0.79	0.36	0.38	0.55
F_{IS}	0.04	0.08	-0.12	-0.05	0.03	0.39	NA	0.08	-0.14	-0.09	0.09	-0.03	0.17	0.31	0.06
A_R	6.00	8.00	3.00	10.00	7.00	7.00	1.00	9.00	4.00	5.00	3.00	14.00	2.00	7.00	6.14
PA_R	0.00	0.00	0.00	0.00	1.00	0.28	0.00	0.43	0.00	0.00	0.00	2.82	0.00	0.00	0.32
LAKE-B	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	10	9	2	10	5	8	2	8	3	6	3	11	3	7	6.21
H_E	0.82	0.66	0.48	0.66	0.70	0.72	0.05	0.79	0.18	0.75	0.47	0.83	0.62	0.68	0.60
H_O	0.80	0.60	0.39	0.73	0.83	0.68	0.04	0.80	0.14	0.69	0.31	0.65	0.62	0.69	0.57
F_{IS}	-0.02	0.09	0.23	-0.11	-0.17	0.02	-0.01	-0.02	0.05	0.12	0.33	0.20	0.12	0.06	0.06
A_R	10.00	9.00	2.00	10.00	5.00	8.00	2.00	8.00	3.00	6.00	3.00	11.00	3.00	7.00	6.21
PA_R	0.00	0.39	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	0.10
HORN-A	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	20	10	4	14	9	8	2	10	6	15	3	22	5	11	9.93
H_E	0.95	0.83	0.43	0.91	0.80	0.83	0.48	0.84	0.71	0.89	0.54	0.96	0.66	0.89	0.77
H_O	0.75	0.78	0.56	0.81	0.76	1.00	0.19	0.74	0.70	0.79	0.40	0.33	0.50	0.84	0.65
F_{IS}	0.09	0.20	0.15	0.01	0.01	0.02	0.22	-0.05	0.03	0.00	0.50	0.08	-0.06	0.00	0.08
A_R	20.00	10.00	4.00	14.00	9.00	8.00	2.00	10.00	6.00	15.00	3.00	22.00	5.00	11.00	9.93
PA_R	0.00	0.02	0.00	0.00	0.00	0.00	0.00	1.00	0.00	0.29	0.00	1.23	0.00	0.00	0.18
HORN-B	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	23	13	4	14	11	13	2	13	10	14	6	29	6	14	12.29
H_E	0.95	0.81	0.50	0.91	0.80	0.85	0.39	0.82	0.75	0.88	0.62	0.95	0.73	0.89	0.77
H_O	0.87	0.67	0.37	0.90	0.79	0.81	0.37	0.88	0.69	0.89	0.27	0.89	0.70	0.89	0.71
F_{IS}	0.01	0.08	0.07	0.03	0.19	0.15	0.09	0.12	0.02	0.07	-0.34	0.05	0.13	0.04	0.05
A_R	23.00	13.00	4.00	14.00	11.00	13.00	2.00	13.00	10.00	14.00	6.00	29.00	6.00	14.00	12.29
PA_R	0.02	0.00	0.00	0.47	1.00	0.00	0.00	0.00	0.00	0.00	0.00	1.82	0.00	0.00	0.24
LAS-10	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	14	10	5	14	8	7	2	9	7	11	4	2	7	14	8.14
H_E	0.92	0.89	0.62	0.94	0.85	0.78	0.28	0.84	0.79	0.89	0.60	0.33	0.53	0.92	0.73
H_O	0.93	0.79	0.44	0.86	0.78	0.73	0.36	0.66	0.66	0.81	0.54	0.79	0.59	0.75	0.69
F_{IS}	0.18	0.12	0.09	0.14	0.10	-0.28	0.32	0.12	0.11	0.12	0.33	0.00	0.06	0.08	0.11
A_R	14.00	10.00	5.00	14.00	8.00	7.00	2.00	9.00	7.00	11.00	4.00	2.00	7.00	14.00	8.14
PA_R	0.00	0.00	1.00	0.00	0.67	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00	1.82	0.32

TABLE S2 – *continued*: Basic descriptive statistics for 14 microsatellite loci for the eight Darnley Bay and Hornaday and Brock River Arctic char sampling locations. Average number of alleles per locus (N_A), expected (H_E) and observed (H_O) heterozygosities, inbreeding coefficient (F_{IS}), allelic richness (A_R), and private allelic richness (PA_R) are shown for each sampling location for each locus and the averages over all loci. For key to sampling location codes, see Table 1 and Figure 1. A_R and PA_R calculated from a sample of 100 genes.

LAS-11	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	28	19	4	18	11	16	2	15	13	20	8	38	8	22	15.86
H_E	0.94	0.80	0.36	0.90	0.74	0.86	0.46	0.77	0.70	0.86	0.57	0.95	0.74	0.89	0.75
H_O	0.77	0.82	0.41	0.77	0.70	0.80	0.52	0.86	0.59	0.95	0.43	0.83	0.61	0.91	0.71
F_{IS}	0.06	0.05	0.05	0.05	0.03	0.15	0.10	0.10	0.07	0.01	-0.16	0.04	0.05	-0.01	0.04
A_R	22.54	12.12	3.44	14.60	9.28	11.88	2.00	9.72	9.13	14.42	6.18	26.82	5.53	14.31	11.57
PA_R	0.33	0.91	0.00	0.18	0.00	0.36	0.00	0.18	0.38	0.39	0.33	0.33	0.30	0.40	0.29
LAS-12	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	23	14	4	16	10	12	2	9	10	13	5	30	5	14	11.93
H_E	0.94	0.78	0.49	0.89	0.75	0.84	0.43	0.76	0.73	0.84	0.43	0.95	0.74	0.89	0.75
H_O	0.88	0.76	0.34	0.85	0.71	0.73	0.41	0.70	0.65	0.85	0.66	0.91	0.70	0.90	0.72
F_{IS}	0.02	0.04	0.07	-0.05	0.05	0.13	0.01	0.10	-0.05	0.00	0.06	0.16	-0.01	0.05	0.04
A_R	21.73	11.79	3.55	13.58	9.00	10.35	2.00	7.85	8.98	11.65	4.98	27.16	5.00	12.98	10.76
PA_R	0.01	0.09	0.00	0.21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.61	0.00	0.00	0.07
HORN-09	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	15	7	3	10	9	9	2	8	7	8	5	21	6	12	8.71
H_E	0.94	0.75	0.41	0.82	0.76	0.86	0.51	0.81	0.70	0.80	0.40	0.96	0.76	0.88	0.74
H_O	0.94	0.74	0.46	0.88	0.65	0.72	0.35	0.71	0.73	0.82	0.84	0.90	0.63	0.85	0.73
F_{IS}	0.17	-0.10	0.01	0.05	0.09	0.07	-0.03	-0.06	0.15	-0.19	-0.08	0.14	0.20	-0.04	0.03
A_R	15.00	7.00	3.00	10.00	9.00	9.00	2.00	8.00	7.00	8.00	5.00	21.00	6.00	12.00	8.71
PA_R	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.14
HORN-10	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	23	13	4	15	10	13	2	11	10	17	5	27	6	13	12.07
H_E	0.94	0.82	0.46	0.90	0.75	0.89	0.40	0.77	0.71	0.90	0.55	0.95	0.76	0.89	0.76
H_O	0.96	0.82	0.32	0.88	0.78	0.69	0.35	0.80	0.70	0.75	0.75	0.88	0.81	0.87	0.74
F_{IS}	0.02	0.05	0.05	0.04	-0.04	0.18	0.09	0.14	0.06	0.09	0.01	0.17	0.22	0.16	0.09
A_R	22.63	12.74	3.91	14.62	10.00	12.88	2.00	10.53	9.35	16.36	5.00	27.00	6.00	12.78	11.84
PA_R	0.37	0.89	0.00	0.00	0.00	0.00	0.00	0.00	1.24	1.10	0.00	1.77	0.00	0.00	0.38
HORN-11	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	24	15	4	13	11	12	2	14	11	15	6	29	5	19	12.86
H_E	0.93	0.79	0.34	0.87	0.80	0.85	0.45	0.79	0.70	0.83	0.61	0.95	0.74	0.88	0.75
H_O	0.91	0.69	0.43	0.82	0.77	0.72	0.43	0.74	0.66	0.85	0.36	0.84	0.67	0.88	0.70
F_{IS}	-0.04	-0.04	0.08	-0.01	0.02	0.19	0.22	0.00	0.01	0.10	-0.23	0.07	-0.10	0.01	0.02
A_R	21.71	12.87	3.83	12.32	10.13	11.61	2.00	11.78	9.32	12.80	5.78	26.26	5.00	15.97	11.53
PA_R	0.06	0.13	0.00	0.29	0.57	0.26	0.00	0.00	0.00	0.00	0.00	0.96	0.00	1.54	0.27
HORN-12	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	24	14	4	19	11	16	2	13	10	21	6	37	8	13	14.14
H_E	0.94	0.77	0.43	0.90	0.78	0.84	0.45	0.80	0.72	0.88	0.43	0.96	0.76	0.89	0.75
H_O	0.92	0.75	0.45	0.94	0.71	0.73	0.42	0.69	0.77	0.84	0.40	0.80	0.75	0.84	0.71
F_{IS}	0.03	0.10	-0.02	0.09	0.01	0.14	0.04	0.09	0.09	0.04	0.16	0.12	0.11	0.01	0.07
A_R	20.69	10.90	3.55	15.27	9.48	12.53	2.00	10.93	8.30	16.24	5.31	29.45	6.21	12.05	11.64
PA_R	0.00	0.37	0.00	0.66	0.36	1.21	0.00	0.00	0.27	0.21	0.37	2.87	0.60	0.11	0.50
ALL	Sco220	Sco200	Sco215	Smm22	Sco202	Sco218	Sfo18	OMM1105	OtsG25	Smm24	SSOSL4	Sco216	Smm17	OtsG83	Avg.
N_A	29	23	5	22	17	19	2	17	16	23	9	57	10	27	19.71
H_E	0.90	0.79	0.46	0.86	0.75	0.81	0.34	0.76	0.66	0.85	0.50	0.87	0.67	0.84	0.72
H_O	0.84	0.74	0.43	0.84	0.72	0.72	0.31	0.74	0.62	0.83	0.51	0.80	0.63	0.82	0.68
F_{IS}	0.07	0.09	0.06	0.03	0.04	0.09	0.08	0.04	0.06	0.01	0.05	0.08	0.09	0.05	0.06
A_R	17.30	10.55	3.54	13.01	8.65	9.64	1.92	9.34	7.31	11.64	4.37	20.29	5.06	12.18	9.63
PA_R	0.06	0.22	0.08	0.13	0.42	0.16	0.00	0.13	0.24	0.26	0.14	1.02	0.16	0.28	0.24

TABLE S3. STRUCTURE (Pritchard et al., 2000) results showing the mean log-likelihood values (LnP[D]) for different hypothesized numbers of genetic populations (K) and the mean value of the ΔK statistic of Evanno et al. (2005). Red values represent the most likely number of genetic groups indicated by ΔK. Dashes = not applicable given that ΔK cannot be calculated for these values of K. Results of the STRUCTURE analysis are also shown in Figure 3.

	All sampling locations			Baseline sampling locations		
K	Mean LnP[D]	SD LnP(D)	ΔK	Mean LnP[D]	SD LnP(D)	ΔK
1	−49842.50	0.21	—	−11735.73	0.53	—
2	−48447.65	10.17	69.94	−10887.00	55.29	7.41
3	−47763.99	105.77	0.36	−10448.19	264.11	0.19
4	−47118.34	59.47	2.82	−10058.96	4.12	114.66
5	−46640.16	254.68	0.59	−10142.44	69.82	1.57
6	−46312.71	16.63	23.91	−10116.28	62.34	1.54
7	−46382.94	215.63	0.80	−10185.98	75.10	0.95
8	−46279.65	286.75	0.04	−10327.05	105.09	1.34
9	−46188.96	257.61	0.53	−10608.53	208.96	0.40
10	−46235.90	276.09	0.20	−10807.44	140.01	—
11	−46337.43	335.21	0.84			
12	−46155.79	283.00	1.05			
13	−46272.63	233.68	0.15			
14	−46424.82	221.40	0.45			
15	−46477.28	338.38	—			

TABLE S4. Results of the 100% simulations performed using the program ONCOR (Kalinowski et al., 2007) to evaluate the power of our baseline sampling locations for genetic stock identification (GSI) and for subsequent mixed-stock fishery analysis, using empirical baseline sample sizes and simulated sizes of 100 and 200. This analysis creates simulated mixture and baseline samples by randomly drawing allele frequencies from each baseline (i.e., 100% of the simulated mixture is from one baseline population). ONCOR then estimates the proportion of the simulated mixture sample that is assigned back to the baseline. Values close to 1.0 suggest that the baseline sampling location performs well in GSI, and values greater than 0.9 are suggested to be informative for management purposes.

Baseline sample	Empirical			100			200		
	Average	SD	95% C.I.	Average	SD	95% C.I.	Average	SD	95% C.I.
BRK-A	0.731	0.018	(0.696, 0.761)	0.977	0.012	(0.948, 0.994)	0.995	0.005	(0.982, 1.000)
BRK-B	0.908	0.012	(0.887, 0.933)	0.996	0.004	(0.989, 1.000)	0.999	0.001	(0.995, 1.000)
HORN	0.951	0.010	(0.931, 0.966)	0.983	0.007	(0.967, 0.996)	0.994	0.005	(0.981, 1.000)