Ocean Resources Enhancement and Hatchery Program Scientific Advisory Committee Meeting Minutes

TELECONFERENCE ONLY
Date: Wednesday, February 22, 2023
Time: 11:00 a.m. – 2:00 p.m. (PST)

Attendees:

Scientific Advisory Committee (SAC) members:

Lee Blankenship; Ken Cain, Ph.D.; Tanya Darden, Ph.D.; Mike Franklin, Ph.D.; Jackson Gross, Ph.D.; Ken Leber, Ph.D.; Kai Lorenzen, Ph.D.; Matt Powell, Ph.D.; Nicole Williamson; Greg Wiens, Ph.D.; and Ron Zweig.

Reviewers:
Michael Tringali, Ph.D. and Mark Christie, Ph.D.

California Department of Fish and Wildlife (CDFW):
Adam Frimodig, Kathryn Johnson, Kirsten Ramey, Jeff Rodzen, and Valerie Taylor

Guests and members of the public:
John Ballotti (Ocean Resources Enhancement Advisory Panel [OREAP] member), Lyall Bellquist (The Nature Conservancy), Michael Denson (National Oceanic and Atmospheric Administration [NOAA]),Mark Drawbridge (Hubbs-SeaWorld Research Institute [HSWRI]), Luke Gardener (California Sea Grant, OREAP member), Ruari MacNamara (HSWRI), Madison Powell, Mike Raabe, Ellen Reiber (South Carolina Department of Natural Resources [SCDNR]), Mike Rust (HSWRI), Mike Shane (HSWRI), Bruce Williams, and Lengxob Yong (SCDNR).

1. **Introductions and announcements**

   Ron Zweig and Valerie Taylor

2. **Brief overview of background, SCDNR white seabass genetics study, peer review findings, and study team response**

   Ron Zweig and Kai Lorenzen Ph.D.

   Kai Lorenzen gave a brief PowerPoint presentation:
   - Genetics study needs to be reviewed for reliability before deciding where to go using the genetics tool and assessing wild populations for hatchery contribution.

- Typical terms of reference and questions asked when reviewing a document - Is the overall approach suitable? Are the methods sound? Is the statistical analysis sound? How should a sampling program be designed if we use this tool to analyze hatchery contribution in the future?
- Main take-homes from the review were that the overall approach is suitable; however, there are some caveats with the statistical analysis. The methods were implemented properly overall. Both reviewers highlighted some concerns and questions about the statistical analysis and possible false assignments of some fish as hatchery fish.
- Reviewers have various suggestions for modified analyses.

3. Question and answer session

Tanya Darden, Ph.D., Michael Tringali, Ph.D., and Mark Christie, Ph.D., SAC

- Mike Tringali – CERVIS finds the likelihood of a certain relationship. In terms of sampling a system that includes hatchery and wild fish, you're still sampling and testing both hatchery and wild fish. You should be testing everything against itself. CERVIS doesn't compute when a lot of different relationships apply. It tries to apply some correction. CERVIS wasn't built to do this type of analysis where some are wild and some are hatchery fish. We need to adopt an inductive approach. Simulations can be used to address this omission.
- Dr. Christie – How many loci were used?
    - Tanya Darden– 15 loci
- Jeff Rodzen (reviewer from CDFW) – Is the intent of this to be able to get away from tagging and rely solely on genetics tags?
    - Tanya – yes
- Mike Tringali - It's hard to get DNA from bone (otoliths). I applaud your efforts. Sampling moving forward could include tissue preserved for future tests.
    - Tanya – HSWRI is already moving forward in taking samples from their broodstock. Samples were genotyped multiple times for low quality samples.
- Mark Christie – Population genetics of the study are solid but would like to discuss the parentage assignments more. For the Mexico samples, three individuals were assigned to broodstock parents. Considering the relatively huge population sizes and the small sample size, the idea that 3/40 fish could be attributed back to hatchery parents seems unlikely.
    - Discussion about adding more loci.
    - Discussion about trio analysis, mutations, and mismatches.
- Mark Christie – Worth putting more effort into making sure these results are accurate. According to these findings, 30% of the pop in Oceanside are hatchery fish – this is a huge amount. These results have huge implications for management if they are accurate.
    - Tanya – We must be very careful here, this isn't a random sample of the whole population. Different questions require different sampling designs. The samples for this study were not collected in a way that would answer those questions.

- Mike Tringali – CERVUS assumes that parents and parent offspring pair are unrelated but we can't assume that there isn't background relatedness going on in the background.
- Kai – Both the juvenile samples and the adult head collection program are systematic sampling programs. We know the selectivity pattern of the gill nets. I think we're not giving these samples enough credit as good samples – we just need to make sure they're appropriately assigned.
- Tanya – Juvenile surveys were done over a large time scale without having age data captured. We don't know how to assign these fish to a year class, but it is giving us an idea that hatchery fish are surviving. The contribution changes over time – we've been looking at stock enhancement since 1996. There is full recruitment at age one. We can sample adults and see how that translates.
- Mark Christie – Broodstock DNA samples are very important and need to be preserved carefully. They should be treated like gold.
    - Tanya - HSWRI has been doing a really good job on that since their interest in implementing a genetic tagging aspect to the program.
- Discussion of use of x-ray to detect tags
    - HSWRI – work in progress, has not been completed yet
- Microsatellite tags?
    - Tanya – Don't know that there's a need for development of another molecular marker; might be better off going forward designing a sampling program that would get at the questions we need going forward.
- Discussion of false assignments
    - Skepticism in assigning something as a mutation that is mismatched at multiple loci
    - Discussion of using additional juvenile samples from California State University Northridge
    - Discussion of null alleles, inbreeding, possibility of broodstock inbreeding
- Lyall Bellquist – You have three sample groups being compared to broodstock fish and only a subset of those were actually genotyped and used. 97% of the samples being used come from the gillnet program. Kai had a really good way of characterizing the sample collection. Why were the juvenile sample collections systematic – to understand population contribution more from a perspective of movement. It was designed to catch hatchery fish. I would say you want to be cautious.
    - Kai - Sampling locations are not randomly assigned for the juvenile sampling program. Population modelling looks at dispersal, calculates survival rates. If you're doing random sampling, you wouldn't have to do these complicated analyses, and this is important when you design your sampling program.
    - Discussion on using simulations

- Question about using otoliths to see if there's a chemical signature in wild or hatchery fish
    - There is a stable isotope method.
    - Pilot studies with collaborators in Mexico with a relatively small subsample. Can determine hatchery fish from wild fish.
    - Difference in growth rings on otoliths?
        - HSWRI did look at otoliths and sectioned them for wild and hatchery fish coming up with different growth curves. But didn't really look at the first year of growth to see if the hatchery fish is different than wild fish.
- Continued discussion of simulations
    - Using wild fish as the parents – false assignment error
    - Using California State University Northridge fish to compare – false rejection error
    - Simulate offspring and broodstock data sets; perform parentage analyses using the CERUS model; expectation is that low levels of parent –offspring matches would occur
        - Error rate would represent an estimate of false assignments.

4. **Public comment on agenda items**

   Valerie Taylor and Ron Zweig

5. **Formulate SAC conclusions regarding SCDNR genetics study**

   SAC

   - Additional analyses to be completed before the review is completed.

6. **Discussion of implications and development of next steps**

   SAC

   - SCDNR will run the suggested parentage analyses and reach out to Mark Christie and Mike Tringali regarding the simulations if assistance is needed.
   - Another meeting will be scheduled in a couple of months to allow SCDNR to perform the additional analyses.

7. **Public comment on agenda items and closing of meeting**

   Valerie Taylor and Ron Zweig

   - John Ballotti – With the Advisory Panel meeting coming up next month, is there enough information to formulate a Scope of Work yet?
   - Mike Tringali – Three suggestions moving forward: sample fin clips; make sure to get a full genotype, sample, and gender all parents; use trio assignment exclusively.

- Kai – we do want the additional information from Tanya before moving forward making sure that information is reliable as far as the genetics tool.
- Discussion about funding and designing a robust field sampling program.

Questions about the meeting or agenda can be directed to the OREHP Coordinator, Valerie Taylor, at Valerie.Taylor@wildlife.ca.gov or OREHP@wildlife.ca.gov.

Meeting agendas and minutes can be found at https://wildlife.ca.gov/Conservation/Marine/OREHP/Scientific-Advisory-Committee.