# Alaska Hatchery Research Program Science Panel meeting December 21, 2020

## Virtual meeting via Microsoft Teams

## Summarized meeting notes and decision points

### Attendees

**Science Panel**

Milo Adkison, University of Alaska

John Burke, ADF&G and Southern Southeast Regional Aquaculture Association (SSRAA; retired from both)

John H. Clark, ADF&G (retired)

Chris Habicht, ADF&G

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

Callie Simmons, SSSC

Kristen Gruenthal, ADF&G

Garold V. "Flip" Pryor, ADF&G

Kyle Shedd, ADF&G

Forrest R Bowers, ADF&G

Erica Chenoweth, ADF&G

Mike Wells, Valdez Fisheries Development Association (VFDA)

Thane Miller, VFDA Board

Ron Heintz, SSSC

Geoff Clark, Prince William Sound Aquaculture Corporation (PWSAC)

Eric Prestegard, Douglas Island Pink and Chum, Inc (DIPAC)

Katrina Hoffman, Prince William Sound Science Center (PWSSC)

Peter Rand, PWSSC

Dion S. Oxman, ADF&G

Scott Wagner, Northern Southeast Regional Aquaculture Association (NSRAA)

Trenten Dodson, Kodiak regional Aquaculture Association (KRAA)

## 2021 Planning

- o **SEAK Stream Sampling (Chum salmon, SSSC contractor)**
    - **Chance Gray** presented the SSSC proposed operational plan outlining scenarios to improve sample collection in study streams mindful of the high variability in weather and chum returns in previous years
        - Mark/recapture effort to be added to the study this year (to collect genetic samples and establish an escapement estimate)
            - o Discussion
                - o trade-offs of different tag types (disc tags versus Floy);
                - o Pre-purchased Floy tags are available from **GCL** to use (est. 5,000) with tagging guns;
                - o Beach seine will be used and pinks will be sorted out by crew; different net types available; **Peter W.** offered use of his juvenile beach seine with fine mesh to reduce tangling
                - o In the case of strays ("nose-ins") surveying nearby systems for tagged chum salmon is not recommended as it would impact survey efforts on the study streams but DIPAC monitor for tagged chum salmon and collect any tags that arrive at the hatchery.
                - o Mark/recapture will need to have same level of effort through time so adjust effort at the peak of the season and use mutilation marks
            - o **Decision point** – Genetic sampling will be conducted as frequently as possible throughout the season with sampled fish Floy tagged and adipose fin clipped. Genetic samples from these fish will be stored in wells containing the end of the Floy tag (double-numbered tags). Throughout the season, mutilation marking will be done every other day to get Mark-Recapture estimates. Mutilation mark will be varied every week (opercle, varying location). Recapture of marked fish would occur during standard stream surveys (normal carcass sampling). If Floy tags are lost, the missing adipose fins will identify dead tagged fish and the tissue sample will allow tracing back to the Floy tag ID that was lost to match otolith reads.
        - Carcass Weirs
            - o Prospect and Sawmill will be less problematic than Fish Creek but will install carcass weirs in all three streams with the option for pulling/disabling the weir midseason if not doable.
            - o **Decision point** – use carcass weirs to increase sample numbers at all three streams. Signage recommended to reduce vandalism at Fish and Sawmill creeks. SSSC will alert and ask for input from SP if midseason changes are needed.
        - Field Crews

- o Successful chum sampling in the years 2021/22/23 is critical to the success of this study. Sampling on all three streams will continue this year with the possibility of revisiting the number of streams sampled in future years
- o **Decision point** – Pursue the option *Field Camp at Prospect Only* outlined in *SITKA SOUND SCIENCE CENTER AHRP SE ALASKA Chum Sampling 2021* submitted to the SP on 12/4/2020 by Chance Gray.  This plan will:
  - o Set up a field camp at Prospect Creek only
  - o Establish a 3rd field crew. This would allow each crew to conduct surveys on a single study stream.
  - o Install partial carcass weirs on each stream to reduce carcass loss due to flooding.
  - o Conduct a mark/recapture component on each stream to collect genetic samples and establish an escapement estimate.
  - o Add an additional field technician during the peak season
  - o Cost $454,417 in 2021 and $1,290,417 from 2021-2023.

## Funding Updates

- o Hatchery component and Processor component zeroed out this year (and possibly future years)
  - • Work might need to be reorganized; analysis might be delayed
- o Northern Fund application for FY21
  - • $180,000 requested. (Likely to be less)
- o Allocations for the GCL may be double entered and reflect higher expenditures than anticipated in FY21.  Some FY21 GCL funding will be moved forward to FY22 as a result of the shipping issue.
  - • Chris H. will work with Flip and Sam on the Proforma
- o Other soft funds can be explored going forward

## RRS results

- o See supplementary web notebook "New RRS Results for Science Panel Dec2020"
  - o Preliminary analyses for two generations of even-year lineages in Stockdale and Gilmour creeks (2014-2016-2018) and among-among stream results for Stockdale, Gilmore, and Hogan (2014-2016):
    - ▪ Stockdale Creek (2016–2018)
      - ▪ Almost all exclusion probabilities were equal to 1; we are confident our marker set will correctly assign parents to offspring.
      - ▪ Of 4,048 total offspring genotyped, 499 were assigned to 383 total parents, for an assignment rate of 12.3%.
      - ▪ A total of 67 offspring were assigned to two parents (triads).
      - ▪ RRS (with 0s) was significant for females at 0.37 (95% CI [0.16, 0.73]) but not males at 0.60 (95% CI [0.27, 1.14]).
      - ▪ There were not enough triads to make meaningful comparisons among cross types (only 1 NN and 55 NH were observed).

- ▪ Family size varied from 0-7 for females and 0-8 for males.
- ▪ Stockdale Creek (2014–2016–2018)
  - ▪ A total of 63 unique grandparents were identified that produced 90 F2 offspring, 76 of which had one grandparent assigned and 14 of which had two grandparents assigned.
  - ▪ F1 to F2 RRS was 0.94 (95% CI [0.61, 1.42]).
- ▪ Gilmour Creek (2014–2016)
  - ▪ Almost all exclusion probabilities were equal to 1.
  - ▪ Of 3,345 successfully genotyped, 975 offspring were assigned to 309 parents for an assignment rate of 29.2%.
  - ▪ A total of 274 offspring were assigned to two parents (triads).
  - ▪ RRS was borderline significant for females at 0.85 (95% CI [0.74, 0.98]) and males at 0.78 (95% CI[0.66, 0.93]).
  - ▪ There was enough cross type data (triads) to make meaningful comparisons
  - ▪ NH and HN crosses were of intermediate success, with NN bracketing at the high end and HH at the low end
  - ▪ There may be a maternal effect as natural origin females exhibited higher success than hatchery origin females regardless of male origin
  - ▪ Family size varied from 0-18 for females and 0-21 for males.
- ▪ Gilmour Creek (2016–2018)
  - ▪ Again, almost all exclusion probabilities were equal to 1.
  - ▪ Of 2,710 total offspring genotyped, 635 were assigned to 395 total parents, for an assignment rate of 23.4%.
  - ▪ A total of 168 offspring were assigned to two parents (triads).
  - ▪ RRS (with 0s) was not significant for females at 0.62 (95% CI [0.10, 1.69]) or males at 0.62 (95% CI [0.10, 2.05]), but this data is incomplete given all the unread otoliths.
  - ▪ Otolith information is still missing for a majority of the 2016-2018 data, and meaningful comparisons among cross types could not be made.
  - ▪ Family size varied from 0-14 for females and 0-11 for males.
- ▪ Gilmour Creek (2014–2016–2018)
  - ▪ A total of 129 unique F0 grandparents were identified that produced 269 F2 offspring, 175 of which had one, 84 of which had two, and 10 of which had three grandparents assigned.
  - ▪ F1 to F2 RRS was 0.84 (95% CI [0.68, 1.02]).
- ▪ Among Stockdale, Hogan, and Gilmour (2014–2016)
  - ▪ Almost all exclusion probabilities were equal to 1; we are confident our marker set will correctly assign parents to offspring.
  - ▪ Of over 12K successfully genotyped, 2,605 offspring were assigned to 917 parents for an assignment rate of 20.8%.
  - ▪ A total of 498 offspring were assigned to two parents (triads).

- There was a highly significant difference in the proportion of offspring assigned to hatchery- and natural-origin parents relative that of potential parents sampled.
- Over 94% of fish sampled were sampled in their natal streams. Different straying patterns were observed among streams. More non-natal fish were observed in nearby streams (Stockdale to Gilmour and vice-versa than in more distant streams (Stockdale or Gilmour to Hogan, and vice versa). Sampling rates among streams and within and among years, combined with only 3 streams sampled makes calculating donor stray rates not straight forward.
  - Discussion
    - Exciting to see; confirmation of known facts like both sexes are promiscuous and stray; lots more interesting things to explore to look at here with some modeling, architecture of dispersal, straying, possibly look at strength of selection on traits being measured; lots of major added value for this project in these data.

## Data Sharing

- o Wording in letter sent from Bill (as representative of SP) to data requester reviewed and finalized. **Decision point:** Data sharing documents accepted by SP

## CICOES PostDoc opportunity

- o Peter W. identified possibility to apply to NOAA for two year fellowship for a post-doc
  - o Would need a NOAA based mentor; Charlie Waters
  - o Help conduct simulations, modeling, scenario building, especially to help with grandparentage questions
  - o Moving forward thinking about policy implications
  - o **Decision point:** SP supports pursuing the application for this postdoc fellowship