Salmon Genetics workgroup report
April 2016

1 BACKGROUND

In April 2015 in conjunction with reviewing the 2013 reports on salmon bycatch genetics in the Bering Sea and Gulf of Alaska, the Council put forward the following motion:

> *The Council requests staff provide a white paper evaluating the feasibility of further temporal and spatial refinements of stock composition data, including identification of the minimum number of samples necessary to meet accuracy and precision standards:*

> - *BSAI Chinook and chum salmon: temporal within season (e.g., by statistical week and month); and spatially within NMFS areas, in particular within Areas 517 and 509.*
> - *GOA Chinook salmon: temporal within season (e.g., by statistical week and month); and spatially within NMFS areas.*

> *In addition, the Council would like to highlight the following suggestions from the SSC minutes:*

> - *Future genetic reports should identify whether a subsample is used, and any potential tradeoffs in precision relative to using a subsample. Identify data standards used to achieve stock composition estimates.*
> - *The CGOA rockfish dataset (2013 – 2015) that includes coded wire tag (CWT) and genetic samples should be analyzed to determine what fraction of the bycatch was from hatchery production. This sample set will also be useful in determining future sampling goals in the GOA for a combined genetic/CWT sampling program.*

> *The Council requests NMFS continue to pursue the more rapid timelines for both BSAI and GOA genetic reports, similar to the GOA reports provided in the past year (target final reports in December.)*

To meet this request a group of analysts from NMFS AFSC (Juneau, Seattle), ADF&G (Anchorage, Juneau), and NPFMC met in person, teleconference, and via email correspondence in March 2016 to discuss and draft responses and plans for addressing the Council's request. Participants in the meeting and discussions to draft this paper included the following: Jeff Guyon, Chuck Guthrie, Chris Kondzela, Andy Gray, Jim Ianelli, Diana Stram, Alan Haynie, Craig Faunce, Sarah Power, Michele Masuda, Ellen Yasumiishi, Bill Templin, Jim Jasper, and Andrew Munro. Discussion topics and relevant recommendations are included in sections below. The informal workgroup intends to meet again following the Council's review to address ongoing work and additional recommendations based on SSC and Council review in April 2016.

2 2014 CHINOOK AND CHUM REPORTS

Jeff Guyon, Chris Kondzela, and Chuck Guthrie provided an overview of results of 2014 genetic analyses on chum and Chinook salmon taken as bycatch in the Bering Sea pollock fishery and in GOA groundfish

fisheries (mainly pollock but also some samples from the arrowtooth flounder fishery and central GOA rockfish fishery). These three documents will be provided and presented to the Council for the April meeting since several of the requests from the Council are addressed within these reports.

The group discussed that Chinook samples in the Bering Sea continue to represent only the pollock fishery due to regulations implemented following Amendment 91 that only specify catch monitoring and control plans for AFA pollock (approximately 3,000 unsampled Chinook salmon PSC per year are caught by fisheries other than AFA pollock in the BSAI (https://alaskafisheries.noaa.gov/sites/default/files/reports/chinook_salmon_mortality2016.pdf and https://alaskafisheries.noaa.gov/sites/default/files/reports/chum_salmon_mortality2016.pdf).

Samples of these (e.g., from Amendment 80 vessels) could provide stock of origin estimates that contrast to those taken from AFA pollock vessels. Direction from the Council and regulatory changes would likely be required should such an additional sampling program be implemented.

2.1 AREA SPECIFIC RESULTS (NMFS AREAS 509 AND 517) IN AFA POLLOCK FISHERY

In response to the Council's April 2015 motion, the analysts worked to refine stock composition estimates in NMFS management areas 509 and 517 (specifically, Guthrie et al. 2016). These areas were selected by the Council because analysts had indicated there were sufficient samples for making comparisons. For example, Tables 3-5 and Figure 5 of Guthrie et al. (2016) (below) show comparative results by these regions (and seasons).
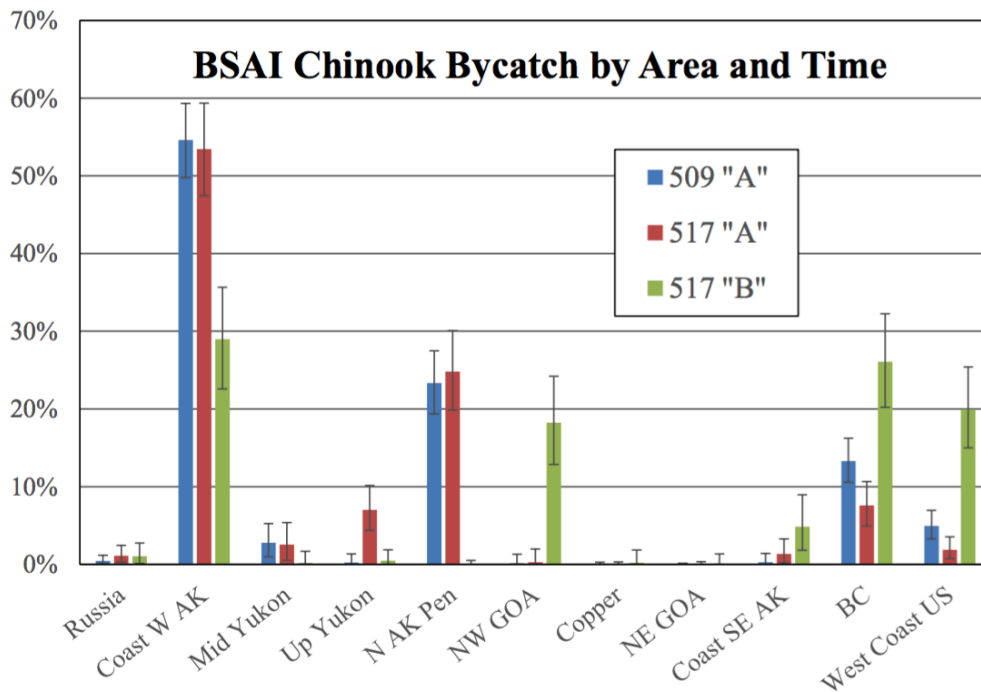

Figure 5. -- Comparison of area and time stock composition estimates from the 2014 BSAI Chinook salmon bycatch for NMFS Area 509 "A" (604 samples), Area 517 "A" (371 samples), and Area 517 "B" (241 samples). BAYES 95% credible intervals are plotted for yearly estimates.

In light of this spatial issue of NMFS management areas, Chuck Guthrie and Chris Kondzela updated the group on recent developments in refining genetics data to ADF&G statistical areas. The analysts have worked with AKFIN and FMA to refine and display genetics information to ADF&G statistical areas and can easily examine sampling levels important for estimating relative stock compositions of the bycatch. Some caveats associated with that include that data must be aggregated at spatial and temporal scales to fulfill confidentiality requirements which is not built into the AKFIN report at this time and that for the mapping tool in AKFIN, the bycatch is assigned to the ADFG area with the largest target species catch if a vessel fished in more than one area.

Using these newly developed tools available on AKFIN, the group evaluated the locations of the 2015 Chinook salmon samples by ADF&G statistical areas in relation to the NMFS management areas. From this comparison, the NMFS management areas appear to be poorly specified for purposes of evaluating spatial differences. One cluster of bycatch occurrence (north of Unimak Island) is divided by NMFS areas 509 and 517 and a separate cluster closer to the Pribilof Islands is split between NMFS areas 517 and 521. Not only are the clusters split into at least two NMFS areas, one NMFS area (517) contains parts of two clusters. It was noted that re-aggregating samples relative to the observed clusters could be done and may be more informative for discerning patterns of stock distribution in the bycatch.

Areas were also identified in the GOA (Sand Point, southeast of Kodiak Island, and Shelikof Strait) for possible alternative spatial resolution of bycatch stock compositions. The group recommended that investigations on spatially explicit estimates should be linked with studies on variability in different years and seasons.

The group discussed the need for some consistent standards for precision and accuracy when estimating the composition of bycatch by stock of origin. Bill Templin provided an overview of efforts underway previously through the Western Alaska Salmon Stock Identification Program (WASSIP) efforts and Yukon River Panel work on establishing accuracy and precision recommendations in genetics. The standards set for WASSIP were set to achieve estimates of stock composition that were within 5% of the true value 90% of the time (Weir et al. 2012). A related and more difficult standard was also proposed (to detect a 1% contribution of a stock 99% of the time) but this was considered unachievable with the available sample sizes. The 1997 report from the Stock ID Subcommittee of the Yukon River Joint Technical Committee proposed a different standard of achieving a CV or and RRMSE of ≤ 20% for all stock groups that compose at least 20% of the total (JTC 1997). The meeting also included discussions on sample size considerations for detecting a stock that comprises less than 2% of the bycatch similar to the idea considered for WASSIP. This would provide for an objective focused upon the explicit resolution of rarer/weaker stocks. The group emphasized that such minimum sample size considerations should be consistent with management objectives and relative impacts and risks.

Bill Templin updated the group on efforts to refine the baselines used for stock composition estimates in the BSAI and GOA. This revised baseline would allow for estimation of stocks currently aggregated within the Coastal Western Alaska (CWAK) group. Specifically, preliminary results suggest that the CWAK aggregation could be separated into three groups including Norton Sound, lower Yukon, and Kuskokwim/Nushagak stocks. Once completed, the baseline could then be used to re-examine historical genetics samples and estimate stock compositions at the refined stock resolution. However, progress on developing this baseline is hampered by a lack of funding. Provided funds are secured, the baseline could be completed and used for analyses as soon as Winter 2016/2017.

An improved baseline is also under development for the GOA and U.S. west coast stocks for studies supported by the Pacific Salmon Commission. This new baseline would be incorporated within the

existing one (which is also used for the Bering Sea) and would provide further refinements to the aggregated groups currently in the GOA including West Coast U.S. and B.C. stocks.

Similar to the expansion of the Chinook salmon baseline that will provide higher resolution groups of western Alaska populations, an ongoing CIAP-WASC chum salmon baseline project supports efforts by ADF&G, NMFS, and UAF to develop new genetic markers with a goal to resolve the CWAK chum salmon populations into finer-scale spatial groupings, e.g., Norton Sound, lower and middle Yukon, Kuskokwim, and Bristol Bay (poster at http://dnr.alaska.gov/commis/CIAP/Fall2010/WASC.pdf and proposal at http://access.afsc.noaa.gov/pubs/posters/pdfs/pGuyon01_western-ak-chum.pdf).

In summary, the group clarified that stock composition estimates depend on:

1. The resolution available in the genetic "baseline" samples (some improvements are forthcoming here—namely for Norton Sound Chinook salmon stocks based on ADFG work)
2. The number of effective samples relative to the total bycatch (i.e., sampling design considerations); and
3. The number of samples in the genetic stock ID process (i.e., the sample size reflecting the accuracy of the genetic data processing)

For the AFA pollock samples at the seasonal level (combined areas), the current system of sampling each 10th Chinook salmon in the bycatch systematically appears to work very well and improvements in the baseline (item 1. above) will presumably allow for more stocks to be included in the composition estimates. However, finer resolution (in space or time) will increase uncertainties in the estimates due to factors 2. and 3.

The Workgroup requests guidance from the SSC and the Council on the following questions regarding priorities: Is spatial or temporal resolution more important? Analysts could provide some examples such as the first priority is to provide estimates by area for A and B/early and late seasons. After that, if sample sizes are large enough, estimates by area and by month? Or is the monthly estimate important enough that rolling up adjacent areas would be acceptable to achieve sample size requirement (noting that the AKFIN information might be helpful to focus samples on high sample regions that might cross management areas). Is relaxing sample size standards from the ideal level (which has yet to be determined) to an acceptable level preferable in order to be able to provide finer temporal or spatial resolution? Is there interest in accurately estimating the proportion of smaller stocks or is the general pattern acceptable?

2.2 SPATIAL MODELING

Alan Haynie provided the group with some ideas to move forward with more explicit spatial modeling of bycatch and fleet behavior specifically attempting to develop a more predictive measure of bycatch occurrence. The refinements to ADFG statistical area spatial scales for genetics may assist in any modeling efforts moving forward (EBS only). For this to be effective inter-annual variability in the stock composition would have to be addressed but could provide insight on ways to reduce impacts to specific stocks of concern (at the fleet management level).

2.3 PROGRESS ON AGE DATA FOR CHUM AND CHINOOK

Ellen Yasumiishi provided an overview of plans for ageing Bering Sea chum and GOA Chinook. She noted that ageing Bering Sea Chinook could also be done but needs prioritization.

The group discussed the genetic results in the GOA pollock fishery as compared with the results in the rockfish and arrowtooth flounder (ATF) fisheries, noting both genetic differences and apparent size composition differences between the fisheries. The group recommended that in addition to the planned ageing of the 2013-2014 GOA Chinook salmon bycatch scales from the pollock fishery, similar data could be processed for the ATF and rockfish fisheries to further investigate perceived size and genetic differences in salmon caught across those three fisheries. Stock composition estimates for each ocean-age was also recommended should sufficient samples be available. A recommendation was also made to evaluate the length composition estimates available.

2.4   ISSUES RELATED TO GOA ANALYSES

Jeff Guyon provided an overview of results of GOA Chinook analyses for 2014, including voluntary efforts by industry to census all Chinook in the ATF and CGOA rockfish fisheries for stock of origin, prevalence of CWTs and biological samples. Michele Masuda then provided an overview of recent analyses of 2013–2015 CWTs recovered in the GOA rockfish trawl fishery (paper appended).

The Council requested the CWT analysis and the implications of the work on estimating the percentage of bycatch from hatchery production. The group discussed that the higher CWT recoveries in 2013 compared to years 2014 and 2015 (see Tables 1 and 2 from document below) reflects the higher Chinook catch that year. Most of the CWT recoveries originated from stocks in Washington and Oregon, followed by British Columbia, Alaska, and Idaho.

Table 1.   Numbers of Chinook salmon that were caught, sampled, adipose fin clipped (ad-clipped), ad-clipped with coded-wire tags (CWTs), and not ad-clipped with CWTs in the prohibited species catch of the Gulf of Alaska rockfish trawl fishery. The actual numbers of CWTs that were decoded are in parentheses.

Year	Number caught	Total sampled		Ad-clipped		Ad-clipped with CWTs		Not ad-clipped with CWTs		Total CWTs	
		Number	Percent of catch	Number	Percent of sample	Number	Percent of sample	Number	Percent of sample	Number	Percent of sample
2013	2,128	2,111	99.2	300	14.2	87[1] (86)	4.1	27	1.3	114[1] (113)	5.4
2014	483	468	96.9	74	15.8	17 (17)	3.6	0	0	17 (17)	3.6
2015	641	638	99.5	100	15.7	23[1] (22)	3.6	5	0.8	28[1] (27)	4.4
Total	3,252	3,217	98.9	474	14.7	127 (125)	3.9	32	1.0	159 (157)	4.9

[1]One tag was lost before it could be read.

Table 2.   Observed and expanded numbers of coded-wire tagged Chinook salmon, numbers sampled and caught, and percentages in the prohibited species catches of the 2013–2015 Gulf of Alaska rockfish trawl fisheries.

Year	Number of CWTs	Number sampled	Percent of sample	Expanded number	Number caught	Percent of catch
2013	114[1] (113)	2,111	5.4	346.5	2,128	16.3
2014	17 (17)	468	3.6	84.2	483	17.4
2015	28[1] (27)	638	4.4	144.0	641	22.5
Total	159 (157)	3,217	4.9	574.7	3,252	17.7

[1]One tag was lost before it could be read.

[1]Issues with visual detection of CWTs by observers were discussed. A 20% sampling fraction is considered adequate to detect CWTs (Nandor et al, 2010). Observers collect salmon genetics and CWT from all Chinook and Chum salmon they encounter in their at-sea samples in all GOA fisheries. In addition, for catcher vessels in the GOA trawl pollock fishery, the observer monitors the offload and takes genetics from all Chinook and Chum salmon encountered as well as examines these for CWT. At-sea sampling rates at the trip for each fishery are determined by which vessels participate in the fishery, the deployment strata they belong in for each year, and the sampling rates in that year. Observer program deployment strata and deployment rates are defined in Annual Deployment Plans.

The overall percentage of the catch that was estimated to originate from hatchery release groups, by expanding observed numbers with sampling and marking expansion factors, was approximately 18%. Some basic assumptions of the estimation method used include tagged fish from release groups represent untagged fish in catches, the marking fraction of juveniles in release groups is a fair estimate of the tagged and untagged ratio in catches, and tagged and untagged fish experience similar mortality.

With regard to genetic sampling of the Chinook salmon bycatch in the GOA, the following sampling protocols have been used for the pollock, rockfish, and arrowtooth flounder GOA trawl fisheries:

1. Prior to 2014, Amendment 93 to the GOA groundfish fishery management plan required industry to retain all Chinook salmon bycatch in the GOA pollock trawl fishery. This retention requirement was aimed at providing observers with complete access to the bycatch to support genetic stock composition analyses. However, Amendment 93 did not mandate complete observer coverage, and not all GOA pollock trips were observed at sea. Consequently, the North Pacific Groundfish and Halibut Observer Program (Observer Program) lacked the ability to know in advance the delivery times and locations of all GOA pollock deliveries. Recognizing these limitations in the GOA, starting in 2014, the Observer Program implemented a simple random sampling (SRS) protocol with respect to trip for the collection of genetic samples in the GOA. This method randomly samples from trips and censuses the salmon bycatch encountered in each associated delivery to the processor.
2. Since 2013, genetic samples have been collected from the Chinook salmon bycatch of the central GOA rockfish trawl fishery by the Alaska Groundfish Data Bank (AGDB). Although there is no requirement for sample collection, the AGDB implemented a census approach whereby samples and biological information are collected from every Chinook salmon encountered.
3. Since 2013, genetic samples have also been collected from the Chinook salmon bycatch of the GOA arrowtooth flounder trawl fishery by the Alaska Seafood Cooperative. Although there was no requirement for sample collection, the Alaska Seafood Cooperative implemented an opportunistic sampling approach to collect genetic samples from this fishery.

2.5   TIMEFRAME FOR PRODUCTION OF REPORTS AND STREAMLINING
Jeff, Chris, and Chuck provided an overview of the timing of producing the technical reports and discussed opportunities for streamlining. Chris provided a chart of the current timeline for the next 18 months or so and showed that a limited shortening of the production of reports was possible. Jeff

[1] **NOTE THIS PARAGRAPH HAS BEEN REVISED FROM THE PREVIOUSLY POSTED VERSION. See C-4 page 6-stike-out posted separately for detailed revisions.**

indicated the need for additional staffing to support improved turnaround time for the genetics reports. In the interim, Bill Templin offered to work with Jeff to find additional means to more efficiently process and genotype samples. As with other issues, additional funding is required in accord with associated workload and sample processing so a cost-benefit analysis would be helpful. Some participants agreed to further explore means to streamline the process.

2.6 AEQ FOR GOA SALMON

The AFSC has begun to compile a process for routine AEQ calculations with a view to extend analyses to GOA Chinook bycatch (chum bycatch in the GOA is low and likely a lower priority). Given the Council's interest in improving analysis and data collection for GOA trawl bycatch, this work is considered timely and perhaps useful for future planned EIS analysis for GOA bycatch to better evaluate the impact of management alternatives on Chinook salmon stocks. The work required to implement AEQ estimates for GOA salmon includes:

- Determining the appropriate spatial and temporal strata given the extent of available bycatch (and length data) and genetics samples
- Compile length frequencies, bycatch totals, and genetic stock ID results by strata for each year
- Convert length frequencies of bycatch to age compositions (either using direct age-length keys or some other method) to obtain bycatch numbers at age (by year)
- Input age-specific oceanic mortality rate
- Estimate of maturity rate (in ocean) based on age composition of in-river runs (weighted by expected contribution) and oceanic mortality rate

3 SUMMARY OF WG RECOMMENDATIONS FOR 2015 ANALYSES AND WORKPLAN

The workgroup recommended analysis of smaller spatial resolutions for stock composition estimates to the extent samples are sufficient. For example, as discussed under section 2.1, Chinook salmon bycatch samples in the BSAI A-season could breakout St. George Island and Area 509, for B-season 517/519 and 521 or alternatively include the northwestern most samples from 517 with 521; in GOA Shelikof Strait early, Sandpoint/Shumagin Late (which are most of the samples in 610), Southeast Kodiak early and late (which are most of the samples from 630).

The workgroup intends to continue to consider alternative analyses of the available genetic samples. For example, one suggestion was to re-estimate stock compositions by year for specific size groups (closely aligned to ages) to compare variability across years.

Below are tables and figures for the 2015 chum salmon bycatch samples from the Bering Sea pollock and GOA groundfish fisheries. Mixed-stock analyses will be run as in the past (Tables A-C), and as an example, an additional analysis could be performed based on four clusters of ADFG statistical areas and two time periods (Table D, Figure 1). However, the sample sizes of sub samples are really too small in a couple of categories. One option would be to add samples that were not subsampled. Another option would be to pool ADFG statistical areas differently or to combine the Early and Middle categories. Analyses can be run on other subsets of samples that may be of interest to the Council. We will analyze all 146 samples from the Bering Sea A-season (Figure 2), the most we have ever received in this season, and the 156 samples from the GOA (Figure 3). As with the 2014 chum salmon samples, the 2015 samples were subsampled in order to minimize laboratory costs while limiting bias of mixed-stock estimates. The total sample set of approximately 7,500 chum salmon was sorted by cruise and specimen number and then

every 4th sample was selected for analysis. This is sufficient to determine the stock composition of the overall bycatch and some subsets of samples, but additional samples beyond those subsampled may be required for other spatial-temporal categories.

Table A. Number of chum salmon genetic samples collected from the 2015 Bering Sea pollock A- and B-seasons and Gulf of Alaska groundfish fisheries by NMFS reporting area. Areas were aggregated where fewer than 3 vessels fished. The samples collected by the Observer Program in the B-season were sub-sampled for genetic analysis (every 4th sample).

Bering Sea A-season		Bering Sea B-season			GOA	
NMFS Area	#samples	NMFS Area	#samples	#sub samples	NMFS Area	#samples
509/516	68	509/513/517	5,696	1,407	610	39
513	14	519	127	40	620	87
517/519	27	521	1,760	439	630	30
521	37	523	26	6		
		524	3	0		

Table B. Temporal groups from the genetic sample sets of chum salmon caught in the 2015 Bering Sea, B-season pollock fishery.

Period	Weeks	Dates	total #samples	#sub samples
Early	24-29	10 June - 18 July	632	164
Middle	30-34	19 July - 22 August	3,994	989
Late	35-42	23 August - 17 October	2,986	739

Table C. Spatial and temporal groups from the genetic sample sets of chum salmon caught in the 2015 Bering Sea, B-season pollock fishery at three periods for the NMFS reporting areas with the most samples.

NMFS Area	Period	Total #samples	#sub samples
517	Early	277	72
	Middle	2,949	721
	Late	2,452	609
521	Early	314	82
	Middle	972	242
	Late	474	115

Table D. Spatial and temporal groups from the genetic sample sets of chum salmon caught in the 2015 Bering Sea, B-season pollock fishery at two periods and four clusters of ADFG statistical areas. The number of sub-samples is approximate. Colors match those in Figure 1.

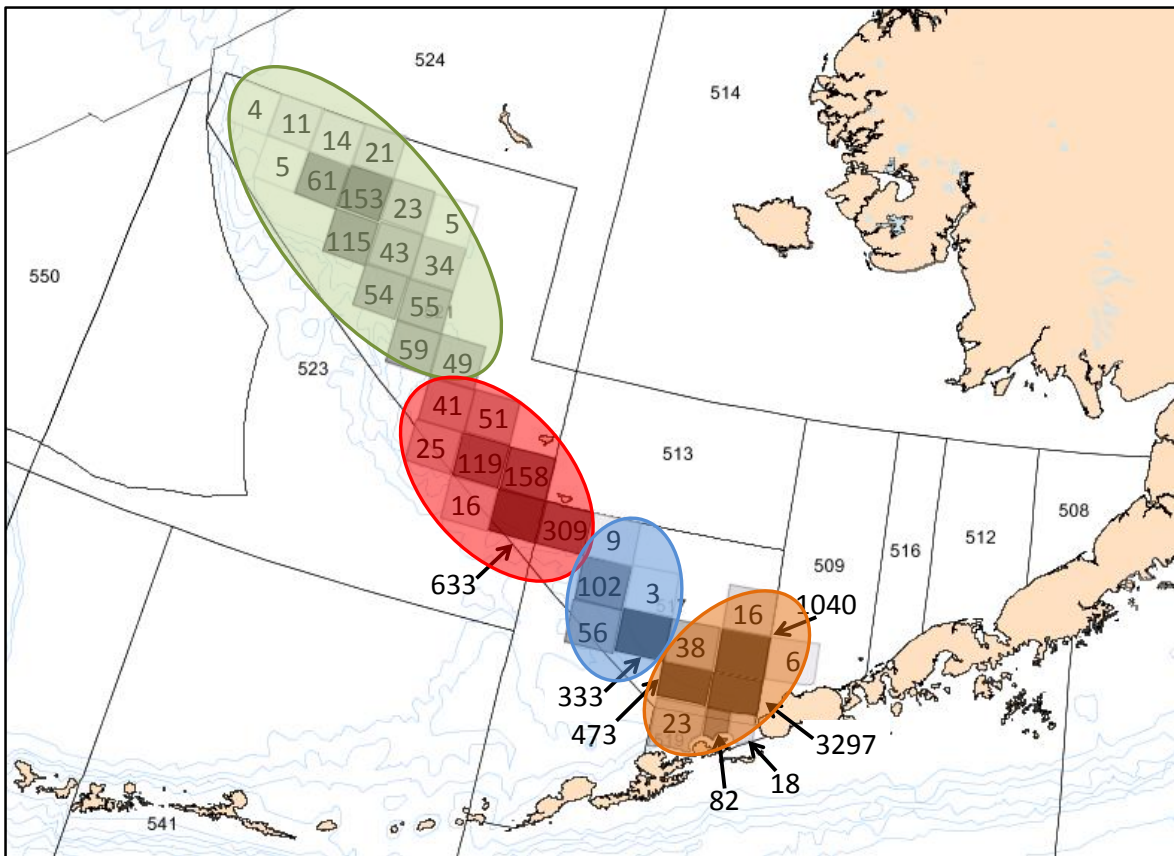| ADFG areas	Period (weeks)	Total #samples	#sub samples
635504-665530	24-32	860	215
	33-43	4141	1035
675500-685600	24-32	206	52
	33-43	298	75
695600-735700	24-32	500	125
	33-43	886	222
725730-785930	24-32	246	62
	33-43	471	118

Figure 1.   Number of chum salmon bycatch genetic samples from the 2015 Bering Sea pollock fishery during the B-season in ADFG statistical areas (smaller squares) where at least 3 vessels fished. Colored areas match those in Table D.
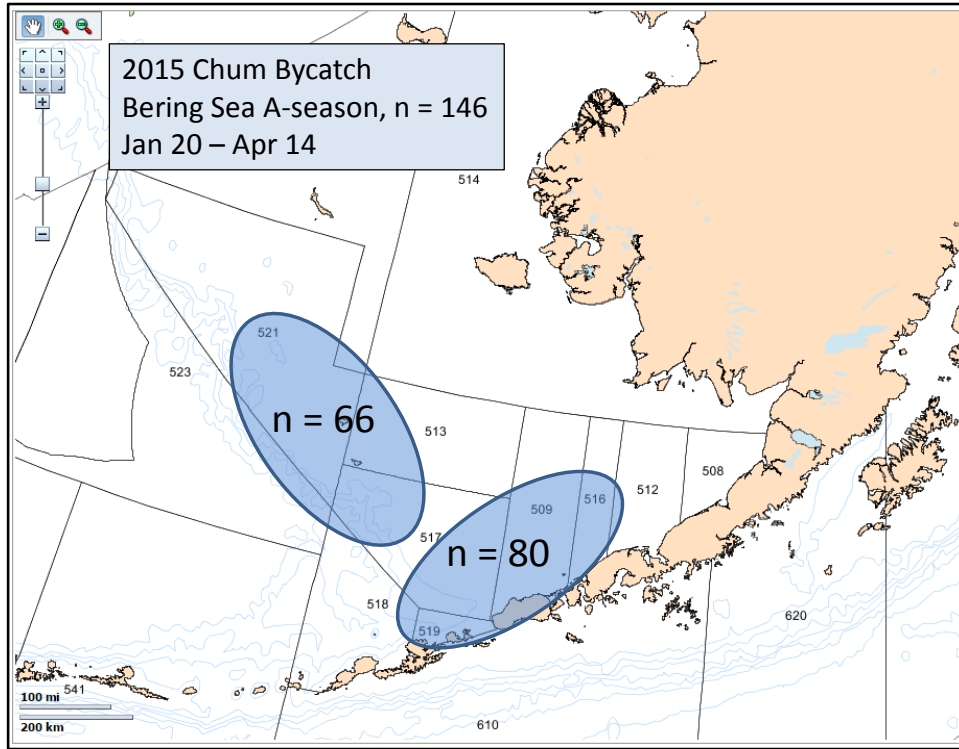
Figure 2. Number of chum salmon bycatch genetic samples from the 2015 Bering Sea pollock fishery during the A-season.
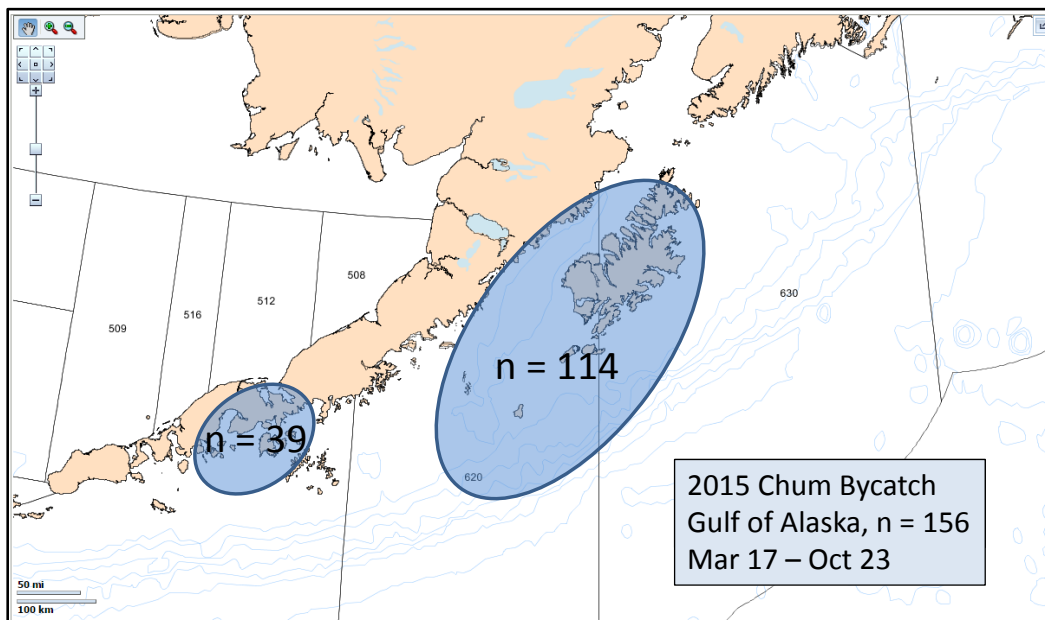

Figure 3. Number of chum salmon bycatch genetic samples from the 2015 Gulf of Alaska groundfish fisheries.

4 REFERENCES

JTC (Joint Technical Committee of the Yukon River US/Canada Panel). 2008. Summary and 2008 season outlook. Alaska Department of Fish and Fisheries, Regional Information Report No. 3A08-01, Anchorage.

Weir, B. S., R. S. Waples and T. P. Quinn. 2012. Western Alaska Salmon Stock Identification Program Technical Document 1: Technical committee comments and review of the original proposal. Alaska Department of Fish and Game, Division of Commercial Fisheries, Regional Information Report 5J12-06, Anchorage.