



Salmon Bycatch Workshop MINUTES

Alaska Fisheries Science Center, Seattle, WA, April 15-16, 2019

The North Pacific Fishery Management Council (NPFMC) held a public workshop on the state of knowledge, and future potential research avenues, for genetic stock identification of salmon bycatch in Gulf of Alaska (GOA) and Bering Sea and Aleutian Island (BSAI) groundfish fisheries. The purpose of the workshop was to facilitate feedback on how stock composition reports can be improved to better inform industry bycatch avoidance efforts, discuss appropriate spatial and temporal resolution of stock identification, and identify other associated analyses that could be used by stakeholders to better understand the causes of, and potential measures to minimize, salmon bycatch.

Committee Members in attendance:

Jim Ianello (AFSC) Workshop Chair	Karl Haflinger (SeaState)	Megan Mackey (AKRO)
Diana Stram (NPFMC)	Marlon Concepcion (AFSC)	Jennifer Cahalan (PSMFC)
Jordan Watson (AFSC)	Lisa Thompson (AFSC)	Ruth Christiansen (UCB)
Alan Haynie (AFSC)	Gwynne Schnaittacher (AFSC)	Bob Foy (AFSC)
Julie Bonney (AGDB)	Adriana Meyers (AFSC)	Shannon Carroll (Trident)
Andrew Munro (ADF&G and SSC)	Lisa Seeb (UW)	Jeremy Rusin (AFSC)
Dayv Lowry (WDFW and SSC)	Jim Seeb (UW)	Craig Faunce (AFSC)
Garrett McKinney (NWFSC)	Megan McPhee (UAF)	Noëlle Yochum (AFSC)
Karla Bush (ADF&G)	Chris Kondzela (AFSC)	Arthur Severance (CVRF)
Chuck Guthrie (AFSC)	Chris Habicht (ADF&G)	Dani Evenson (ADF&G)
Ellen Yasumiishi (AFSC)	Eric Volk (AEB)	John Gruver (UCB)
Stephanie Madsen (APA)	Dion Oxman (ADF&G)	Jennifer Ferdinand (AFSC)
	Sara Gilk-Baumer (ADF&G)	
	Patrick Barry (UAF)	

Webex participants:

Anne Vanderhoeven (Arctic Storm), James Mize (Golden Alaska), Jackie Whittle (AFSC), Jason Gasper (AKRO), Mellisa Heflin (Bering Sea Elders Group), Ernie Weiss (AEB), Steve Marx (ODFW), Paul Wilkins (CVRF), Katy McGauley (AGDB), Curry Cunningham (APU), Sarah Power (ADF&G), Michele Masuda (AFSC)

Abbreviations

ABL	Auke Bay Laboratories (Division of AFSC)	NPFMC	North Pacific Fishery Management Council
ADF&G	Alaska Department of Fish and Game	NWFSC	NOAA Northwest Fisheries Science Center
AGDB	Alaska Groundfish Databank	ODFW	Oregon Dept. of Fisheries and Wildlife
AEB	Aleutians East Borough	SSC	Scientific and Statistical Committee of the NPFMC
AFSC	NOAA Alaska Fisheries Science Center	UAF	University of Alaska Fairbanks
AKRO	NOAA Alaska Regional Office	UCB	United Catcher Boats
APA	At-Sea Processors Association	UW	University of Washington
APU	Alaska Pacific University	WDFW	Washington Department of Fish and Wildlife
CVRF	Coastal Villages Relief Fund		

Presentations

- A series of presentations were centered around three main topics:
- State of the knowledge
- Developing capacities
- Recommendations and priorities

The agenda is attached. All presentations were posted to the meeting agenda site and made publicly available here: [Salmon Bycatch Agenda](#)

Three guiding questions for the workshop were provided by Council staff:

- Can we gain efficiencies within the current system?
- What can be answered with the current design, and are changes needed?
- What resources (funding, etc.) can be leveraged to make changes?

State of the knowledge

The first session provided an overview of the current management of salmon bycatch in both the BSAI and GOA, including industry management within different fisheries as well as the observer program sampling design and methodology in the North Pacific. The second part of this session provided information on the current results of Chinook and chum salmon bycatch genetic stock composition analyses. The authors of each talk, and abstracts from each presentation, are provided below.

NPFMC management and industry efforts in bycatch

Diana Stram¹, Karl Haflinger², Julie Bonney³

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Salmon bycatch management measures are implemented in the Eastern Bering Sea (EBS) pollock fishery, the Gulf of Alaska (GOA) pollock fisheries, the Central GOA catcher vessel Rockfish fishery, the GOA catcher vessel non-pollock/non-rockfish fisheries, and the GOA catcher processor fisheries (flatfish and rockfish). These fisheries have very different management and operational characteristics which affect how salmon bycatch is both estimated and managed. The EBS pollock fishery (which operates under a cooperative structure) has a complicated Chinook and chum management program incorporating Chinook prohibited species catch (PSC) limits allocated by season and sector with Incentive Plan Agreements (IPAs) managed by sector to provide for additional bycatch reductions and management provisions (excluders, seasonal constraints) as well as considerations for chum bycatch reduction. SeaState Inc. is contracted by the fishery to provide bycatch management services that include facilitating data flow between NMFS and cooperatives which all have complex rules regarding Chinook usage by individual vessels and by establishing bycatch avoidance areas by sector for both Chinook and chum (with Chinook avoidance taking priority over chum). For the GOA, only the rockfish fishery in the central GOA operates under a cooperative structure while the GOA pollock, GOA non-pollock/non-rockfish shoreside fisheries and offshore non-pollock fisheries are open access with each having their own binding Chinook PSC limit. Voluntary actions are sometimes taken in the pollock fisheries for bycatch avoidance and to slow the pace of the fishery to allow for better management of salmon bycatch. The catcher vessel rockfish coops implement mandatory salmon bycatch avoidance measures such as a slow start and bycatch rate standards through the intercooperative agreement. Sampling provisions differ between the EBS and GOA. In the EBS there is 100% observer coverage, a complete count (census) of all salmon (carried out shipboard on CPs and motherships and at the processing plants for pollock

delivered shoreside) with systematic sampling of all Chinook and chum for measurements and genetic material at rates of 1 in 10 Chinook and 1 in 30 chum. In the GOA, the pollock fishery has partial observer coverage and a shoreside salmon census when observed while the rockfish fishery operates under a cooperative management structure, has 100% observer coverage, and Chinook PSC is estimated from at-sea samples collected by vessel observers. In the limited access GOA catcher vessel non-pollock/non-rockfish fisheries (flatfish and cod, also under partial observer coverage), and the GOA catcher processor fisheries (flatfish and Western GOA rockfish, 100% observed), Chinook is also estimated from observer at-sea samples.

The observer genetic sampling protocols for the Gulf trawl fisheries differs from those in the Bering Sea: for the pollock fisheries, rather than following a random systematic sampling protocol, genetic specimens (pelvic axillary processes [PAP] plus 5 scales) are collected by the observer from every Chinook and chum salmon encountered during the pollock offloads at the plant. If no scales are present, only PAPs are collected. Length, weight, and sex are also recorded for each encountered Chinook and chum salmon. For the CV and CP non-pollock fisheries, observers collect genetic specimens and biological data from every Chinook and chum salmon encountered in their at-sea species composition samples. No specimens are collected from coho, pink, and sockeye salmon.

For Kodiak's CGOA Rockfish Program shoreside fishery, industry has been collecting genetic samples (PAPs) and biological data at the Kodiak plants from all landed Chinook salmon since 2013 (there is a 100% salmon retention requirement for all trawl fisheries in the CGOA and WGOA). Otolith collection was added in 2017. Due to lack of scales on the Chinook, they have rarely been collected for this industry-funded project.

North Pacific Groundfish Observer Program Sampling Design and Methods

Jennifer Cahalan¹ and Marlon Concepcion²

¹Pacific States Marine Fisheries Commission

²Fisheries Monitoring and Analysis, Alaska Fisheries Science Center, NOAA

The North Pacific Observer Program is a multi-objective monitoring program which collects data to meet a wide range of management and research needs. In addition to mandates for data collections in support of catch and bycatch estimation and stock assessment, observers also collect data used for a range of scientific activities. Data collected includes fishing locations and effort, species composition of the catch, biological specimen data (length, weights, tissues collected for genetic, diet, or other analyses), and data related to protected species.

The Observer Program uses a randomized hierarchical, stratified sample design with two coverage categories: full coverage where observers are onboard for every trip and partial coverage where a portion of trips are randomly selected to be observed in five gear-based strata and an electronic monitoring (EM) stratum. Vessels less than 40 ft length overall (LOA) and all vessels using jig gear are not required to have observer coverage. Observer coverage strata and coverage rates are defined in the Annual Deployment Plan (NMFS 2018). Within each of these strata, sampling is hierarchical with randomized selection of fishing trips. Within each trip, observers randomly select hauls to be sampled. Within each haul, a random sample of the unsorted catch is collected, and from within that sample individual fish are randomly selected for the collection of biological data and specimens. This is an efficient sample design that makes the best use of observers' limited time and energy while collecting high quality data. Detailed descriptions of the sampling methods can be found in the Observer Sampling Manual, prepared each year by the Alaska Fisheries Science Center (AFSC 2019). A description of sampling methods and catch estimation is also available (Cahalan et al., 2010).

Observer sampling related to salmon falls largely outside of this hierarchy. Initially, the collection of Chinook and chum salmon tissues used in genetics sampling was implemented as a special project. With Amendment 91 to the Bering Sea and Aleutian Islands (BSAI) Fishery Management Plan (FMP) in 2011 these data collections became part of the observer’s standard duties. In the BSAI pollock fishery, all salmon are set aside by industry for the observer who counts all salmon by species and collects tissue samples (the pelvic axillary processes [PAP] plus 5 scales) from Chinook salmon (every 10th fish) and chum salmon (every 30th fish). Since BSAI pollock is a full coverage fishery, this represents a complete enumeration of salmon and a systematic random sample taken directly from the bycatch. To accommodate this change in sampling, the Observer Program was no longer able to support shoreside sampling for other prohibited species (crab, halibut), resulting in a decrease in the numbers of halibut viabilities and lengths collected. The methods used in the BSAI have remained relatively stable since 2011. Salmon tissue samples for genetics are not collected outside the pollock fishery in the BSAI.

Since the implementation of Amendment 93 to the Gulf of Alaska (GOA) Groundfish FMP in 2014, fisheries observers on pollock trawl vessels enumerate all salmon by species and collect genetic tissue samples from all Chinook and chum salmon encountered either at-sea in their samples or shoreside in the delivery on **observed trips**. On non-pollock trips, the observer only collects salmon tissue samples from Chinook and chum salmon in their species composition samples collected at-sea. The majority of the GOA fisheries fall under the partial coverage Observer Program and observers only collect salmon data from observed trips. Prior to 2014, several data collection methods were implemented, however, the methods currently in place have proven to be logistically feasible and have remained relatively unchanged since 2014. These different data collections are summarized in the figure below (Figure 1).

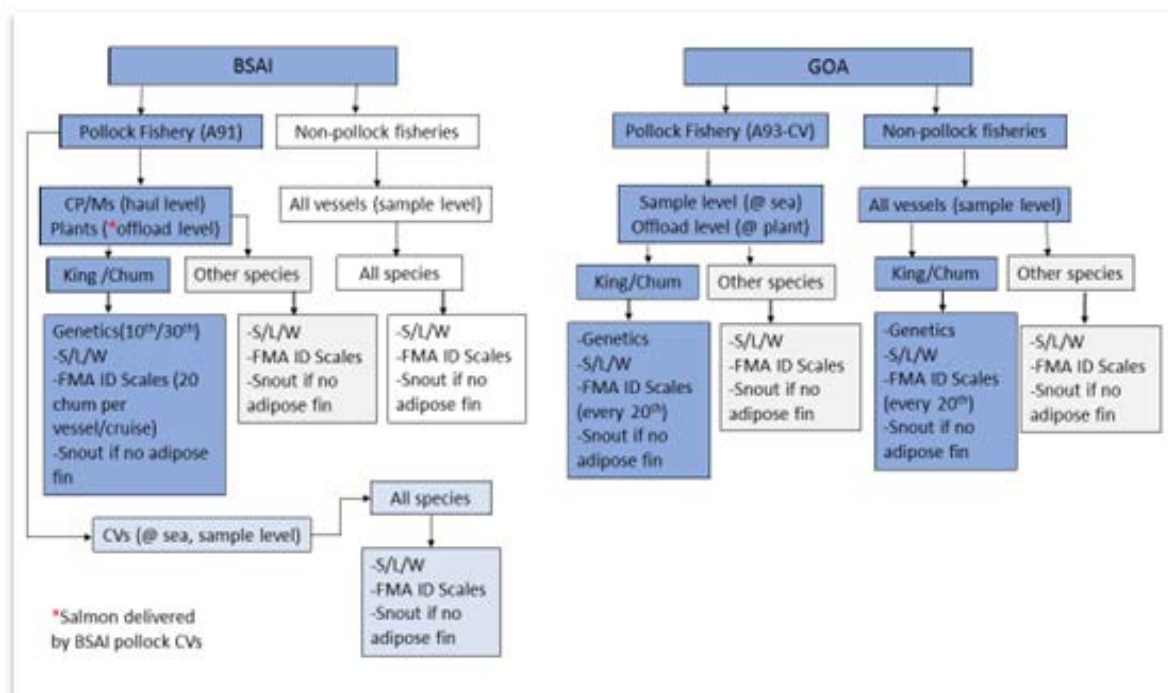


Figure 1: Summary of data collections for salmon specimens in the BSAI and GOA trawl fisheries

Sampling methods used by observers in the BSAI are different from those used in the GOA; details can be found in Faunce (2015). In the BSAI, genetics samples are collected from the full coverage pollock fishery only. Industry conducts the sorting and since plant observers are available for shoreside data collections, the observer has access to all salmon both at-sea (vessel observer) and shoreside (plant observer). The bycatch estimate is the complete enumeration of Chinook and chum salmon. The genetic

tissue samples are collected directly from the bycatch using a systematic random sample of every 10th Chinook salmon and every 30th chum salmon. In contrast, in the GOA, tissue samples are collected from the partial coverage trawl fisheries (pollock and non-pollock fisheries). In the pollock fishery only, the vessel observer is responsible for sampling at-sea and monitoring the delivery of observed trips at shoreside processing plants. Since these are partial coverage fisheries, the estimate of bycatch is based on an observer data-derived bycatch rate from observed trips applied to fisheries landings. In addition, genetic tissue samples are collected from a portion of bycatch. On observed pollock trips, the observer obtains tissue samples from all Chinook and chum salmon encountered for the trip (at-sea and in the delivery) while on non-pollock trips, the at-sea observer obtains tissue samples only from Chinook and chum salmon in their samples. Because these tissue samples are collected from a portion of the bycatch, the hierarchical sample weightings become an important part of the estimation process.

Once an observer has finished their deployment, tissue samples for genetic analysis are returned to one of four Observer Program offices in Dutch Harbor, Kodiak, or Anchorage, Alaska or Seattle, Washington. Data collected with the tissues samples are tracked and undergo several quality control checks in addition to data quality evaluations that are part of the observer debriefing process. Salmon genetic tissue samples and salmon snouts (with coded wire tags) are then shipped to the NMFS AFSC Auke Bay Laboratory twice a year in coordination with Auke Bay Lab staff.

References

AFSC (Alaska Fisheries Science Center). **2019 Observer Sampling Manual**. Fisheries Monitoring and Analysis Division, North Pacific Groundfish Observer Program. AFSC, 7600 Sand Point Way N.E., Seattle, Washington, 98115. <https://www.fisheries.noaa.gov/resource/document/north-pacific-observer-sampling-manual>

Cahalan, J.A., J. Mondragon, J. Gasper. 2014. Catch Sampling and Estimation in the Federal Groundfish Fisheries off Alaska: 2015 Edition. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-286, 41 p. <http://www.afsc.noaa.gov/Publications/AFSC-TM/NOAA-TM-AFSC-286.pdf>

Faunce, C. H. 2015. Evolution of observer methods to obtain genetic material from Chinook salmon bycatch in the Alaska pollock fishery. U.S. Dep. Commer., NOAA Tech. Memo. NMFS-AFSC-288, 28 p. doi:10.7289/V5MG7MFF. <http://www.afsc.noaa.gov/Publications/AFSC-TM/NOAA-TM-AFSC-288.pdf>

NMFS. 2018. **2019 Annual Deployment Plan for Observers in the Groundfish and Halibut Fisheries off Alaska**. National Oceanic and Atmospheric Administration, 709 West 9th Street. Juneau, Alaska 99802. <http://meetings.npfmc.org/CommentReview/DownloadFile?p=13252b3a-482b-4009-85ad-727d01384735.pdf&fileName=B2%202019%20ADP.pdf>

Primer on Genetic Mixed Stock Analysis

Chris Habicht, Alaska Department of Fish and Game, Gene Conservation Laboratory

This primer on genetic mixed stock analysis (MSA) is designed to provide a foundation for discussions on how MSA of salmon bycatch from the groundfish trawl fisheries can be used by industry to avoid critical stocks. We review the components of MSA and the errors that must be considered when designing MSA sampling and analyses. The three major components of MSA are: 1) the baseline, which is the genetic characterization of populations (spawning aggregates) that represent all populations that may be present in the mixture; 2) the mixture, which is made up of genotypes from individual fish representing a fishery of interest; and 3) the analysis, which identifies the best fit of combined mixture genotypes to the baseline populations, which are then aggregated into stock groups. We also discuss the two types of errors that must be considered when designing MSA sampling and analysis: 1) sampling error and 2) genetic

error. Sampling error is the chance that a sample contains the true proportions in the fishery it represents, which can be reduced by increasing sample size. Genetic error is caused by the misclassification of mixtures because of genetic similarity among stock groups, which can be reduced by only including genetically distinguishable stock groups and by increasing sample sizes. Finally, we provide guidelines for best practices for genetic MSA to help guide discussions on how to develop analysis plans to best respond to stakeholder needs.

Chinook Salmon Bycatch Genetic Stock Composition: Current Capabilities and Analyses

Chuck Guthrie

Auke Bay Laboratory, Alaska Fisheries Science Center, NOAA

For mixed-stock analyses of Chinook salmon bycatch from the Bering Sea and GOA groundfish fisheries, we use a genetic baseline of 172 populations and 43 SNP markers developed by the ADF&G Gene Conservation Laboratory. These populations are aggregated into eleven stock groups for which stock composition is estimated. In addition to annual and seasonal estimates of stock proportions by fishery, we estimate stock proportions of bycatch from finer-scale strata specified in the ANSWERS tool developed by AKFIN in 2015. Geographical aggregations of ADF&G statistical areas were developed to provide stock composition estimates with greater spatial precision than is possible with the large NMFS statistical areas. Examples were shown of the current strata used for stock composition analysis of Chinook salmon. A timeline was presented of the processing and analyzing of genetic samples, and reporting of stock composition results. Hatchery production of Chinook and chum salmon by country was summarized. Most (84%) of the Chinook hatchery production is from the U.S. About half (53%) of the chum hatchery production is from Japan, with 22% from each of Russia and the U.S.

Chum Salmon Bycatch Genetic Stock Composition: Current Capabilities and Analyses

Chris Kondzela

Auke Bay Laboratory, Alaska Fisheries Science Center, NOAA

The analyses of Bering Sea chum salmon bycatch by the Auke Bay Laboratories (ABL) are summarized. Since systematic sampling was implemented in 2011, over 55,000 genetic samples have been shipped from the AFSC's Fisheries and Monitoring Analysis Division (Observer Program) and received by ABL. High chum salmon bycatch in recent years has been further subsampled, resulting in a total of more than 17,000 samples genotyped since 2011. The AKFIN reporting tool developed by the PSMFC was used to specify strata for sample datasets from the B-season when most chum salmon are caught. Shifts in peak bycatch of 3-4 weeks earlier in 2017-2018 was noted. The genetic samples collected across statistical weeks, NMFS areas, and by fishing vessels closely match the 1 in 30 systematic sampling protocol implemented by the Observer Program. Currently, mixed-stock analysis of the chum bycatch samples is done with the BAYES software program using a coastwide genetic baseline of 11 microsatellite markers surveyed in 381 populations grouped into 6 stocks. Stock estimates for the 2017 B-season were compared with estimates from other years, and across areas, time periods, fishing sector, and fish age strata. Stock estimates are reported annually in NOAA Technical Memoranda and at NPFMC meetings.

Age information for salmon bycatch from fish scales

Ellen Yasumiishi

Auke Bay Laboratory, Alaska Fisheries Science Center, NOAA

Age information is being developed for the genotyped salmon bycatch samples from the pollock trawl fisheries in the Bering Sea and Gulf of Alaska. Individual fish age information is available from scales for the genotyped Bering Sea chum salmon from 1997-2017. Time series of age composition are dominated by age-4s followed by age-3 and age-5 chum salmon. A high occurrence of age-3 chum salmon in the Bering Sea during the 2015 warm blob year corresponded with a higher proportion of fish identified from southern origin stocks. Upcoming efforts will focus on processing scales for age of Chinook salmon from the Bering Sea (2005-2018) and Gulf of Alaska (2011-2018). Updating these datasets through 2018 would require two years of lab work. Applications of the age information include estimating age composition, bycatch by age, stock composition by age, size-at-age curves for the Adult Equivalency model, spatio-temporal modeling, and estimating marine mortality rates.

Developing Capacities

The second session focused upon improving current capabilities and analyses as well as innovative approaches to develop new capacities.

Looking for better ways to use genetic data to avoid critical Chinook stocks in groundfish fisheries: Update on current work and possibilities for future efforts

Sara Gilk-Baumer¹, Garrett McKinney², and Lisa W. Seeb³

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²*Northwest Fisheries Science Center, NOAA*

³*University of Washington, School of Aquatic and Fishery Sciences*

This presentation discusses the current state of the Chinook salmon genetic baseline for Pacific rim applications of mixed stock analysis (MSA). We briefly provide an overview of the history of baseline development, and touch on recent developments in technology and regional applications. We then discuss the challenges associated with differentiating fine scale stock groupings in Western Alaska, and review specific projects designed to work towards solutions. These include a project that identified 96 high powered single nucleotide polymorphism (SNP) genetic markers that allowed differentiation of three stock groupings, and another project that compiled over 1,000 new and existing SNPs intended to further distinguish one of these stock groups. The relative cost of implementing these different methodologies is discussed, and the need to balance those costs with project needs. Finally, work is ongoing to improve resolution of stock groups in Western Alaska, and future work may involve innovative approaches such as new statistical analyses for unbalanced baselines or incorporating technological advances. This presentation will provide a foundation for the discussions on how to improve estimates of MSA to best respond to stakeholder needs of groundfish trawl fisheries.

Looking for better ways to use genetic data to avoid critical chum salmon stocks in groundfish fisheries: A partnership of science and industry

Chris Kondzela¹ and Megan McPhee²

¹*Auke Bay Laboratory, Alaska Fisheries Science Center, NOAA*

²*University of Alaska Fairbanks*

A review of chum salmon genetic baselines was provided. Mixed-stock analysis of the chum bycatch is only possible because of the extensive collaborations of state, federal, university, and international fishery researchers that resulted in standardized coastwide genetic baselines. The current baseline used for estimating the stock composition of chum salmon bycatch is the coastwide microsatellite baseline, which was the only DNA-based baseline available when the Auke Bay Laboratories' Genetics Program began analyzing chum salmon bycatch in 2009. Since that time, substantial efforts have been made to develop single nucleotide polymorphism (SNP) baselines on both the coastwide and regional scale. SNPs are easier to standardize across laboratories and equipment, and are generally less expensive to process than microsatellites. At this time, the most complete SNP baseline with coastwide coverage is the 96-SNP Western Alaska Salmon Stock Identification Program (WASSIP) baseline developed by the Alaska Department of Fish and Game. The WASSIP baseline has a single coastal western Alaska group. A more recent focus on finding SNPs that separate coastal western Alaska populations into finer-scale stock groupings, e.g., Norton Sound, lower Yukon, Kuskokwim, and Bristol Bay, led to the development of a panel of 448 SNPs that separates Norton Sound from the other coastal western Alaska stock groupings. Other recent efforts have resulted in a 350-SNP panel of finer-scale stock groupings in southern British Columbia and Washington. Use of the regional SNP panels for analysis of chum salmon bycatch will require further work: currently there is only partial overlap of SNP markers of limited geographic scope.

Chum genetics: Update on current work and possibilities for future efforts/timing, What else might be possible?

Chris Habicht¹, Jordan Watson²

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²*Auke Bay Laboratory, Alaska Fisheries Science Center, NOAA*

This component of the developing capacities section examines what new or different genetic mixed stock analyses (MSA) might be useful to provide answers to questions from the pollock fishery industry. We review potential questions that might be of interest to industry and provide some guidelines and suggestions on how answers might be provided. We review the following five questions: 1) What stocks do you need to identify?; 2) How accurately do you need to estimate?; 3) What fishing area/time scales do you need analyzed?; 4) When do you need the results?; and 5) What result formats do you need? We discuss the tradeoffs between stratum resolution and stock composition accuracy. We provide methodical alternatives and considerations for providing results within a day, a week, and a year. Finally, we provide some alternatives for data representation that allows for user-defined analyses of data collected since inception and for methods that allow the incorporation of data from outside sources, such as satellite environmental data. We also briefly address efforts to standardize genetic analysis methods across labs.

Use of tags, thermal marks, and scales to determine origin and age of salmon

Dion Oxman, Alaska Department of Fish and Game, Mark, Tag, Age Laboratory

Coded wire tags (CWTs) and otolith thermal marks provide an inexpensive and relatively easy alternative to genetic analyses when trying to determine the origin and movements of salmon caught as bycatch. The CWT, which is applied to hatchery-origin Chinook salmon, is a length of magnetized stainless steel wire approximately 0.25mm in diameter and 1.1 mm long, injected into the snout of a fish, that contains a specific code denoting an individual's birth date, age, hatchery of origin, and release location. Because the application process is labor intensive, hatcheries usually tag 1 in 10 Chinook salmon with CWTs. CWTs are typically not used with chum salmon. The application of CWTs to Chinook salmon is mandated by the U.S./Canada Pacific Salmon Treaty. Otolith marking, which is applied to both Chinook and chum salmon, is a process that uses short-term temperature fluctuations to create a series of distinctive growth rings in the otoliths of embryonic fish. By exposing broodstock to a series of temperature changes, hatcheries can create unique patterns of rings in the otoliths of all exposed fish. The resulting mark patterns provide the same information about an individual's history as the CWT. Both CWTs and thermal marks are easily recovered and, unlike genetic markers, provide information on fish age and require no specialized training. Demographic data can also be obtained from analyzing growth patterns on scales and otoliths of both hatchery and wild fish. The data acquired from tag and mark recoveries, however, are only applicable to that portion of the bycatch originating from hatcheries, whereas genetic analyses can be applied to an entire sample of fish caught as bycatch regardless of origin. These marking techniques should not be considered mutually exclusive because both CWTs and thermal marks can be used to validate the results of genetic analyses.

Alternatives for updating AEQ analysis and prioritizing data needs

James Ianelli

Resource Ecology and Fisheries Management, Alaska Fisheries Science Center, NOAA

Extensive observer data on the biological attributes (size and age composition) of Chinook bycatch were used to estimate the impact on specific regional stock groups (RSGs), as defined given available genetic stock identification estimates. The model provides estimates of the impact on Chinook salmon RSGs, given seasonal and spatial variability in the bycatch, estimated run-strengths and in-river age compositions, uncertainty in age-specific oceanic natural mortality of Chinook salmon, and between-year variability in genetic information. The upper Yukon River stock is transboundary and subject to heightened management interest and international management agreements on escapement goals. In 2018, results were updated from an earlier analysis used to develop the management regulations that went into place in 2011. It shows that the new data result in slight changes in previous estimates, and that the lower overall Chinook salmon bycatch since 2008 has resulted in lower impacts to the main western Alaskan RSGs. New analytical updates included sensitivity analyses to illustrate potential effects of changes in size-at-age of Chinook salmon from the age-length keys used in the original model. Length frequency data show differences in the EBS (pollock fishery) with fewer fish measured compared to before 2011 (only the fish sampled for genetic tissues are measured for length whereas prior to that, all observed salmon were measured). In the GOA, length frequency sampling for salmon has remained stable. From previous communications with the Council, there was some concern about using historical age-length data since there has been some indication of growth changes in recent years. Consequently, a "what-if" analysis was conducted and presented during the workshop. This sensitivity analysis examined what happens if growth is shifted to be older given the same size (by about one half a year). Results showed slight increases in the relative impact for Chinook salmon but the relative impact remains low.

Biology, behavior, and bycatch reduction devices: conservation engineering approaches to salmon bycatch mitigation

Noëlle Yochum

Resource Assessment and Conservation Engineering, Alaska Fisheries Science Center, NOAA

An overview of the motivations and recent experiments in salmon bycatch reduction through fishing gear modification was provided. Excluder devices that promote escapement of salmon from groundfish trawls during fishing operations include a suite of configurations and strategies. To measure the efficacy of these devices, cameras are often mounted inside the trawl to observe gear and fish behaviour. Video footage has indicated that there might be a link between artificial lighting (i.e., camera lights) and salmon behaviour, which has been observed in other fisheries. Experiments to evaluate whether artificial lights can be used to elicit behaviours from salmon were discussed, including an evaluation of light color, strobe rate, and intensity. Preliminary results indicate that these light properties (e.g., color) play a role in salmon response type and strength to the artificial lights. Further study on both salmon excluder design and salmon behaviour in response to artificial light is planned for 2019 by the Conservation Engineering group (CE) within the AFSC, and industry led studies evaluating salmon excluder designs are on-going. Critical to CE research is collaboration with industry partners and the incorporation of diverse perspectives and expertise.

Priorities and workshop recommendations

The final session was designed as a group discussion amongst participants to provide feedback on a range of issues and develop priorities and recommendations moving forward. The group developed a number of policy and management priorities based upon discussion and consideration of overall utility, and short- and long-term feasibility. The group also provided a short list of additional considerations for forthcoming analyses and continued baseline development for genetics.

1. Chinook AEQ

GOA: Industry expressed interest in an AEQ in the GOA to look at the relative impact of the GOA pollock fishery on stocks of interest.

Discussion included challenges to the development of an AEQ in the GOA. Methods to estimate AEQs are confounded by the large number of potential stock groups contributing to the bycatch. In the Chinook AEQ presentation, it was noted that the length distribution of Chinook in the GOA was substantially smaller than in BSAI samples. Reasons for this are unclear, though the different stock assemblages and life history types likely contribute. Further discussion will be necessary to develop appropriate methods.

BSAI: A major potential improvement to the AEQ analysis currently lies in the backlog of Chinook scale samples that have not been aged. The AEQ currently uses an age-length key from several decades ago but scale-based ages provide an opportunity to update the AEQ analysis to account for potential changes in size-at-age and age-at-maturity. Efforts should be made to evaluate sample sizes and impacts on AEQ. A “what-if” analysis presented during the workshop which shifted the growth to be older given the same size (by about one half a year) resulted in slight increases in the relative impact of bycatch on regional stock groups.

2. GOA Chinook hatchery contribution

There is concern regarding the impending ~20% increase in production of hatchery Chinook salmon to support southern resident killer whales because increased hatchery production may affect bycatch

numbers in coming years. Hatchery contribution information is desirable to establish a baseline before substantial production increases occur as well as help inform impact rates on wild stocks of interest.

Methods to estimate hatchery contribution given the large mix of stocks encountered have yet to be developed. The group discussed potential approaches to combine genetic, otolith, CWT, and scale information.

3. Utility of comprehensive Chinook data collection efforts from rockfish fishery bycatch

Tremendous effort has been directed at sampling 100% of the Chinook bycaught in the Central GOA Rockfish fishery for genetics, otoliths, CWTs, sex, and length. An evaluation of the utility of this information for management or policy decisions is warranted.

4. BSAI Chum variation in space and time

Recommend continuation of current efforts and spatial clusters. There was particular interest in developing the capability to separate hatchery chum salmon from wild chum. There is continued interest in being able to break-up genetic information across spatial strata (clusters) over time. Such approaches will help to resolve spatiotemporal patterns of different stock groups. It was questioned whether finer spatial and temporal scales in the data analysis may be useful and it was subsequently noted that in years during which higher bycatch occurs, some finer spatial and temporal strata can be examined.

With the transition to different mixed-stock analysis (MSA) software, it will be easier for staff at ABL to more quickly explore different spatial clustering over time. Additionally, now that sufficient data exist from a number of years of systematic sampling, we will explore a more systematic approach (e.g., k-means clustering) to determine persistent boundaries for spatial clusters of chum bycatch.

5. Evaluate policy implications of increased proportion of Pacific Northwest/BC fish in BSAI bycatch as it relates to management under lower caps tied to 3 River index.

Western Alaska stock proportions (for Chinook) have decreased in recent years while British Columbia and Pacific Northwest stock proportions have increased. Industry acknowledged the value of post-season analysis of stock composition for Chinook salmon in providing this information. Chinook bycatch is currently managed to incentivize avoidance of all Chinook salmon regardless of origin. Some additional analysis may be warranted to look at the efficacy of the current management structure as it relates to avoidance of Western Alaska (WAK) Chinook stocks and/or the potential for perverse incentives given the current cap structure. Continued update and monitoring of the WAK AEQ as it relates to previous estimates, WAK run sizes as represented by the 3 River index, and breakpoint analysis of the 250,000 fish threshold under the 3 River index relative to bycatch and PSC cap levels should be considered.

Methods to estimate hatchery contribution given the large mix of stocks encountered have yet to be developed. The group discussed potential approaches to combine genetic, otolith, CWT, and scale information.

6. Evaluate utility of time and area genetic evaluations of Chinook

The current management system in both the Bering Sea and GOA mandates that industry avoid all salmon regardless of origin. Thus, while spatiotemporal patterns in stock composition are interesting and informative, they are not currently being used in bycatch avoidance efforts as the mandate is to avoid *all* Chinook salmon. The Council should consider how and if this information can be used in management under current or future revised management efforts for bycatch reduction.

7. Improved efficiency in sample collection and processing

- A. **Field.** Determine the feasibility of deploying detector wands in the field to determine whether CWTs are present. A missing adipose fin is an indicator of a hatchery-origin fish. Since the rise of mass marking to support mark selective fisheries in the Pacific Northwest, many hatchery fish have an adipose fin clip but no CWT. Wanding these fish in the field saves on shipping costs of snouts that have no CWT.
- B. **Lab.** Expedite ageing by combining preparation/processing of scales and genetic tissue samples. There has been no Chinook scale ageing since 2011 so there is a large backlog and would require two years of agency time to catch up. In the future it would be best to prepare scales (mount scales on gum cards and press gum cards onto acetates to make impressions of scales) for ageing at the same time that they are processing genetic tissues since going back through the collections for each fish is time consuming and inefficient. To process both at the same time would require additional personnel but in the long run would be much more cost and time efficient. Transition to new software for analysis of genetic data that is faster and more flexible than BAYES.

8. Improving use of the Chinook genetic baseline

The present genetic baseline being used for analysis of Chinook bycatch was developed independently of its current usage in management and could be improved to be more responsive to current and future policy and management objectives. The 11 stock groupings in use now were initially based on political boundaries and, in particular, some areas in the Pacific Northwest could be better defined based on biological differences. Improvements could also be made in grouping stocks by hatchery production areas versus wild stocks.

Future Directions

1. Strategies for interactive data visualization

Each year, the NMFS ABL genetics group has sought to explore more spatial and temporal aspects of mixed-stock analysis (MSA) data. These data can now be examined across a suite of dimensions (e.g., year, season, spatial cluster of statistical areas, age, stock origin), but plotting these data to explore trends across time can be difficult and onerous. Staff are developing a suite of interactive online visualizations using R Shiny that will allow users to select the dimensions or filters of interest to answer different questions, e.g., “In 2017, in which spatial cluster was the majority of age-3 Russian-origin chum salmon caught?”. As several of the different strata have been added over time, full development of these visualizations will first require some additional historic MSA analyses to be run in order to fill out time series. Data will also be downloadable through the Shiny interface, allowing users to explore the data on their own.

2. Upgrade technological capacity in Auke Bay genetics lab

The ABL has recently advanced computational power through virtual machine computing, which will allow them to increase processing speed, versatility, and remote access. Additionally, the lab is exploring implementation of the rubias package in R Statistical Software, which will provide greater flexibility for running MSA, but more importantly, result in greater automation. Together, the combined automation and flexibility will allow a more thorough exploration of the different strata in time and space for which sufficient sample sizes exist for MSA. Furthermore, as the industry standard in MSA, rubias receives regular support and updates that allow it to regularly interface with new developments in parallelization, visualization, and standardization.

The ABL has recently acquired an instrument capable of performing genotyping-by-sequencing (GBS). This technology provides opportunities for increased workflow, more automated and replicable genotyping, and increased stock resolution. Implementing GBS panels may provide additional opportunities to reconfigure stock groupings to better answer questions of interest to the public, fisheries managers, and industry. A baseline containing 96 SNPs appropriate for stock composition analyses of chum salmon captured in the Bering Sea and the GOA exists and has been incorporated into a GBS panel. A SNP baseline for Chinook salmon analysis over an appropriate area already exists and a GBS panel is in progress, but additional baseline collections from Asia, Alaska, and Canada will need to be screened before using this method for stock compositions of mixtures from the Bering Sea and Gulf of Alaska. To implement this new methodology, ABL will require additional staff and training for the laboratory and statistical methods and may require higher-throughput GBS equipment.

3. Continue to explore application of shipboard genetic stock identification

Of the three options for increasing the turn-around speed for stock composition analyses (1 day, 1 week, 1 year), the 1-day turn around option was only of interest to industry representatives for chum salmon in the Bering Sea. Given current management regulations, industry representatives were not interested in quicker analysis speeds for Chinook salmon since the objective is to reduce catch regardless of stock. The Pollock Conservation Cooperative Research Center has funded a study by Dr. McPhee to investigate the potential utility of the MinION nanopore sequencing platform for shipside stock composition estimates of chum salmon bycatch. If this methodology is successful, it may provide vessels with real-time stock composition estimates for two stocks: Asian and North American. Results for this project are due in 2020.

NPFMC Salmon Bycatch Workshop

Date: April 15-16, 2019
Location: Traynor Room, Alaska Fisheries Science Center, Seattle, WA
Duration: 1.5 days
Scope: Information needs for Chinook and chum salmon PSC

WEBEX information is listed on: <https://meetings.npfmc.org/Meeting/Details/603>

Agenda

Note:

- Lead presenter in parentheses, additional collaborators may also present during agenda item;
- Each session will include facilitated discussion after the presentation at the discretion of the Chair

Monday, April 15

9:00 a.m. 1. **Review of agenda and workshop format** – Jim Ianelli (Workshop Chair)

9:15 a.m. 2. **State of knowledge**

- a. NPFMC programs and actions on salmon bycatch and industry efforts in BSAI and GOA groundfish fisheries –Diana Stram
- b. North Pacific Groundfish Observer Program Sampling Design and Methods: (Jennifer Cahalan)

Overview of the NPGOP sampling design including integration of electronic monitoring and highlighting aspects of sampling tailored to meet data collection needs for PSC species.

- c. Primer on Genetic Mixed Stock Analysis (Chris Habicht)
- d. Chinook Salmon Bycatch Genetic Stock Composition: Current Capabilities and Analyses (Chuck Guthrie lead)

Chinook salmon: Description of genetic stock identification (GSI) of bycatch, NPFMC stock composition update. Data sources for BSAI and GOA. Hatchery production summary.

10:30 a.m. *Break (15 mins)*

- e. Chum Salmon Bycatch Genetic Stock Composition: Current Capabilities and Analyses (Chris Kondzela)

Chum salmon: Description of GSI of bycatch, NPFMC stock composition update. Data sources for BSAI and GOA. Hatchery production summary.

11:15 a.m. 3. **Developing capabilities**

- a. Looking for better ways to use genetic data to avoid critical Chinook salmon stocks in groundfish fisheries: A partnership of science and industry (Sara Gilk-Baumer)
- b. Looking for better ways to use genetic data to avoid critical chum salmon stocks in groundfish fisheries: A partnership of science and industry (Chris Kondzela)
Chum genetics: Update on current work and possibilities for future efforts/timing
- c. What else might be possible? (Chris Habicht and Jordan Watson)

12:00 p.m. Lunch (90 minutes)

1:30 p.m. Resume #3 **Developing capabilities**

- d. Use of tags, thermal marks, and scales to determine origin and age of salmon (Dion Oxman)
- e. Alternatives for updating AEQ analysis and prioritizing data needs (Jim Ianelli)
- f. Biology, behavior, and bycatch reduction devices: conservation engineering approaches to salmon bycatch mitigation (Noelle Yochum)

2:30 p.m. **4. Facilitated discussion: What can we do to improve our estimates of GSI and what potential changes we can make to best respond to stakeholder needs?**

Discussion to identify challenges, generate ideas and begin to develop possible solutions to address needs from of industry and other stakeholders. We intend to build upon an initial list of stakeholder requests and to prioritize the information needs, current capacity to address and/or capacity building needs to move forward. This discussion should set the stage for Day 2 follow-up. *There will be a mid-afternoon break scheduled at the discretion of the Chair.*

5:00pm Adjourn for Day 1

Tuesday, April 16

8:30 a.m. **6 Day 1 recap** (Jim Ianelli)

8:45 a.m. **7 Designing methods to get answers** (Facilitated discussion with all)

- a. What can be answered with the current design and are changes needed?
- b. Refining the questions to answer and/or information necessary moving forward

- c. Revising sampling design and discussion of observer coverage levels needed to meet stakeholder and Council objectives.

10:00 a.m. *Break (15 minutes)*

- d. Data acquisition and access

11:00 a.m. 8 Next Steps and Recommendations

12:00 p.m. Adjourn Workshop

1:00pm-5:00pm Work session for report drafters