MEMORANDUM

State of Alaska

Department of Fish and Game
Division of Commercial Fisheries

TO:	Jeff Regnart Division of Commercial Fisheries Director And Charles Swanton Sport Fish Division Director	DATE:	November 30, 2012
THROUGH:	William Templin Fisheries Scientist I	PHONE NO:	267-2290
FROM:	Andrew Barclay Fishery Biologist III	SUBJECT:	ESSN Chinook salmon MSA

From 2010 to 2012 genetic tissue samples were collected opportunistically from Chinook salmon harvested in the Upper Cook Inlet (UCI) Upper Subdistrict set gillnet fishery, commonly referred to as the East Side Set Net (ESSN) fishery. Tissue samples were collected from Chinook salmon during regular openings at receiving sites and occasionally from a fish processor the following day. The sampling goal for each fishing period was to sample as many Chinook salmon as possible during each tide from all areas of the ESSN fishery. Because there was only one dedicated person to collect these samples, some areas of the ESSN fishery could not be sampled during each tide. Additionally, some areas were targeted for sampling because they were expected to have larger Chinook salmon harvests, while some areas with lower harvests were not sampled. A total of 885, 1281, and 185 Chinook salmon genetic tissue samples were collected in 2010, 2011, and 2012, respectively.

In 2012 the ESSN fishery was closed for much of the season to protect Chinook salmon returning to the Kenai River. In the fall of 2012, the Gene Conservation Laboratory was directed to proceed with analysis of the collected samples to determine the stock composition the ESSN during the three years. Based on discussions with biologists and biometricians from both Commercial Fisheries and Sport Fish divisions, the 2012 samples were excluded from the analysis because of the low sample size and restricted fishing periods from which they originated. The GCL generally does not release estimates that might have management or allocation implications until data are collected over a minimum of three years. However, due to the public interest in this question, the GCL has analyzed the 2010 and 2011 collections and the results are provided in this memo. These estimates should be viewed as preliminary until data from a more structured study plan from additional years are analyzed.

The current genetic baseline for UCI Chinook salmon contains a total of 66 individual collections representing 32 populations which have been analyzed for 40 single nucleotide polymorphism loci (Table 1; Figure 1). This baseline contains the same set of loci and collections as the baseline reported in Barclay et al. (2012) with the exception of two additional Kenai River populations (Grant Creek and Lower Kenai River mainstem). The updated baseline was used in the analysis of the ESSN fishery samples; however, Slikok Creek (Kenai River) was removed from the baseline because it is a very small population and it is genetically similar to Crooked Creek (Kasilof River). Initial tests of the baseline (which included Slikok Creek) for mixed-stock analysis (MSA) indicated that a large portion of Crooked Creek fish misallocated to Slikok Creek. Once Slikok Creek was excluded, MSA tests of the baseline indicated that adequate genetic differentiation existed among all the reporting groups and that they could be used with high confidence (at least 90% correct allocations in 100% proof tests; see methods in Barclay et al. 2010). These reporting groups include: 1) all UCI Chinook population North and West of the Kenai River; *NorthwestCI*, 2) Kenai River tributary populations (excluding Juneau Creek); *KenaiTrib*, 3) Kenai River mainstem populations including Juneau Creek; *KenaiMainstem*, 4) the Kasilof River mainstem population; *KasilofMainstem*, and 5) Anchor River, Ninilchik River, Deep Creek, and Crooked Creek; *CoastalSKenaiPen* (Table 1; Figure 1). Although Juneau Creek is a tributary of the Kenai River it was included in the Kenai River mainstem reporting group because it is genetically similar to Kenai River mainstem populations.

For the 2010 and 2011 collections, tissues were subsampled in proportion to the harvest within statistical areas of the Upper Subdistrict (Ninilchik, Cohoe, South K. Beach, North K. Beach, South Salamatof, and North Salamatof), with a goal of 400 individuals per year. Some tissue samples in 2010 and 2011 were collected at processors which received deliveries from multiple statistical areas. Because the specific statistical area of these samples was not identified, these samples were excluded from analysis. A total of 376 and 347 samples were selected for analysis from 2010 and 2011, respectively. Several samples from 2010 (3) and 2011 (5) were excluded from the analysis because they failed to genotype at more than 20% of loci screened (see methods in Barclay et al. 2012). These individuals were removed because the inclusion of individuals with poor quality DNA might introduce genotyping error and reduce the accuracy of the MSA. The final number of successfully analyzed samples was 373 and 342 samples in 2010 and 2011, respectively.

The MSA program BAYES was used to estimate the proportions of the 5 reporting groups (stocks; Figure 1) contributing to each fishery sample. The analysis employed a similar the BAYES protocol reported in Barclay et al. (2010) for baseline evaluation tests, except that each fishery sample was analyzed for 5 chains with 40,000 iterations per chain. Estimates and 90% credibility intervals for each fishery sample were tabulated from the combined set of the second half of each chain (100,000 iterations).

The stock composition estimates for 2010 and 2011 were similar. In both years the Kenai River mainstem reporting group had the greatest contribution followed by the Kasilof River mainstem reporting group. The combined contribution of all other reporting groups in both years did not exceed 2.4% (Table 2; Figure 2).

Please let me know if you have any questions regarding this analysis.

REFERENCES CITED

Barclay, A. W., C. Habicht, W. D. Templin, H. A. Hoyt, T. Tobias, and T. M. Willette. 2010. Genetic stock identification of Upper Cook Inlet sockeye salmon harvest, 2005–2008. Alaska Department of Fish and Game, Fishery Manuscript No. 10-01, Anchorage.

Barclay, A.W., C. Habicht, R. A. Merizon, and R. J. Yanusz. 2012. Genetic baseline for Upper Cook Inlet Chinook salmon: 46 SNPs and 5,279 fish. Alaska Department of Fish and Game, Fishery Manuscript Series No. 12-02, Anchorage.

Table 1.- Tissue collections of Chinook salmon collected throughout Upper Cook Inlet including the year sampled, number of samples collected (N), the number of individuals analyzed from each collection included in the baseline and their assigned reporting group for the analysis of the East Side Set Net fishery collections. Unique population numbers represent all the analyzed collections that contribute to a single population.

Pop. No.	Reporting Group	Location	Year Collected	N	Analyzed
1	NorthwestCI	Straight Creek	2010	105	95
2		Chuitna River	2008	20	20
2			2009	122	122
3		Coal Creek	2009	42	42
3			2010	35	35
4		Middle Fork Chulitna River	2009	72	72
4			2010	97	97
5		Stephan Lake weir	2008	19	19
5		Prairie Creek	1995	52	52
5			2008	98	98
6		Chunilna Creek	2009	50	50
7		Montana Creek	2008	33	33
7			2009	155	155
7			2010	30	30
8		Deception Creek	2009	122	100
8		Willow Creek	2005	74	74
9		Moose Creek	1995	51	51
9		Deshka River weir	2005	200	200
10		Talachulitna River	1995	58	58
10			2008	74	72
10			2010	48	48
11		Sunflower Creek	2009	53	53
12		Little Susitna River	2009	3	3
12			2010	122	122
13		Moose Creek	1995	20	20
13			2008	33	33
13			2009	22	22
14		Ship Creek	2009	311	311
15		Chickaloon River	2008	2	2
15			2010	66	65

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Pop. No.	Reporting Group	Location	Year Collected	N	Analyzed
16	KenaiTrib	Grant Creek	2011	23	23
16			2012	32	32
17		Quartz Creek	2006	35	34
17			2008	34	34
17			2009	41	41
17		Dave's Creek	2007	8	8
17			2008	5	5
18		Crescent Creek	2006	165	165
19		Russian River	2005	24	24
19			2006	16	16
19			2007	84	83
19			2008	91	91
20		Benjamin Creek	2005	56	56
20			2006	150	150
21		Killey River	2005	68	68
21			2006	190	190
22		Funny River	2005	37	37
22			2006	183	183
23		Slikok Creek	2004	48	48
23			2005	100	95
23			2008	58	57
24	KenaiMainstem	Juneau Creek	2005	32	32
24			2006	100	91
24			2007	24	24
25		Upper Kenai River mainstem	2009	200	200
26		Middle Kenai River mainstem	2003	80	80
26			2004	39	39
26			2006	183	183
27		Lower Kenai River mainstem	2011	90	80
28	KasilofMainstem	Lower Kasilof River mainstem	2005	144	49
28		Middle Kasilof River mainstem	2005	273	273
29	CoastalSKenaiPen	Crooked Creek	1992	95	95
29			2005	212	212
30		Ninilchik River weir	2006	190	162
31		Deep Creek	2009	100	100
32		Anchor River weir	2006	200	200

Table 2.- Stock proportion estimates, standard deviation (SD), sample size (n), and lower (5%) and upper (95%) bounds of the 90% credibility interval for mixtures of Chinook salmon harvested in the east side set net fishery in 2010 and 2011.

	2010 (n= 373)				2011 (n=342)			
Reporting Group	Mean	SD	5%	95%	Mean	SD	5%	95%
NorthwestCI	0.020	0.022	0.000	0.063	0.004	0.007	0.000	0.019
KenaiTrib	0.003	0.006	0.000	0.015	0.004	0.008	0.000	0.021
KenaiMainstem	0.644	0.046	0.566	0.719	0.723	0.041	0.654	0.788
KasilofMainstem	0.331	0.040	0.267	0.398	0.267	0.040	0.203	0.333
CoastalSKenaiPen	0.002	0.004	0.000	0.009	0.002	0.004	0.000	0.009

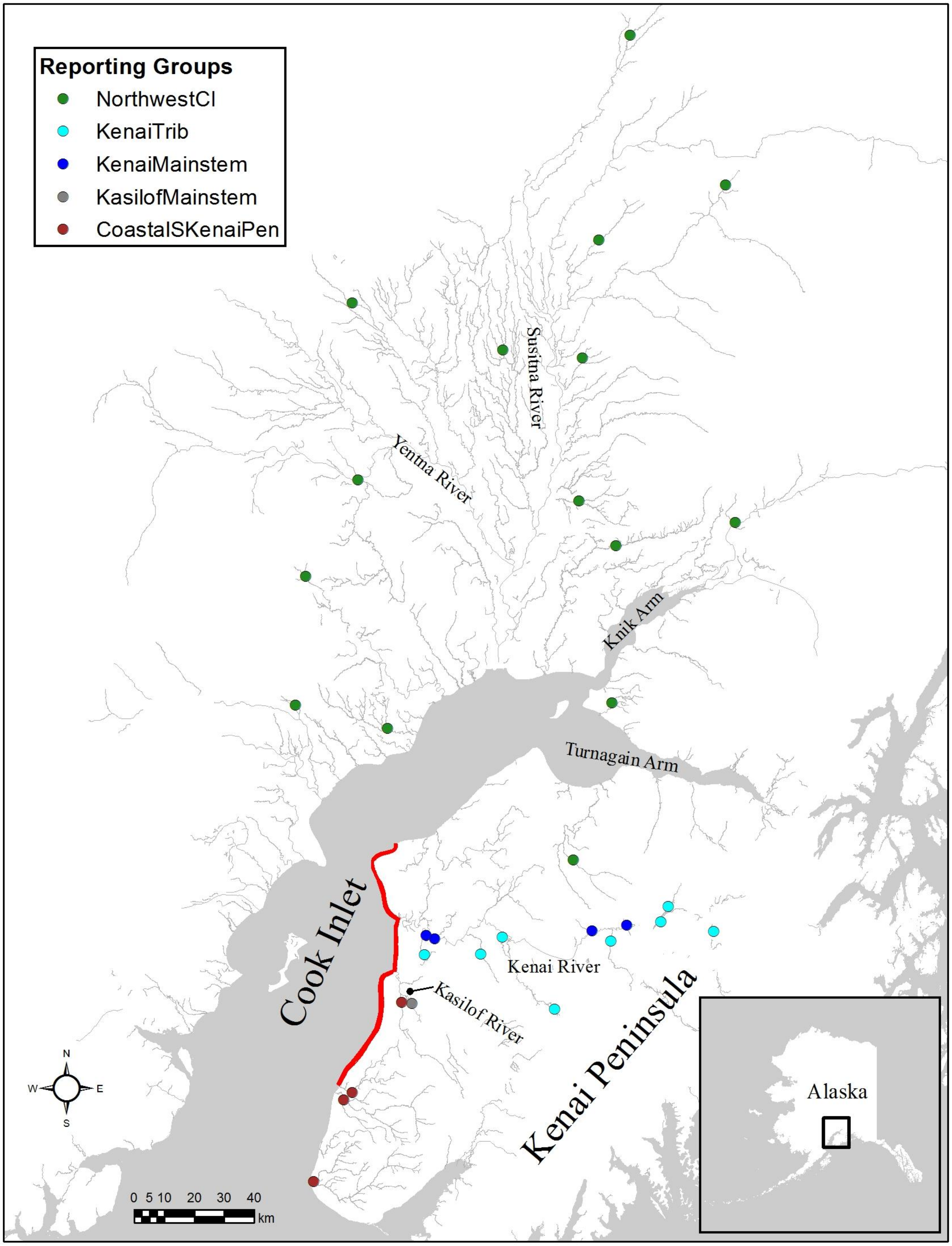

Figure 1.- Sampling locations (dots) for Chinook salmon used to compile a genetic baseline for Upper Cook Inlet. East Side Set Net fishery area is highlighted in red. Colors for each reporting group are indicated in the legend.

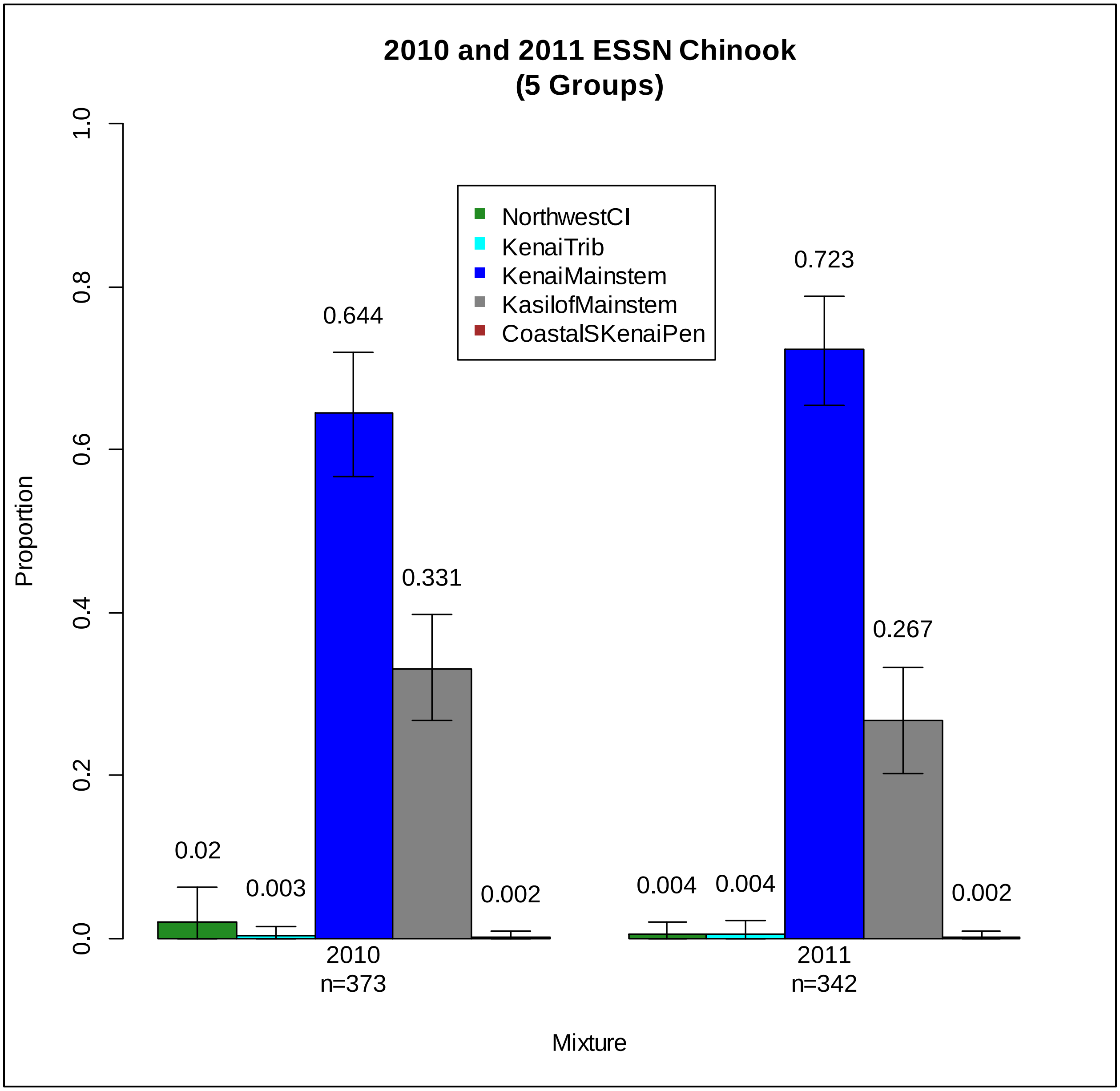

Figure 2.- Stock proportion estimates for Chinook salmon harvested in the East Side Set Net (ESSN) fishery of Upper Cook Inlet in 2010 and 2011. Numbers above the bars are the mean estimates, n is the sample size of the fishery sample for each year, and whiskers indicate the upper and lower bounds of the 90% credibility interval.