

Alaska Hatchery Research Program Science Panel meeting May 14, 2021

Virtual meeting via Microsoft Teams

Summarized meeting notes and decision points

Attendees

Science Panel

Milo Adkison, University of Alaska
David Bernard, ADF&G (retired)
John Burke, ADF&G and Southern
Southeast Regional
Aquaculture Association
(SSRAA; retired from both)
John H. Clark, ADF&G (retired)
Chris Habicht, ADF&G
Jeff Hard, Northwest Fisheries
Science Center, National
Marine Fisheries Service
(NMFS; retired)
Ron Josephson, ADF&G (retired)
Bill Smoker, University of Alaska
(retired)
Bill Templin, ADF&G
Alex Wertheimer, NMFS (retired)
Peter Westley, University of Alaska

Other Attendees

Sam Rabung, ADF&G
Tommy Sheridan, Sheridan Consulting, LLC
Chance Gray, Sitka Sound Science Center
(SSSC)
Chris Barrows, Pacific Seafood Processors
Association
Kristen Gruenthal, ADF&G
Garold V. "Flip" Pryor, ADF&G
Kyle Shedd, ADF&G
Erica Chenoweth, ADF&G
Ben Adams, Northern Southeast Regional
Aquaculture Association (NSRAA)
Mike Wells, Valdez Fisheries Development
Association (VFDA)
Ron Heintz, SSSC
Geoff Clark, Prince William Sound
Aquaculture Corporation (PWSAC)
Samuel May, PhD candidate, UW
Tessa Frost, Southern Southeast Regional
Aquaculture Association (SSRAA)
Chris Barrows, Pacific Seafood Processors
Association (PSPA)
Charlie Waters (NMFS)

AHRP Meeting Minutes

- **December AHRP Meeting Minutes approved**
- **Approval of meeting minutes**
 - **Decision point** –Going forward, email comments on draft meeting minutes would be available for two weeks; after that time, the meeting minutes would be considered approved by the group and ready for posting to the public on the website

2021 Field Season Planning

- **Sitka Sound Science Center Field Season Planning**
 - **Ron Heintz** presented on the SSSC 2021 field season mark/recapture study plan
 - Overview of their approach to the experimental design to estimate escapement with mark/recapture method
 - Based on the classic Petersen estimation (main assumptions: population closed, equal capture probability, no tag loss, tagging status known without error, tagging has no effect on behavior); they will meet/check the assumptions of the model by the following:
 - Releases being done just above tidal influence, nearby locations being surveyed for tagged fish, tests for closure, double tagging to estimate tag loss and double-check release/return identification, g-tests to examine stream distribution of tagged and untagged fish, and comparison of the size distributions of tagged and untagged fish.
 - Current experimental design does not constrain the analysis to only the classical Petersen model
 - Open population models are less biased
 - Sampling efforts should be well within the limits of doing a pooled Petersen estimate, based on previous year fish handling counts.
 - Field Methods for Marking include
 - Capture with beach seines, release just above tidal area
 - Sample every other day beginning with first fish
 - Mark with spaghetti tags
 - Double mark with opercular punch (different mutilation mark with each release date, as opposed to each week)
 - Record data: Date, tag, sex, punch location, scale number, live recaptures, axillary well number, length.
 - Field Methods for Recapture include
 - Recover marks throughout stream
 - Use carcass weir near first mortality site to increase recapture odds and handle high water events
 - Follow previous season methods
 - Inspect previously unsampled fish
 - Verify tag recoveries
 - Record data: Date, sex, condition, punch location, heart well location, location, length, tag status/number, scale number, otolith location

AHRP May 2021 Meeting Summary

- Analysis methods
 - Conducted in R and in Mark
 - Stratified Petersen estimate with testing for closure
 - Provides estimate of N and error
 - Requires pooling
 - Separate analysis for groups i.e. sex, age
 - Open population models – Jolly-Seber with covariates
 - Provides estimate of N and error
 - Capture probabilities by group
 - Losses due to emigration by group
 - Migration phenology by group
 - Residence time by group
- Discussion
 - Fish will be mark/recaptured indiscriminate of a certain length (**Decision point** – **Ron H.** will correct the planning document by removing the typo that “all fish longer than 400mm be marked”)
 - Bear and Bird Predation concerns
 - Even with some data that bears don’t target tagged fish over un-tagged, Hot pink floy tags might be suboptimal color in general; **Decision point** – meet and look into purchasing a less brightly colored tag, if they are available in time for field work.
 - Number of samples being collected per fish evaluated
 - Given the number of data points being documented and collected per fish, is it possible to replace genetic axillary with an opercle punch if successfully collected
 - **Decision point** – Use opercle punches if obtainable with axillary sample as optional for genetics. Field tests with different punches will be tried before the season and the decision revisited if need be.
 - **Decision point** – Do not use scales as substitute for genetic sample due to contamination/quantity concerns.
 - The possibility of doing a genetic mark recapture as a tool was discussed; trade-off between physically tagging the fish versus relying solely on genetics was discussed, but no change to experimental design was made at this point.
 - Only spit-balled estimates based on mutilation data could be used for population estimates if did only genetics mark/recapture since genetic results would not likely be through the lab, quality control, and analysis until the spring following the field season.

Otolith Shipping Incident Update and MTAL Flood

- **New Extraction Method now in place**
 - **Chris Habicht** reviewed the experiments done by GCL team to develop a effective method of extracting DNA safely from the otoliths where pairing was compromised

AHRP May 2021 Meeting Summary

- With 17% of that shipment to MTAL affected, anticipate 2% loss of data after this new method reconnects otoliths with their respective heart tissues
- **MTAL Flood**
 - **Chris Habicht** confirmed that the flood caused by a faulty fire sprinkler system did not affect the room where study otoliths were. Even if it had, they were protected with rubber mats so water exposure to the plates was not an immediate threat to any samples.

RRS results

- See supplementary web notebook “AHRP SP New Results RRS summary to date and preliminary heritability estimation” by Kristen Gruenthal, Kyle Shedd, and Chris Habicht
 - **Kristen G.** gave an overview of analyses of parentage results for even and odd lineages of pink salmon in Stockdale and Hogan Creeks in Prince William Sound, as well as even year results for Gilmour Creek.
 - We do not have full otolith reads for Gilmour 2016/2018 or Erb 2016, but these analyses include all fish sampled; analyses will need revision once otolith heart re-pairing has been completed.
 - Summary of single-generation and multi-generation RRS results
 - Single-generation RRS (Table 1) is <1 globally thus far, with 21 of 26 (81%) of estimates significantly <1 (in bold).
 - Four of six estimates of multi-generation RRS (Table 2) are also below 1.
 - One estimate is significantly <1 (Hogan 2015-2019; in bold)
 - two are borderline (Hogan 2014-2018, Gilmour 2014-2018),
 - one is still compromised by the shipping issue (Gilmour 2014-2018),
 - Two are based on extremely small sample size (Stockdale 2013-2017, Hogan 2013-2017).
 - Identifying great grandparents/great grandoffspring has been difficult as sample sizes winnow markedly through the generations.
 - Almost all exclusion probabilities were equal to 1; we are confident our marker set will correctly assign parents to offspring.
 - Mating Patterns
 - Kristen G. overviewed the general mating patterns for the 2014 parental generation.
 - Data are partitioned according to cross type, but trend lines represent the overall patterning.
 - Streams are those for which we have prepared the GIS location data (currently Stockdale and Hogan only)
 - Evidence of size assortative mating
 - Stockdale – no overall trend
 - Hogan – bigger fish may tend to mate with bigger fish but results are largely inconclusive

AHRP May 2021 Meeting Summary

- Gilmour – TBD
- Paddy – TBD
- Erb – TBD
- When were dams and sires that mated sampled:
 - Stockdale – females were sampled later on average than males likely due to earlier run timing in males
 - Hogan – females and males were sampled about the same on average, although there may be some variability among the cross types
 - Gilmour – TBD
 - Paddy – TBD
 - Erb – TBD
- Where were dams and sires that mated sampled:
 - Stockdale – dams and sires were found in generally the same area
 - Hogan – dams tended to be found further upstream on average than males
 - Gilmour – TBD
 - Paddy – TBD
 - Erb – TBD
- A summary was presented of an exploration of the parent-pair offspring trio/triad data (i.e. cross data) in terms of spatiotemporal patterning and generating preliminary estimates of narrow-sense heritability of body length, sample date, and RS according to cross type for Stockdale, Hogan, Gilmour, and Erb Creeks for the 2014 brood year; location information is not yet available for the bulk of our samples.
 - Correlation between parent-offspring body length
 - Stockdale – slight positive trend but low correlation between parent and offspring body lengths
 - Hogan – slight positive trend but low correlation between parent and offspring body lengths, except between female parents and male offspring (no trend)
 - Gilmour – slight positive trend but generally low correlations except between a hatchery female parents and natural male parents and offspring
 - Paddy – TBD
 - Erb – slight positive trend but low correlation between parent and offspring body lengths; sample size for HH was too small to make meaningful conclusions
 - Narrow-sense heritability of body length
 - Stockdale – heritability of body length is low except for the HH cross type, which had the fewest number of samples
 - Hogan – sample size too small
 - Gilmour – heritability of body length high for NN and especially HN cross types
 - Paddy – TBD

- Erb – highest heritability in HH cross type, but sample size was too small to make meaningful conclusions. Heritability for NN, with the largest sample size, was generally higher, too, however, lending support to the idea that body length is heritable (not surprising, but a good result).
- Correlation between parent-offspring sample dates
 - Stockdale – higher correlation between parent and offspring sample date for natural vs hatchery fish of both sexes; better sample sizes for natural-origin fish, however
 - Hogan – higher correlation between parent and offspring sample date for natural vs hatchery fish of both sexes except male parents with female offspring; generally small sample sizes, however
 - Gilmour – higher correlation between parent and offspring sample date for natural vs hatchery fish of both sexes except male parents with female offspring
 - Paddy – TBD
 - Erb – higher correlation between parent and offspring sample date for natural vs hatchery fish of both sexes except female parents with male offspring; better sample sizes for natural-origin fish, however
- Narrow-sense heritability of sample date
 - Stockdale – heritability of sample date (run time) is high in NN crosses, moderately so in HN crosses, and below 0.1 otherwise, although sample size is somewhat low for the HH cross
 - Hogan – sample sizes are too small
 - Gilmour – strong heritabilities overall for sample date, with good sample sizes
 - Paddy – TBD
 - Erb – sample size for HH was too small to make meaningful conclusions
- Correlation between parent-offspring sample location and narrow-sense heritability of sample location not yet available for parental years beyond 2014.
 - GIS-based stream distance mapping is in progress by Chase Jalbert.
- Narrow-sense heritability of RS (fitness)
 - It should be noted that estimation of the heritability of fitness (RS) here will be problematic because it does not account for sampling rates or productivity/year effects.
 - There are large reductions in sample size across generations within pedigrees rooted in incomplete sampling across brood years.
 - As a reminder, for example, few grandoffspring have more than 1 or 2 grandparents assigned.

AHRP May 2021 Meeting Summary

- Stockdale – negative, but small sample size for F2 generation grandoffspring
- Hogan – h^2 estimates suggest heritability of RS for Hogan, but the sample sizes were too small to make any meaningful interpretation
- Gilmour – also negative; results prompted exploring this metric by dyad to increase dataset size for F2 generation
- Paddy – TBD
- Erb – TBD; heritability analysis of RS requires Erb 2016-2018 data
- RS by dyad
 - Results: Negative; dyad data did not help because F2 generation dataset likely too small.
- Summary:
 - There is some evidence for heritability of body length, but there is more for heritability of sampling date (i.e. run timing).
 - Distance data are not yet available beyond the 2014 parental generation and are thus not yet included in analyses.
 - Analysis of heritability of RS is unsatisfactory due to reductions in sample size across generations.
 - Caveat: Some heritabilities were >1 . There are biological reasons this could happen, such as higher relationships between (inbreeding) and/or among parents than expected or trait measurement error, under a controlled experimental design. These events are unlikely in our datasets, however.
 - Our issues likely stem from the fact that we estimate narrow-sense heritability from $r = \sqrt{(\frac{1}{2})h^2}$, and therefore, correlations >0.7 result in $h^2 > 1$. Small sample sizes, and depending on cross type, can likely artificially elevate.
 - The effect of small sample size is particularly apparent for the Hogan 2014-2016 sample date analysis, which results in h^2 values far out of the range of acceptability
 - Estimation of overall heritability, independent of cross type, will likely be the most immune.

Funding Updates

- **Kristen G.** provided an update on the SeaGrant proposal that will bring additional money into the project, replacing some of the chum work that was supposed to be funded as part of the overall project
 - Application will be submitted by May 28, won't announce awards until October
 - Proposed collaboration with Megan McPhee to develop a GTseq panel for chum salmon so that work can be done on chum salmon from this project similar to work done for pinks
 - Develop GTseq panel with 300-500 markers including higher diversity markers, with a grad student built into the proposal
- Pink Salmon Disaster funding

AHRP May 2021 Meeting Summary

- \$1.7 million dollars available from pink salmon disaster funding will be applied towards pink salmon analyses under this project
- Pink salmon portion of AHRP will be completely funded.

Manuscript Updates

- Prince William Sound Pink/Chum stray rates paper is published:
 - Knudsen, E. E., Rand, P. S., Gorman, K. B., Bernard, D. R., and W. D. Templin. 2021. *Hatchery-Origin Stray Rates and Total Run Characteristics for Pink Salmon and Chum Salmon Returning to Prince William Sound, Alaska, in 2013–2015*. *Marine and Coastal Fisheries: Dynamics, Management, and Ecosystem Science* 13:41–68. <https://doi.org/10.1002/mcf2.10134>
 - This paper was chosen as a featured article in the “Journal Highlights” article by AFS and publicized in the May issue of Fisheries magazine
- Southeast Alaska chum paper is available online
 - Josephson, R., Wertheimer, A., Gaudet, D., Knudsen, E. E., Adams, B., Bernard, D. R., Heintz, S. C., Piston, A. W., and W. D. Templin. 2021. Proportions of hatchery fish in escapements of summer-run Chum Salmon in Southeast Alaska, 2013–2015. Accepted Article (online access). *North American Journal of Fisheries Management*. <https://doi.org/10.1002/nafm.10580>
- RRS paper
 - Chris and Bill have finished reviewing the latest version after revisions
 - Emily L., the first author will be able to meet early the week of 5/17 to finish up revisions and submit back to the editors for publication

Cooperative Institute of Climate, Ocean, and Ecosystem Studies (CICOES) postdoc

- **Peter W.** introduced Sam May the recipient of the CICOES postdoc
 - **Sam May** is a PhD candidate at the University of Washington’s School of Aquatic and Fishery Science studying quantitative and population genomics; Fall 2021 thesis defense expected then joining the project.
 - This component will help with moving forward thinking about policy implications
 - Charlie Waters – NOAA mentor; Peter Westley – Academic Mentor