Coastwide Salmonid Genetics CONFERENCE

May 12-15, 2025

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Alaska Native Land Acknowledgement

We acknowledge that we are on traditional territories of the many Indigenous peoples of this place, whose footsteps have marked these lands for centuries. The Coastwide Salmonid Genetics Conference 2025 is on the ancestral and unceded territory of the Dena'ina Ełnena peoples. We make this acknowledgement as an act of gratitude to those whose territory we reside on or are visiting.

An excerpt from https://www.anchorage.net/plan-your-trip/about-anchorage/the-denaina-people/

> Anchorage is located within Dena'ina Ełnena, the traditional homelands of the Dena'ina Athabascan people. One of Alaska's many distinct and diverse Indigenous groups, the Native people of Knik Arm are the K'enaht'ana, members of the Eydlughet (Eklutna) and K'enakatnu (Knik) tribes.
>
> The Upper Cook Inlet regions between the Chugach and Talkeetna Mountains have long provided abundant fishing, hunting, and gathering grounds, and the Anchorage Bowl area is filled with historically significant spots known for their roles in Dena'ina life. Traditional place names describe the areas' geographical features and cultural uses: Point Woronzof, with its steep bluffs, was originally known as Nuch'ishtunt, meaning "Place Protected from Wind." Earthquake Park, where land famously broke and shifted and sank into Cook Inlet during the 1964 Good Friday Earthquake, was originally and aptly named Nen Ghiłgedi — "Rotten Land." Kincaid Park was known as "Ułchena bada Huch'iłyut," meaning "Where We Pulled up the Alutiiq Boats," a name that tells the story of the last battle between the Upper Inlet Dena'ina and Ułchena raiders from Prince William Sound.
>
> In the 20th century, the construction of the Alaska railroad and the ensuing development of the city of Anchorage brought significant disruptions to Dena'ina life in the area, and the 1918 influenza epidemic devastated local Dena'ina communities.
>
> But the Anchorage area's Dena'ina roots remain strong. Today, residents preserve the culture in world-class institutions like the Alaska Native Heritage Center and the Anchorage Museum, through traditional subsistence activities like berry picking in the Chugach Mountains or fishing in Turnagain Arm, and via captivating public art installations, live performances, and arts and crafts handmade by modern Dena'ina artists.
>
> Learning about the land's Dena'ina heritage is an important part of any visit to Anchorage.

Welcome!

Greetings and welcome to the 2025 Coastwide Salmonid Genetics Conference, co-hosted by the Alaska Department of Fish and Game's Gene Conservation Lab, American Fisheries Society (AFS) Genetics Section, and Alaska Chapter AFS! Since 1984, this biennial conference has served as a forum for exchanging information in the field of salmonid genetics. The AFS Genetics Section became active with Coastwide beginning in 1997 and officially began sponsoring meetings in 2018. The AFS Genetics Section strives to provide a better understanding of the role of genetics in aquatic sciences, fisheries management, and aquaculture; encourage protection of genetic resources of aquatic species; and promote the accumulation, synthesis, and exchange of genetic information concerning aquatic organisms and their management.

It has been 11 years since Coastwide was held in Alaska. Spring has come early this year to Alaska, and we hope you are able to get out and enjoy everything the area has to offer. Local highlights include the Wednesday evening social at Kincaid Park Chalet and several Thursday afternoon field trip options including visits to the Alaska Wildlife Conservation Center, the William Jack Hernandez Sport Fish Hatchery, or the Alaska Native Heritage Center. Please see a local for tips on the best ways to get out and explore!

Our meeting this year will be kicked off in a keynote address by Drs. Jim and Lisa Seeb, who will explore the history of genetics in Alaska and Coastwide meetings with their talk, "Synergies among ADF&G Genetics, AFS Genetics Section, and Coastwides." This year's program also features 42 oral presentations and 11 poster presentations, including 5 students, covering a wide range of topics in salmon genetics.

A huge thank you to the many dedicated volunteers who made this meeting possible. We also wish to thank our meeting sponsors: Illumina, Standard BioTools, Macherey-Nagel, GTseek, Twist Bioscience, Element Biosciences, Bristol Bay Science and Research Institute, Pioneer Alaskan Fisheries, Alaska Wildlife Conservation Center, Broken Tooth Brewing, Double Shovel Cider Co., and Alaska Chip Company. Their support was instrumental in ensuring a successful meeting experience.

Finally, thank you to all the attendees at this year's meeting. In these times of uncertainty and challenges to the role of science in our ever-evolving world, it is more important than ever for us to gather and share ideas. We look forward to an engaging meeting!

Coastwide 2025 Planning Committee: Jodi Estrada, Sara Gilk-Baumer, Kristen Gruenthal, Heather Hoyt, Bobby Hsu, and Kyle Shedd

Throughout the program:

* Denotes Student Presentation

† Denotes First Author

AFS Code of Conduct

[Text is reproduced from the AFS Code of Conduct.]

Purpose:

American Fisheries Society (AFS) meetings are among the most respected scientific meetings of fisheries professionals in the natural resource scientific community. AFS values the diversity of views, expertise, opinions, backgrounds, and experiences reflected among all attendees, and is committed to providing a safe, productive, and welcoming environment for all meeting participants and AFS staff. All participants, including, but not limited to, attendees, speakers, volunteers, exhibitors, staff, service providers, and others, are expected to abide by this Meetings Code of Conduct. This Code of Conduct applies to all AFS meeting-related events, including those sponsored by organizations other than AFS but held in conjunction with AFS events, in public or private facilities.

Expected Behaviors:

- Treat all participants, attendees, AFS staff, and vendors with respect and consideration, valuing a diversity of views and opinions, and critiquing ideas rather than individuals.
- Refrain from demeaning, discriminatory, or harassing behavior and speech directed toward other attendees, participants, AFS staff, and suppliers/vendors.
- Be mindful of your surroundings and of your fellow participants. Alert AFS staff or venue event staff if you notice a dangerous situation or someone in distress.
- Respect the rules and policies of the meeting venue, hotels, AFS-contracted facility, or any other venue.
- To foster a welcoming environment, assist AFS members with impaired physical or cognitive abilities, if necessary.

Unacceptable Behaviors:

- Harassment, intimidation, or discrimination in any form is unacceptable. Harassment includes speech or behavior that is not welcome or is personally offensive. Behavior that is acceptable to one person may not be acceptable to another, so use discretion to be sure respect is communicated. Harassment intended in a joking manner still constitutes unacceptable behavior. Regardless of your intent, if you are advised directly or by another party that some aspect of your speech or behavior at an AFS meeting is harassment, you are expected to stop engaging in such speech or behavior.
- Do not physically or verbally abuse any attendee, speaker, volunteer, exhibitor, AFS staff member, service provider, or other meeting guest.
- Examples of unacceptable behavior include, but are not limited to, unwelcome or offensive verbal comments related to age, appearance, or body size, employment or

military status, ethnicity, gender identity and expression, individual lifestyle, marital status, national origin, physical or cognitive ability, political affiliation, sexual orientation, race, or religion. Harassment can also include the use of sexual and/or discriminatory images in public spaces or in presentations; deliberate intimidation; stalking; following; harassing photography or recording; sustained disruption of talks or other events; bullying behavior; inappropriate physical contact; and unwanted sexual attention.

- Appropriate and responsible personal use of photographs or posts to social media of another individual's oral presentation, poster, or likeness is acceptable unless permission is specifically denied by the individual.
- Do not disrupt talks at oral or poster session or activities in the exhibit hall or at other events organized by AFS at the meeting venue, hotels, or other AFS-contracted facilities.
- Any retaliation against participants for reporting unacceptable behavior is unacceptable. Like harassment or discrimination, retaliation against reporting poor behavior will be subject to consequences.

Reporting Unacceptable Behavior:

- Anyone experiencing or witnessing behavior that constitutes an immediate or serious threat to public safety at any time should contact local law enforcement (by calling 911) and immediately notifying facility security without delay.
- If you are not in immediate danger but feel that you are the subject of unacceptable behavior, you are encouraged to file a formal complaint to the AFS Ethics and Professional Conduct Committee and/or an AFS officer or the AFS Executive Director which will then be forwarded to the Ethics and Professional Conduct Committee for assessment.

Consequences:

- Anyone requested to stop unacceptable behavior is expected to comply immediately.
- Consequences to unacceptable behavior will be determined by the AFS Ethics and Professional Conduct Committee in conjunction with AFS officers and the AFS Executive Director.
- Consequences may include one or more of the following actions:
    - Dismissal from the meeting without refund
    - Reporting to your agency
    - Exclusion from any future AFS (sub unit/chapter/division) meetings for five years
    - Revoke of AFS membership without the opportunity for renewal for five years
    - If the offense is criminal, local law enforcement will be contacted.

Please report incidents to the Ethics and Professional Conduct Committee using the Code of Conduct Reporting Form.

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Schedule At a Glance

Monday, 5/12

6:00 PM – 9:00 PM Registration, Meet & Greet, cash/credit bar available, hors d'oeuvres provided, pre-function space

Tuesday, 5/13

6:30 AM – 8:00 AM Registration continued, breakfast provided, pre-function space

8:00 AM – 12:10 PM Meeting/talks, Redington Ballroom, Break 10:00 AM – 10:20 AM

12:10 PM – 1:20 PM Lunch provided, pre-function space

1:20 PM – 4:30 PM Meeting/talks, Redington Ballroom, Break 2:50 PM – 3:10 PM

4:30 PM – 6:00 PM Poster setup for presenters

6:00 PM – 9:00 PM Poster session and Trade show, Redington Ballroom and pre-function space, cash/credit bar available, hors d'oeuvres provided

Wednesday, 5/14

6:30 AM – 8:00 AM Breakfast provided, pre-function space

8:00 AM – 12:10 PM Meeting/talks, Redington Ballroom, Break 10:00 AM – 10:20 AM

12:10 PM – 1:20 PM Lunch provided, pre-function space

1:20 PM – 2:50 PM Meeting/talks, Redington Ballroom, Break 2:30 PM – 2:50 PM

2:50 PM – 4:30 PM Breakout sessions, suggested topics:

Pacific Salmon Commission Fraser Sockeye; Revised Chinook SNP baseline

6:00 PM – 10:00 PM Social at Kincaid Park Chalet, transportation provided

Thursday, 5/15

06:45 AM – 8:20 AM Breakfast provided, pre-function space

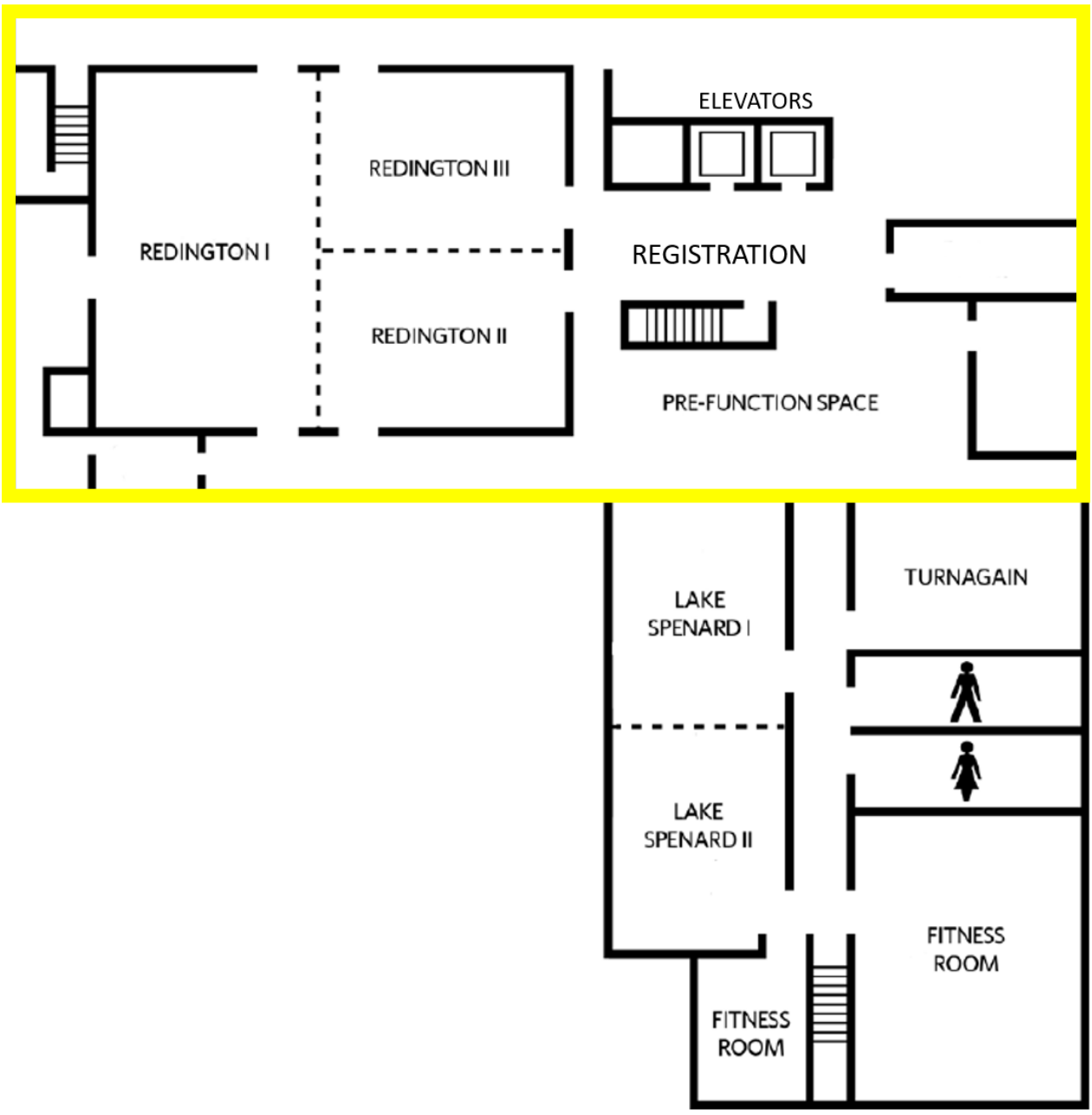
8:20 AM – 12:00 PM Meeting/talks, Redington Ballroom, Break 10:00 AM – 10:20 AM

1:00 PM – 5:00 PM Optional tours, use QRL code for registration:

- Alaska Wildlife Conservation Center
- William Jack Hernandez Sport Fish Hatchery
- Alaska Native Heritage Center

Meeting Space Layout

All events, unless otherwise noted, are at The Lakefront, 3rd floor, Redington Ballroom. Breakfasts and lunches will be served in the pre-function space.



Keynote Abstract

Synergies among ADF&G Genetics, AFS Genetics Section, and Coastwides

Jim and Lisa Seeb

Research Professors Emeriti

School of Aquatic and Fishery Sciences

University of Washington

We were invited to explore the importance of coastwide collaborations to Alaska fisheries management, and as a corollary, the connections among the Gene Conservation Laboratory (GCL), the AFS Genetics Section (cosponsor of this meeting), and the convening of Coastwide Salmon Genetics Conferences (Coastwides). We established the GCL in 1989 at the invitation of two visionaries, Bob Burkett and Doug Eggers, who understood the impact that a genetics lab would have on hatchery and fisheries management. They recognized that the State of Alaska straddles the major high seas migration pathways of maturing salmon. Populations from throughout the Pacific Rim can be found along the continental shelf in Alaska; they co-mingle with Alaskan populations and are often harvested together. Coastwide databases are critical for Alaska to understand the timing, migration pathways, and composition of these fisheries. We revisit the early years of Coastwides and describe the links among the GCL, the Genetics Section, and Coastwides. We review the evolution and adoption of DNA markers and the ongoing efforts of the GCL to construct Pacific Rim-wide databases in partnership with other labs in Asia and North America. Finally, we briefly review the collaborations between the GCL and the Alaska Salmon Program at the University of Washington.

Detailed Conference Schedule

Monday, 5/12

6:00 PM – 9:00 PM Registration, Meet & Greet, cash/credit bar available, hors d'oeuvres provided, pre-function space.

Tuesday, 5/13

6:30 AM – 8:00 AM Registration continued, breakfast provided, pre-function space.

8:00 AM Introduction, Welcome, Land Acknowledgement, and Overview, Sara Gilk-Baumer

8:15 AM Keynote Speakers: Jim and Lisa Seeb, Research Professors Emeriti, University of Washington, "Synergies among ADF&G Genetics, AFS Genetics Section, and Coastwides"

9:00 AM Break (10 minutes)

Session 1: *Close kin mark-recapture (CKMR)/Parentage*

> **9:10 AM** Matthew Campbell, "Evaluating Genetic Introgression from Hatchery-Origin Steelhead in the Snake River Basin Using Advanced Grandparentage Inference"
>
> **9:30 AM** Audrey Harris, "Clearing the hurdle: How arrival timing and size influence reproductive success in steelhead returning to Fish Creek, Idaho"
>
> **9:50 AM** Sponsor: Illumina, Sandi Calhoun, "Introducing the Illumina MiSeq i100"

10:00 AM Morning Break (20 minutes)

> **10:20 AM** Mary Commins*, "Evaluating the second-generation effects of hatchery supplementation in Auke Lake sockeye salmon"
>
> **10:40 AM** Zachary Robinson, "Estimating Chinook Salmon Escapement Using Transgenerational Mark-Recapture (tgMR) in the Presence of Precocial Parr"
>
> **11:00 AM** Scott Blankenship, "Estimating abundance of *Oncorhynchus mykiss* In Anadromous Waters Using CKMR Approach"
>
> **11:20 AM** Alana Luzzio*, "Using parentage-based tagging to identify natal origins of Chinook salmon (*Oncorhynchus tshawytscha*) returning to a restored creek"
>
> **11:40 AM** Brice Adams, "Migratory form Bull Trout parentage in the Clark Fork River, Montana"
>
> **12:00 PM** Sponsor: GTseek LLC, Nathan Campbell, "Salmonid genome structure and implications for GT-seq marker selection"

12:10 PM Lunch provided, pre-function space (70 minutes)

Tuesday, 5/13, continued

Session 2*: Genetic Stock Identification (GSI)/Population Genetics (Popgen)*

1:20 PM Todd Seamons, "Genetic discovery and description of a Nisqually River Chinook salmon population"

1:40 PM John Hargrove, "Temporal trends in hybridization between native and non-native salmonids in the Clearwater and Lochsa Rivers, Idaho"

2:00 PM Adrian Spidle, "Rescue program for South Fork Nooksack Spring Chinook salmon"

2:20 PM Rebecca Cheek, "Scaling up: Harnessing the power of an updated regional baseline for broad scale genetic stock identification of Chum Salmon (*Oncorhynchus keta*)"

2:40 PM Student Travel Grant Awards, Sara Gilk-Baumer

2:50 PM Afternoon Break (20 minutes)

3:10 PM Eric Rondeau, "A SNP-based coastwide sockeye salmon baseline for genetic stock identification in British Columbia"

3:30 PM Andy Barclay, "An updated coastwide baseline for genetic stock identification of chum salmon: a resource for examining stock-specific marine migration and harvest"

3:50 PM Kyle Shedd, "A range-wide genetic baseline for Chinook salmon improves resolution for stock identification in Alaska and northern Canada"

4:10 PM Erika King, "Updated status of Southeast Alaska coho salmon genetic baseline"

4:30 PM Closing, Sara Gilk-Baumer

4:30 PM – 6:00 PM Break, Poster Session Setup

6:00 PM – 9:00 PM Poster session and Trade show, cash/credit bar available, hors d'oeuvres provided, Redington Ballroom and pre-function space.

Wednesday, 5/14

6:30 AM – 8:00 AM Breakfast provided, pre-function space

8:00 AM Welcome and Day overview, Sara Gilk-Baumer

Session 2: *Genetic Stock Identification (GSI)/Population Genetics (Popgen) continued*

8:10 AM Chase Jalbert, "Alaska's Other Potential Eruption: Illuminating Fish Stocks with MAGMA"

8:30 AM Bobby Hsu, "Using computer simulation to assess sample size for mixed stock analysis"

8:50 AM Elizabeth Lee, "Genetic Stock Identification from Gravel to Gravel: Use of Genetic Tools in Forecasting and Monitoring Yukon River Chinook Salmon Runs"

9:10 AM Tyler Dann, "GSI of South Alaska Peninsula Chum Salmon Harvests: genetic tools inform management of fisheries that connect stakeholders amid conservation crises"

9:30 AM Jon Hess, "Genetic identification of lamprey genera and anadromous ecotypes in watersheds of the Northeastern Pacific Ocean"

9:50 AM Open timeslot

10:00 AM Morning Break (20 minutes)

Session 3: *Genomics*

10:20 AM Christopher Setzke*, "Mechanisms of specialist-generalist tradeoffs for IHNV in salmonids"

10:40 AM Kyle Wellband, "Shared patterns of DNA Methylation variation in hatchery-origin Coho Salmon and implications for developing molecular monitoring tools"

11:00 AM Samuel Rosenbaum*, "Chromosome-level reference genome for male brook trout (*Salvelinus fontinalis*) from a long-term genetic rescue study"

11:20 AM Timothy Healy, "Genomic estimates of climate change vulnerability in Sockeye Salmon"

11:40 AM Shawn Narum, "Conservation of Neutral and Adaptive Genomic Variation in Anadromous Fishes of the Columbia River"

12:00 PM Element Biosciences, Amy Klegarth, "Shift Your Science"

12:10 PM Lunch provided, pre-function space (70 minutes)

Wednesday, 5/14, continued

1:20 PM Wes Larson, "Understanding the genetic basis of run timing diversity in four species of Pacific salmon"

1:40 PM Kristen Gruenthal, "Genomic signatures of natural and domestication selection in wild and hatchery pink salmon"

2:00 PM Anna Tigano, "Fine-scale population genomics of chum from the southern Canada/USA border based on whole genome data"

2:20 PM Sponsor: Twist Biosciences, Paul Doran, "Twist's FlexPrepTM: Accelerating the Transition from Microarrays to Next-Generation Sequencing in Agrogenomic Applications"

2:30 PM Afternoon Break (20 minutes)

2:50 PM Breakout Sessions, suggested topics:

Pacific Salmon Commission Fraser Sockeye

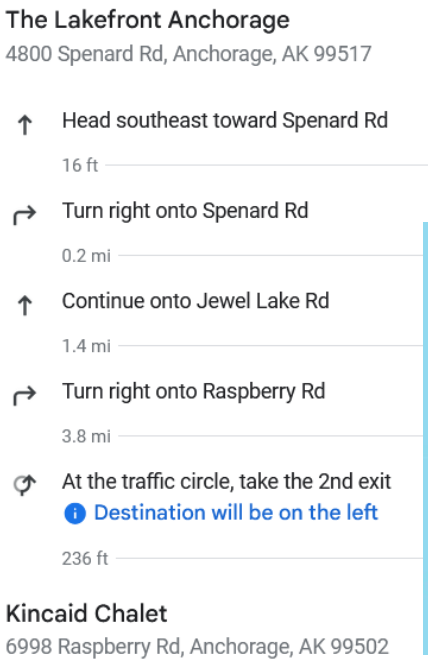
Revised Chinook SNP baseline

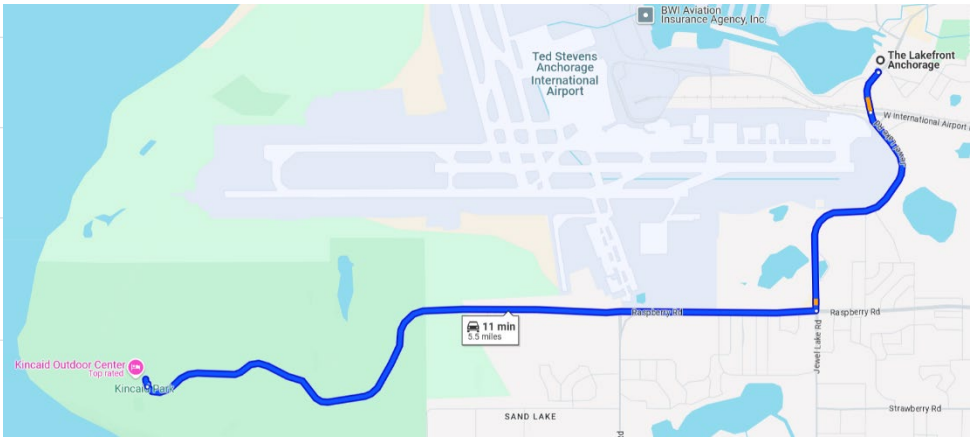
4:30 PM Closing, Sara Gilk-Baumer

6:00 PM – 9:00 PM Social at the Kincaid Park Chalet, transportation provided, see below for details. Appetizers, salad, Moose's Tooth Pizza, desserts, Broken Tooth Brewery, and Double Shovel Cider provided.

Wednesday Evening Social

A 56-person coach bus will make two trips each way to and from The Lakefront and Kincaid Park Chalet. The first bus departs The Lakefront at 5:40PM; the first return bus departs Kincaid at 8:30PM. However, if you choose personal transportation, see the following graphics for directions and a map.





Thursday, 5/15

6:45 AM – 8:20 AM Breakfast provided, pre-function space

8:20 AM Welcome and Day Overview, Sara Gilk-Baumer

Session 3: *Genomics continued*

8:30 AM Rebekah Horn, "Genomic insights into local adaptation and migration success in reintroduced Coho salmon of the Wenatchee River Basin"

8:50 AM Stuart Willis, "Heritability and genomic basis of age-at-maturity in Chinook Salmon"

9:10 AM Natasha Howe, "Age at maturity in sockeye salmon has a strong genetic component found on both sex and autosomal chromosomes"

Session 4: *Straying*

9:30 AM Nancy Hillstrand, "What are acceptable hatchery stray proportions in Alaska's anadromous waters?"

9:50 AM Sponsor: Standard BioTools, Zach Farrow, "Fast Answers for Fast Fish"

10:00 AM Morning Break (20 minutes)

Session 5: *eDNA*

10:20 AM Nate Cathcart, "Fish surveys, salmon population genetics, and eDNA detection in Bering Land Bridge National Preserve"

10:40 AM Michael Phelps, "Tracking invasive and threatened salmonid species using real-time and automated systems"

Session 6: *Lab Infrastructure*

11:00 AM Lanie Galland, "Mobile DNA sequencing laboratory for real-time assessment of Columbia River basin fisheries: Genotyping in a van down by the river"

11:20 AM Jodi Estrada, "Non-destructive high-throughput DNA extractions from pink salmon otoliths"

11:40 AM Heather A. Hoyt, "Three million and counting: Genetics sample archiving for the Alaska Department of Fish and Game"

12:00 PM Closing, Sara Gilk-Baumer

Thursday Afternoon Add-On Excursions

Alaska Wildlife Conservation Center

The Alaska Wildlife Conservation Center (AWCC) is a sanctuary dedicated to preserving Alaska's wildlife through conservation, education, research, and quality animal care. AWCC takes in injured and orphaned animals year-round and provides them with spacious enclosures and quality animal care. Most of the animals that arrive at the AWCC become permanent residents and will always have a home here.

A 56-person coach bus will provide transportation to and from The Lakefront and the AWCC. Bus departs The Lakefront at 1:00PM, returning at 5:00PM

William Jack Hernandez Sport Fish Hatchery

Construction of the William Jack Hernandez Sport Fish Hatchery was completed in June of 2011. Located in Anchorage at the intersection of Reeve Blvd. and Post Road, this fully enclosed, recirculating aquaculture system (RAS) based facility uses the best available technology to conserve water and reduce heating demand to produce Chinook and coho salmon, rainbow trout, and Arctic char. With over 100 rearing tanks, there is space for production of more than 6 million sport fish each year. These fingerling (1" to 2"), smolt (3" to 5") and catchable (7" to 12") fish are released throughout South Central Alaska from Cordova to Kodiak, Homer, Kenai, Seward, Anchorage, Mat/Su and Talkeetna. Sport fishing activity supported through these fish releases accounts for over $20 million a year in economic impact on local communities.

Vehicles will be available for transportation to and from The Lakefront and the William Jack Hernandez Sport Fish Hatchery.

Alaska Native Heritage Center

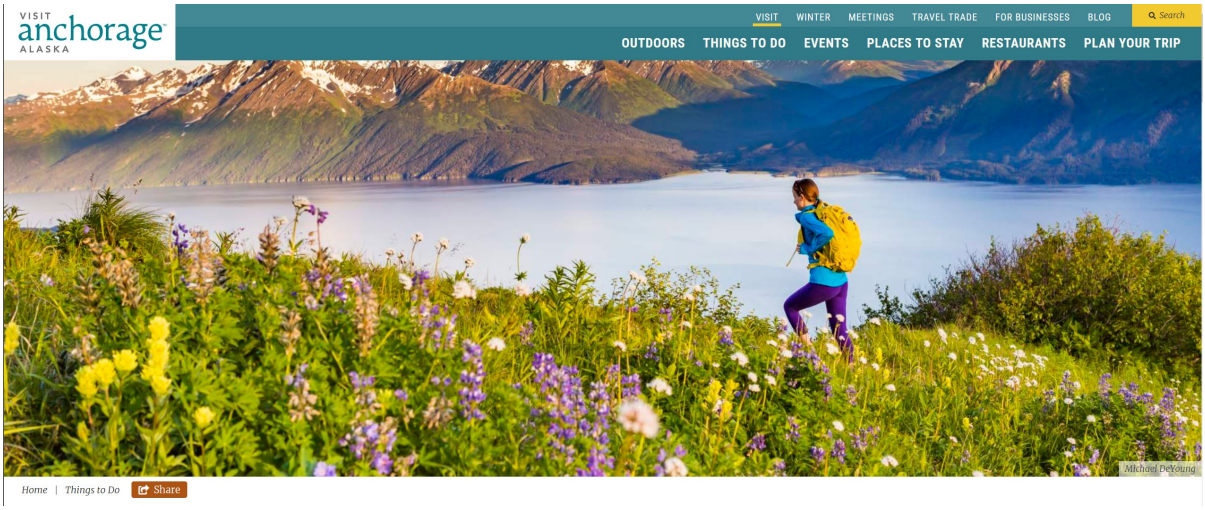
The Alaska Native Heritage Center (ANHC) is the only statewide cultural and education center dedicated to celebrating all cultures and heritages and created by a unanimous vote of the Alaska Federation of Natives in 1987. Two years later, ANHC was officially an incorporated 501(c)(3) non-profit organization and with the help and support of committed community members, in coordination with distinguished organizations like the Alaska Native Corporations, began fundraising to build the Center. ANHC opened its doors to the public in May of 1999, and celebrates its 25th Anniversary in 2024.

Vehicles will be available for transportation to and from The Lakefront and the Alaska Native Heritage Center.

Registration is available via this link:

Local Attractions and Adventures

If you are interested in extending your time in our great State, please enjoy this list of ideas for things to do. https://www.anchorage.net/



Anchorage is the place where young spirits and adventurous souls come to play. Hike a mountain trail under the midnight sun. Paddle turquoise waterways through a vast state park. Learn about incredible Indigenous cultures. Alaska activities and attractions include legendary wildlife, spectacular mountain vistas, fascinating museums and cultural centers, icy blue glaciers, and more. Metropolitan amenities mix with unrivaled natural splendor to make Anchorage an unforgettable destination. Need some help planning? Order a free Official Guide to Anchorage to get started.

4-Wheeling / ATV

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Photography Tours

Private Boat Charters

Rafting & River Trips

Railroad Tours

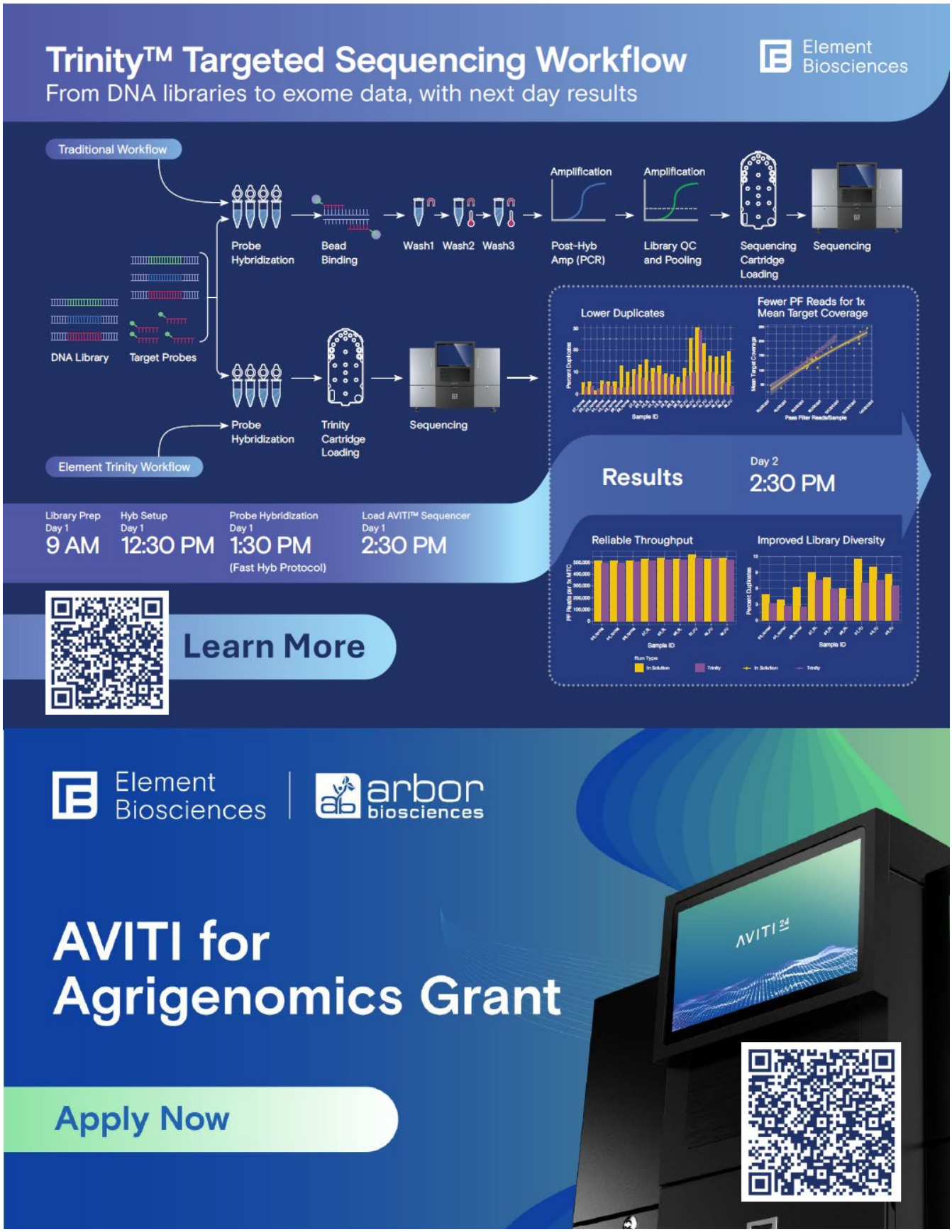
Shopping

Sightseeing Tours & Day Trips

Spas, Health & Wellness

Things To Do With Kids

Wildlife Viewing


Trinity™ Targeted Sequencing Workflow
From DNA libraries to exome data, with next day results
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Bead Binding
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Amplification
Post-Hyb Amp (PCR)
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Sequencing Cartridge Loading
Sequencing
DNA Library
Target Probes
Probe Hybridization
Trinity Cartridge Loading
Sequencing
Element Trinity Workflow
Lower Duplicates
Fewer PF Reads for 1x Mean Target Coverage
Results
Day 2
2:30 PM
Library Prep Day 1 9 AM
Hyb Setup Day 1 12:30 PM
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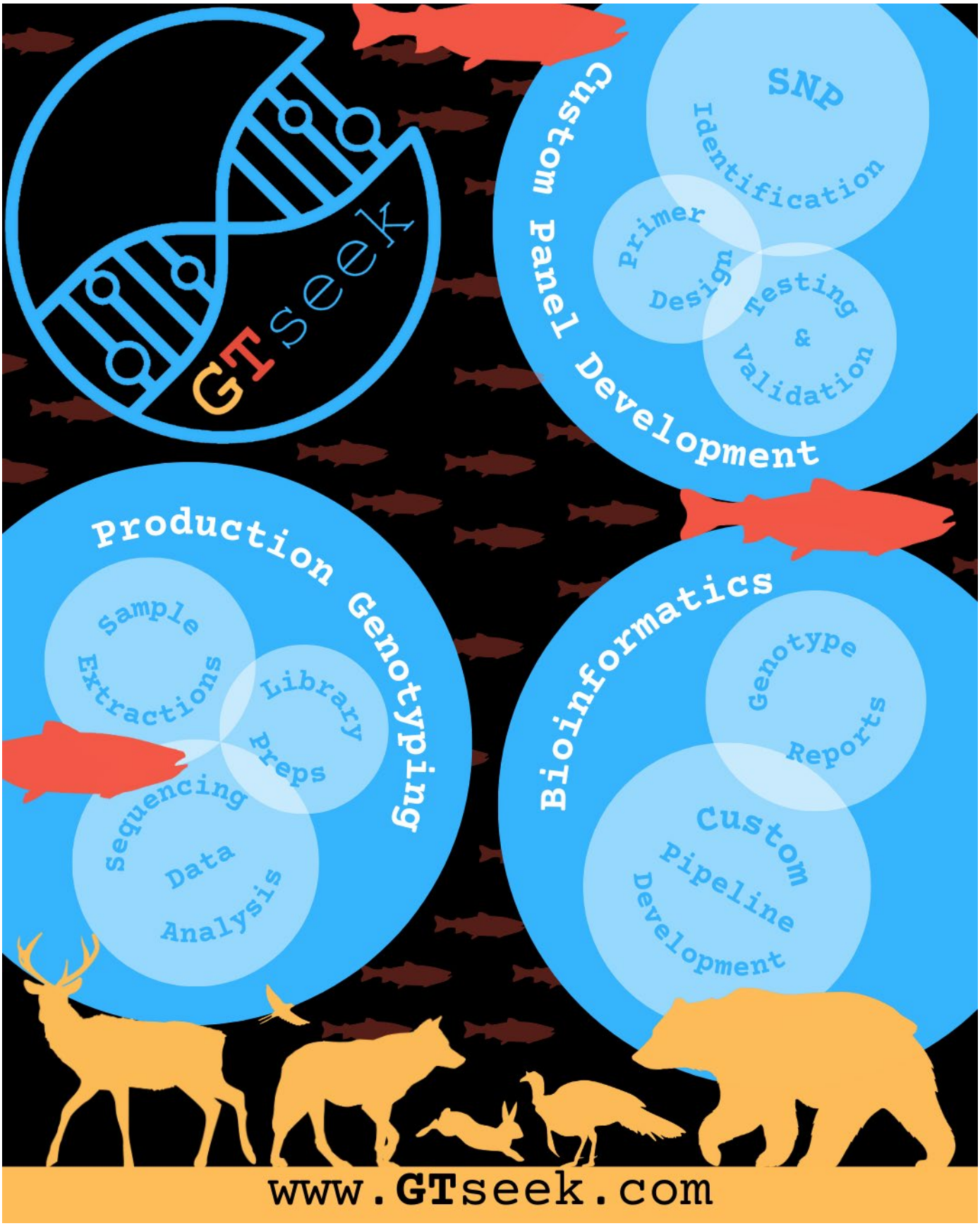
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Oral Presentation Abstracts

[Sorted Alphabetically by Presenter's Last Name]

Adams, Brice; USFWS; "Migratory form Bull Trout parentage in the Clark Fork River, Montana"; *Tues, 5/13, 11:40 AM*

Coauthor(s): Shana Bernall, Avista Corporation

Bull Trout (*Salvelinus confluentus*) have both resident and migratory life history forms. In the lower Clark Fork River, Montana juvenile migratory forms move from their natal tributaries to Lake Pend Oreille, Idaho for growth and rearing. The construction of three mainstem dams on the river blocked upstream passage for Bull Trout attempting to return home to spawn, raising questions about the persistence of the migratory form. Beginning in 2001, Avista Corporation and local stakeholder groups began providing upstream passage for Bull Trout at the lower most mainstem dam, Cabinet Gorge Dam. In 2004, Avista Corporation and Abernathy Fish Technology Center (AFTC), began using genetic assignment tests to inform decisions related to upstream fish passage. To assess the success of the fish passage program, a genetic parentage analysis was conducted to determine if Bull Trout collected downstream of Cabinet Gorge Dam were successfully spawning after being moved over the dam, giving them access to two important Clark Fork River tributaries: the East Fork Bull River and Graves Creek. Overall assignment success in this study was high, with over 90% of juvenile Bull Trout assigned to at least one parent. Upstream transport adults contributed to just under 72% of the collected juvenile Bull Trout, with varied rates between East Fork Bull River (68%) and Graves Creek (99%). This finding demonstrates that assisted fish passage does not negatively impact breeding success and could contribute to the restoration of healthy populations of migratory Bull Trout where habitat connectivity is disrupted by passage barriers.

Barclay, Andy; ADF&G; "An updated coastwide baseline for genetic stock identification of chum salmon: a resource for examining stock-specific marine migration and harvest"; Tues, 5/13, 3:30 PM

Coauthor(s): Tyler Dann, ADF&G; Kristen Gruenthal, ADF&G; Sara Gilk-Baumer, ADF&G

Interannual variation in ocean survival among important chum salmon stocks has been observed in recent years across the Pacific-wide range of the species, leading to questions about the mechanisms driving these changes. Genetic stock identification is the premier method for distinguishing among stocks in fishery mixtures. The method requires a baseline representing all potentially contributing stocks screened for genetic markers that have adequate levels of variation in allele frequencies among stocks. We present a new single-nucleotide polymorphism (SNP) baseline containing genetic data from over 42,000 fish and 91 loci that builds on previous baselines. The baseline was assembled using genetic data from tissue collections sampled over the past 39 years, with contributions from Korea, Japan, Russia, U.S., and Canada made possible through organizations like the NPAFC and PacSNP. In the baseline analysis, we assessed the identifiability of each reporting group by analyzing up to 100 mixture samples with varying compositions drawn from the baseline without replacement and used leave-one-out cross-validation and novel visualization methods to interpret correct allocations to stock and directionality and magnitude of incorrect allocations for individual assignments of fish. The baseline can distinguish 23 fine-scale and 7 broad-scale reporting groups making it a useful tool for estimating the contribution of stocks present in mixtures of fish caught on the high seas. The baseline is also capable of individually assigning fish to 5 reporting groups making it useful when pairing individual fish data with stock of origin. These capabilities make the baseline a key resource for examining stock-specific patterns of migration, harvest, and mortality in the northern Pacific Ocean.

Blankenship, Scott; Genidaqs – a laboratory of Cramer Fish Sciences; "Estimating abundance of *Oncorhynchus mykiss* In Anadromous Waters Using CKMR Approach"; *Tues, 5/13, 11:00 AM*

Coauthor(s): Steven Zeug, Genidaqs; Jasmine Williamshen, Genidaqs; Bobbie Flores, Genidaqs; Alex Constandache, Genidaqs; Jesse Wiesenfeld, Genidaqs; Annie Brodsky, Genidaqs

This presentation is derived from four years of data collection and analysis activities for *Oncorhynchus mykiss* life cycle monitoring in the lower Stanislaus River (California). The goal of this project is to estimate abundance of specific *O. mykiss* life stages and transition rates among life stages to better understand drivers of life history diversity and population dynamics. Abundance is being estimated using Close Kin Mark Recapture methods. Observed parent-offspring pairs across all years (2021-2024) were partitioned by birth year, with two models applied for abundance estimation, an iterative single year, and a multi-year. Within each year the adult abundance estimate generated by each model was statistically equivalent. For the single-year model, adult abundance estimates were 1,778 (1,547-2,039), 2,256 (2,075-2,450), 2,223 (2,031-2,441), and 2,115 (1,830-2,455) for 2021-2024, respectively. For the multi-year model, adult abundance estimates were 1,779 (1,542-2,048), 2,238 (2,063-2,422), 2,198 (2,005-2,404), and 2,011 (1,756-2,308) for 2021-2024, respectively. Other aspects of this project documented age and growth (scale analysis), the frequency of juvenile *O. mykiss* emigration from the lower River, and migrant survival within the Stanislaus River and out to San Francisco Bay (acoustic telemetry).

Calhoun, Sandi; Illumina; "Introducing the Illumina MiSeq i100"; *Tues, 5/13, 9:50 AM*

The new MiSeq i100 Series delivers Illumina's fastest run times yet, breakthrough simplicity, and significant sustainability advancements to empower every lab, everywhere. Please join for an overview of the MiSeq i100 features and a Q&A session.

Campbell, Matthew; IDFG; "Evaluating Genetic Introgression from Hatchery-Origin Steelhead in the Snake River Basin Using Advanced Grandparentage Inference"; *Tues, 5/13, 9:10 AM*

Coauthor(s): Audrey C. Harris, PSMFC; Zachary L. Robinson, CRITFC; Rebekah L. Horn, CRITFC; Shawn R. Narum, CRITFC; Thomas A. Delomas, USDA

Steelhead (*Oncorhynchus mykiss*) hatchery programs in the Snake River Basin (Idaho, Oregon, and Washington) are pivotal for fisheries management and species conservation, yet they pose genetic risks to wild populations through introgression resulting from hatchery-origin fish reproducing in the wild. This study evaluated these risks using an advanced grandparentage inference method, enhancing traditional parentage-based tagging approaches. A novel genetic marker panel composed of 287 microhaplotype loci was developed and rigorously validated, demonstrating high genotyping success rates (>90%) and substantial genetic diversity (heterozygosity ≈ 0.45). Empirical assessments confirmed the panel's efficacy, showing minimal false-positive rates and acceptable false-negative rates, which were further reduced by incorporating detailed hatchery metadata. Genetic analyses of returning wild adult steelhead collected during 2020–2021 at Lower Granite Dam (Snake River) identified 19.1% of individuals as having hatchery-origin grandparents. Leveraging PIT-tag detection data, we determined that most hatchery reproduction occurred in areas specifically managed for hatchery-origin steelhead, whereas reproduction rates were substantially lower in areas managed strictly for wild populations. By utilizing this innovative genetic approach, the study substantially enhances multi-generational genetic monitoring capabilities, providing crucial insights into the impacts of hatchery practices. These advancements support adaptive management strategies and inform regulatory compliance efforts aimed at the conservation of ESA-listed Snake River Steelhead populations.

Campbell, Nathan; GTseek LLC; "Salmonid genome structure and implications for GT-seq marker selection"; *Tues, 5/13, 12:00 PM*

Genotyping-in-Thousands by sequencing (GT-seq) has become a cornerstone technique for genetic analysis in salmonid species due to its efficiency and scalability. In this presentation, I will illustrate an advancement to the GT-seq workflow: a self-normalizing PCR system we developed called *Nate's Plates* (gtseek.com/products), which streamlines amplicon tagging and normalization into a single step. Leveraging this improved method, we demonstrate how GT-seq can be adapted to produce high-resolution genotypes from short tandem repeats (STRs), enabling microsatellite-based studies via sequencing. I will also explore the evolutionary context of genome duplication in salmonids and offer strategies for selecting robust hyper-variable SNP, STR, and microhaplotype markers—key considerations for building effective GT-seq assays in salmon populations.

Cathcart, Nate; ADF&G; "Fish surveys, salmon population genetics, and eDNA detection in Bering Land Bridge National Preserve"; *Thurs, 5/15, 10:20 AM*

Coauthor(s): Duncan Green, ADF&G; Elizabeth Lee, ADF&G; Priscilla Lema, ADF&G; Tyler Dann, ADF&G; Joe Giefer ADF&G; Letty Hughes, NPS; Jenefer Bell, ADF&G

From 2021-2024, the National Park Service and the Alaska Department of Fish and Game performed a project in water bodies of Bering Land Bridge National Preserve with three objectives. First, we documented habitats supporting anadromous and resident freshwater fish species. This identified streams supporting anadromous species such as salmon and some whitefish species and then nominated to the Anadromous Waters Catalog (AWC), which protects habitats pursuant to the Anadromous Fish Act (AS 16.05.871). Second, we established salmon population genetic baselines in the Nuluk, Arctic, Serpentine, and Nugnugaluktuk rivers. Third, we sampled eDNA to detect fishes relative to our physical sampling catches as well as the AWC. We sampled fish via backpack electrofishing, raft electrofishing, gillnetting, seining, minnow trapping, aerial surveys and angling. We visited 96 sites and caught 20 species, 10 of which were anadromous species. We submitted 57 nominations to the AWC for all five species of Pacific salmon, Dolly Varden, pond smelt, rainbow smelt, Bering cisco, and humpback whitefish. AWC nominations included adding or extending 300 kilometers of habitat across 38 water bodies. We sampled 2,094 salmon for genetics, 96% of those samples were for chum and pink salmon. Chum, pink, and coho salmon samples were assigned to genetic reporting groups and filled in large spatial gaps in genetic baseline data coverage. Nine sites across five streams were sampled for eDNA, 17 species were detected and related to our sampling data and the AWC. Integrating fish surveys, genetic sampling, and eDNA detection showed how the Seward Peninsula's fish community distributes across the landscape and in fisheries, relative to statutory habitat protections.

Cheek, Rebecca; WDFW; "Scaling up: Harnessing the power of an updated regional baseline for broad scale genetic stock identification of Chum Salmon (*Oncorhynchus keta*)"; *Tues, 5/13, 2:20 PM*

Coauthor(s): Amelia Louden, WDFW; Maureen P. Small, WDFW (retired); Todd R. Seamons, WDFW

Genetic Stock Identification (GSI) is an important tool for fisheries management to alleviate harvest pressure on at risk stocks. However, identifying stocks of concern in a mixed-stock fishery requires a comprehensive genetic baseline to which samples may be assigned. Here, we compiled a large genetic baseline of 350 single nucleotide polymorphism (SNP) markers for 189 Chum salmon (*Oncorhynchus keta*) collections from across Puget Sound, Washington, Columbia River, Oregon, and Canada. We examined genetic diversity and used leave-one-out cross validation and mixture simulations to test the accuracy of the baseline in generating GSI mixture composition estimates. We found that population structure among Chum populations is primarily driven by run-timing and geography. We also demonstrate high assignment accuracy at both broad and regional scale reporting group levels. However, there are multiple groups that remain unresolved including Chum from the strait of Juan de Fuca, and Lower Columbia River that need additional samples to determine whether current collections are representative of these populations. Simulated mixtures showed effective GSI results for several common mixed-stock fisheries applications. This SNP baseline represents an important advancement in technologies available to managers and researchers of Chum salmon.

Commins, Mary*; University of Alaska Fairbanks; "Evaluating the second-generation effects of hatchery supplementation in Auke Lake sockeye salmon"; *Tues, 5/13, 10:20 AM*

Coauthor(s): Megan V. McPhee, UAF; David A. Tallmon, UAS; Scott C. Vulstek, NOAA; Peter A.H. Westley, UAF

Salmon hatcheries are widespread across the Pacific Rim, providing benefits such as economic gains and increased subsistence and recreational fishing opportunities. However, they are controversial due to risks posed towards wild fish populations, including genetic and phenotypic differences that can cause both inbreeding and outbreeding depression in wild populations. In order to better understand and mitigate the potential risks to wild populations, researchers conducted experimental hatchery supplementation of sockeye salmon in the Auke Lake Watershed in Juneau, Alaska, from 2011 to 2013, through a collaboration between NOAA Fisheries, UAF, and ADFG. Hatchery productivity was high in the first generation, but concerns remain for relative reproductive success in the second generation, where hatchery-origin fish spawn naturally. Additionally, differences in age were observed between offspring of hatchery and wild fish in the first generation, which may influence overall population dynamics. We analyzed the second-generation impacts of this supplementation on the natural population by utilizing a genetic pedigree to explore two objectives. Our first objective was to assess the relative reproductive success of hatchery-origin, wild-origin, and mixed-origin (hatchery-wild) fish in the second generation and the second objective compares the ages of offspring across these groups. Preliminary results show minimal variation in reproductive success and age among the groups, which is encouraging, but concerns about potential impacts on effective population size and genetic diversity in the wild population persist. Results from this study may help inform supplementation programs, including the Transboundary Sockeye Salmon program.

Dann, Tyler; ADF&G; "GSI of South Alaska Peninsula Chum Salmon Harvests: genetic tools inform management of fisheries that connect stakeholders amid conservation crises"; *Wed, 5/14, 9:10 AM*

Coauthor(s): Birch Foster, ADF&G

Commercial seine and gillnet harvests along the South Alaska Peninsula, a fishery known as Area M, target valuable sockeye salmon (*Oncorhynchus nerka*) but incidentally harvest chum salmon (*O. keta*). The fishery has been contentious for decades due to the interception of salmon bound for other regions and has increasingly been scrutinized by Western Alaska user groups and other stakeholders following Chinook (*O. tshawytscha*) and chum salmon crashes and fishery closures in Western Alaska in recent years. The Gene Conservation Laboratory was tasked with analyzing harvests to inform the public regulatory body responsible for defining management plans implemented by the Alaska Department of Fish and Game. We present an example of the role of genetics in a fishery that connects disparate stakeholders in a key salmonid migratory mixing zone of the North Pacific. Results from 2022 were markedly different from a similar study conducted in 2007-2009, indicating changes in relative productivity between Asian and Western Alaskan chum stocks, and played a central role in shaping commercial fisheries policy. Analyses with an updated coastwide baseline provide insight into stock-specific harvests.

Doran, Paul; Twist Biosciences; "Twist's FlexPrepTM: Accelerating the Transition from Microarrays to Next-Generation Sequencing in Agrogenomic Application"; Wed, 5/14, 2:20 PM

As sequencing costs continue to drop dramatically, sequencing-based genotyping approaches are in the process of replacing microarrays. This shift to sequencing is driven by better data, lower cost, and the capability to run a single platform for both discovery and genotyping. Twist recently launched FlexPrepTM: a HTP, self normalizing, high diversity library prep that is speeding up this ongoing transition.

Here we present examples from 1) Hudsonalpha's full service KHUFU genotyping & breeding platform where they are now leveraging FlexPrepTM to generate high quality data from peanut, cannabis, pumpkin, microbiome soil and many other samples. With KHUFU, you can identify the known and de novo markers at a fraction of the cost; 2) a cow-calf operation that has made the switch working in collaboration with Curio Genomics and Twist Bioscience. Using CURIO, we evaluate the concordance of results from arrays and targeted sequencing in the same animals, enabling the switch.

This streamlining of lab processes has profound implications for breeding program efficiency, genetic gain, and the precision of agrigenonic practices.

Estrada, Jodi; ADF&G; "Non-destructive high-throughput DNA extractions from Pink Salmon otoliths"; *Thurs, 5/15, 11:20 AM*

Coauthor(s): Kyle Shedd, ADF&G

We developed a novel method to extract DNA from more than 10,000 otoliths from hatchery- and wild-origin Pink Salmon collected in Prince William Sound, Alaska. A crack team of GCL staff worked for over a year to develop a high-production method of removing potentially contaminating DNA from the otoliths, yet maintaining the small amount of existing source DNA. Not only were we able to extract high-quality DNA from these otoliths suitable for genotyping using GT-seq, we simultaneously retained enough of the otolith structure to allow determination of origin. The otoliths of hatchery Pink Salmon in the state of Alaska are thermally marked with alternating banding patterns specific to brood year and hatchery. In addition, Pink Salmon otoliths are very small, and retention of thermal mark presence/absence and readability, despite the presence of chemicals known to dissolve the aragonite (calcium carbonate) from which otoliths are constructed, is difficult. I will describe the journey to this project's success, with mention of what methods were tried and deemed ineffective, and lessons that we learned from the event.

Farrow, Zach; Standard BioTools; "Fast Answers for Fast Fish"; *Thurs, 5/15, 9:50 AM*

Real world examples for Standard BioTools IFCs in conservation, pathogen detection and other salmon related applications. Showcasing how the BioMark X9 and IFCs offer more data, quicker. Reducing long hours in the lab and decreasing turnaround time at critical times of the year.

Galland, Lanie; CRITFC; "Mobile DNA sequencing laboratory for real-time assessment of Columbia River basin fisheries: genotyping in a van down by the river"; *Thurs, 5/15, 11:00 AM*

Coauthor(s): Shawn Narum, CRITFC

Estimating the migration timing, stock-specific abundance, and ancestry proportions of native salmonids is essential for effective conservation and management in the Columbia River basin. Here, we present an innovative monitoring program intended to provide real-time genetic stock assessment of salmonids from priority fisheries during critical migration, spawning, and harvest periods. We have worked to develop a mobile genetics laboratory where receipt of tissues, completed genotypes, and final parentage-based tagging (PBT) and genetic stock identification (GSI) analyses are intended to be completed within a 24-hour period, providing the most up-to-date genetic assignments for monitoring trends across stocks in the Columbia River and its tributaries. We aim to assess individuals from key migration and spawning sites by utilizing a mobile genetics laboratory. Designed in a custom trailer, the mobile lab will be fully equipped to process DNA samples from tissue collection through genotype, and distribute results to conservation managers. Further, the lab will have the potential to run entirely off grid, providing capacity at remote sites where energy, power, and network settings may be otherwise prohibitive. With the advent of the mobile genetics laboratory, this may facilitate real-time conservation and management of priority fisheries.

Gruenthal, Kristen; ADF&G; "Genomic signatures of natural and domestication selection in wild and hatchery pink salmon"; *Wed, 5/14, 1:40 PM*

Coauthor(s): William Hemstrom†, CSU; Kyle Shedd, ADF&G; Peter Euclide, Purdue University; Morgan Sparks, USDA; Chris Habicht, ADF&G (retired); Lorna Wilson, ADF&G; Mark R. Christie, Purdue University

Understanding the heritable bases for natural and domestication selection is key to managing and conserving wild populations and captively-reared populations that may interact with them. Pacific salmon (*Oncorhynchus spp.*) have outsized ecological, cultural, and economic roles, which can be positively enhanced or, at times, negatively impacted with supplemental propagation via hatcheries. Pink salmon (*O. gorbuscha*) present an uncommon opportunity to explore selection because selective regimes are replicated across wild and hatchery-origin stocks within two independent evolutionary lineages, and all stocks share the same natural environment for most of their lives. Using whole-genome resequencing of 794 fish, we present multiple lines of evidence for selection on gene regions underpinning functional adaptation in natural and artificial environments. First, we identify and characterize haplotypes present in both lineages in a leucine rich repeat containing gene (lrrc9), the frequencies of which vary substantially across wild and hatchery stocks and explain as much as 59% of variation in run timing in sampled pink salmon in Prince William Sound, Alaska. Additionally, we provide lineage- and hatchery- specific evidence for adaptation to artificial environments in genes that have been related to circadian rhythm (hlfb) and immune response (muc2). Our results indicate that response to selection in natural and artificial settings may be swift (allele frequency shifts in these genes occurred in fewer than 15 generations) and may mediate genetic interactions between wild and artificially propagated individuals.

Hargrove, John; PSMFC; "Temporal trends in hybridization between native and non-native salmonids in the Clearwater and Lochsa Rivers, Idaho"; *Tues, 5/13, 1:40 PM*

Coauthor(s): Matthew R. Campbell, IDFG; Joseph D. Thiessen, IDFG; Joseph M. Dupont, IDFG

Hybridization between native and introduced fish species poses a global threat to conservation. Understanding how hybridization dynamics change over time, and identifying factors driving these patterns can help inform management and conservation decisions. In this study, we assessed long-term trends in hybridization between Westslope Cutthroat Trout (*Oncorhynchus lewisi*) and Rainbow Trout (*O. mykiss*) in the North Fork Clearwater and Lochsa rivers in Idaho. We revisited historical sampling sites and utilized a single nucleotide polymorphism (SNP) panel to evaluate changes in the extent of interspecific hybridization over time. Additionally, we tested whether observed introgression was driven by stocking of nonnative coastal Rainbow Trout or native steelhead. Across 59 sampling sites, the proportion of fish carrying Rainbow Trout alleles either decreased or remained stable at approximately 60% of sites. Evidence of ongoing hybridization, indicated by the presence of first-generation hybrids, was observed in 14% of the surveyed Westslope Cutthroat Trout populations. Introgression from coastal Rainbow Trout was absent in the Lochsa River and occurred infrequently at locations within the North Fork Clearwater River. Site-specific characteristics and their influence on observed hybridization levels are also discussed.

Harris, Audrey; PSMFC; "Clearing the hurdle: How arrival timing and size influence reproductive success in steelhead returning to Fish Creek, Idaho"; *Tues, 5/13, 9:30 AM*

Coauthor(s): Marika E. Dobos, IDFG; John S. Hargrove, PSMFC; Nolan R. Smith, IDFG; Timothy Copeland, IDFG; Matthew R. Campbell, IDFG

Steelhead (*Oncorhynchus mykiss)* exhibit a wide array of life history strategies, including freshwater residency versus anadromy, reproductive strategy, age at maturity, and migration timing. However, the influence of life history on steelhead reproductive success remains poorly understood. Since 1994, the IDFG has used a weir to capture wild steelhead in Fish Creek, a tributary to the Lochsa River. Annual adult abundance has been estimated since 1996, and genetic samples have been collected from all captured adults since 1997. We describe the genetic mating system of steelhead in Fish Creek across multiple generations (1997-2022, N = 3,094). Mating and reproductive success were quantified for individuals using dual- and single-parentage, which allowed us to explore the influence of arrival timing, body length, and sex on reproductive success across multiple generations using hurdle models. For fish of average size and arrival timing, reproductive success was similar between males and females. However, the influence of arrival timing and body size on reproductive success varied by sex. Earlier-arriving males produced more offspring, whereas later-arriving females exhibited higher reproductive success. Among successful females, larger body size was associated with greater reproductive success; in contrast, body size had little effect on offspring numbers in successful males. We also inferred significant reproductive contribution from resident males based on ratios of spawning anadromous adults and single-parent assignments. Our study integrates demographic and genetic data over multiple generations to quantify life history diversity, highlighting how diverse life history portfolios may confer resilience and buffer populations against environmental stochasticity.

Healy, Timothy; DFO; "Genomic estimates of climate change vulnerability in Sockeye Salmon"; *Wed, 5/14, 11:20 AM*

Coauthor(s): Braden J. Judson, DFO; Rose-Lynne F. Savage, DFO; Ellika M. Crichton, DFO; Anna Tigano DFO; Eric B. Rondeau, DFO; Kyle W. Wellband, DFO

Novel conditions associated with climate change pose a risk to Pacific salmon in Canada. The resilience of populations will be partially dependent on the capacity for adaptive responses in the face of these new stressors. Genomic tools provide insights into these responses by estimating both genetic diversity within populations in the present (i.e., heterozygosity or nucleotide diversity), and mismatches between putatively adaptive variation under current and future conditions (i.e., genomic offset). As a part of both the Genomic Adaptation and Resilience to Climate Change project and the Pacific Salmon Strategy Initiative, we have applied these approaches to estimate climate change impacts on Canadian Sockeye Salmon. Genome-wide genetic variation was assessed by low-coverage resequencing in approximately 700 individuals across ~90 populations. Heterozygosity estimates suggest standing genetic variation is highly variable among populations even within watersheds or regions. In comparison, genomic offsets suggest populations with inland spawning grounds, especially in the Fraser River watershed, may be particularly vulnerable to forecasted environmental change. Over 4,000 genomic regions were detected as outliers consistent with involvement in environmental adaptation in Sockeye Salmon, and variation in maximum temperature had substantial impacts on genomic offset estimates. Taken together, these results inform the relative climate change vulnerability among Sockeye Salmon populations in Canada, and highlight distinct genetic aspects contributing to climate change risk. Ongoing work will incorporate these data into holistic climate change vulnerability assessments for the species.

Hess, Jon; CRITFC; "Genetic identification of lamprey genera and anadromous ecotypes in watersheds of the Northeastern Pacific Ocean"; *Wed, 5/14, 9:30 AM*

Coauthor(s): Greg S. Silver†, CRITFC; Ralph T. Lampman, CRITFC; Niva Percival, CRITFC; Nataliya Timoshevskaya, CRITFC; Jeramiah J. Smith, CRITFC; Kale T. Bentley, CRITFC; Joy Wade, CRITFC; Shawn R. Narum, CRITFC

Non-parasitic, non-migratory Western Brook Lamprey (WBL; *Lampetra ayresii*) and parasitic, anadromous Western River Lamprey (WRL; *L. ayresii*) are sympatric lampreys representing different life history variations of the same species. Novel genetic tools are crucial for distinguishing between WBL and WRL, as their larvae are morphologically identical. These tools enable the assessment of imperiled native lampreys of the Northeastern Pacific, including WBL, WRL, and Pacific Lamprey (*Entosphenus tridentatus*). Using whole genome resequencing, 47 candidate single nucleotide polymorphism (SNP) markers were developed from WBL (N=24) and WRL (N=15) from Ksi Ts'oohl Ts'ap Creek (Nass River, British Columbia, Canada). These ecotypes are likely distinguished by a few divergent SNPs across multiple chromosomes. Five novel candidate SNPs were used for genetic ID of WBL and WRL ecotypes in mixed lamprey collections from lower Columbia River tributaries (N=1,474), Ksi Ts'oohl Ts'ap Creek (N=352), and ocean-phase WRL from the Georgia Basin (Salish Sea, British Columbia, Canada; N=91). Two previously published SNPs were used to identify genera (*Entosphenus* vs. *Lampetra*). Morphological ID, utilizing photographs from genotyped lampreys, showed high concordance between ID methods for genera (99%) and *Lampetra* ecotypes (>98%). Spatial and temporal compositions of lamprey genera and ecotypes were characterized across NE Pacific tributaries. While lamprey genera proportions varied within regions and across years, *Lampetra* ecotypic proportions were stable. WRL were rare in lower Columbia tributaries (~1% of *Lampetra*) but common further north (>40% of *Lampetra*). Genetic ID methods are powerful monitoring tools, efficiently identifying genera and ecotypes regardless of life stage and biometrics.

Hillstrand, Nancy; Pioneer Alaskan Fisheries; "What are acceptable hatchery stray proportions in Alaska's anadromous waters?"; *Thurs, 5/15, 9:30 AM*

When monitoring in Alaska's river systems and mixed stock fisheries, hatchery straying is often found in proportions above 50% up to 100%. Inter-regional straying from 250 miles away from PWS has consistently been documented in variable proportions to occur in significant pink salmon stocks of Lower Cook Inlet salmon streams for over a decade. Recent adult chum salmon returns from remote hatchery releases in the Northern Southeast Outer NSEO District of Southeast Alaska has resulted in massive straying up to 100% in escapement goal index streams and was a control in the Alaska Hatchery Research Program where stray rates were below 3% before these releases. The stock status in these systems, are now listed as management stocks of concern with an action plan that has initiated a Performance Review. State Performance Reviews have never been initiated before. Chinook salmon have been documented to stray from the Homer Spit up to Ship Creek in Anchorage. The genetics policy does not condone inter-regional straying. Straying at very high levels is counterintuitive for healthy sustainable salmon populations yet has been allowed to continue without solution. Monitoring is minimal so the extent of these events is unknown. The NSEO has now skewed the results of the Alaska Hatchery Research Program where remote releases have now been documented to accelerate straying from 3% to 100% in one year. The Board of Fisheries has requested an acceptable stray rate metric that is safe and sustainable. This aligns with the Wild Fish Priority statute AS 16.05.730. SEAKs Regional planning Team's April meeting also asked for acceptable genetic straying metrics. What modeling is required to protect wild fish of Alaska, to create a species specific stray rate % that removes risk of adverse effects to wild fish, jeopardized by hatchery genetic straying.?

Horn, Rebekah; CRITFC; "Genomic insights into local adaptation and migration success in reintroduced Coho salmon of the Wenatchee River Basin"; *Thurs, 5/15, 8:30 AM*

Coauthor(s): Jeff Caisman, Yakama Nation Fisheries; Cory Kamphaus, Yakama Nation Fisheries; Shawn R. Narum, CRIFTC

Reintroduction of salmonids to regions where they have been extirpated is a common conservation strategy, often implemented through natural recolonization, translocation of natural populations, or hatchery-based programs. Locally adapting to specific environmental conditions is critical for long-term population viability, particularly for species like Coho salmon, which face diverse selective pressures during their migration. This study focuses on the Mid-Columbia River Coho salmon reintroduction program, managed by the Yakama Nation Fisheries, which has successfully reintroduced Coho salmon to the Wenatchee and Methow river basins. Notably, these populations have adapted to the longer migration route than those in the founding stock, with selection favoring individuals that can navigate a challenging 15 km high-gradient canyon to reach optimal spawning grounds. The objectives of this study were to investigate whether specific genomic regions are under selection for traits associated with return location and timing in Coho salmon. A weak, polygenic signal in female Coho salmon was found to be linked to return location with a subset of candidate adaptive regions across eight chromosomes. Genomic variation among broodlines was also detected that could impact interannual migration timing and successful navigation to upriver spawning habitat. These findings provide insights into the genomic mechanisms underlying local adaptation in reintroduced salmon populations and inform broodstock selection strategies aimed at promoting natural production and long-term population sustainability.

Howe, Natasha; PSMFC; "Age at maturity in sockeye salmon has a strong genetic component found on both sex and autosomal chromosomes"; *Thurs, 5/15, 9:10 AM*

Coauthor(s): Patrick D. Barry, NOAA; Samuel W. Rosenbaum, University of Montana; Megan V. McPhee, UAF; Wesley A. Larson, NOAA

Pacific salmon display myriad life history traits that allow for diversification within and among species, and one of the most pronounced is age-at-maturity. Each salmon species has a different ensemble of freshwater and saltwater residence times that influence reproductive success and gene flow between age classes. One well-studied reproductive strategy is that of sneaker males, or jacks, that return to spawn after just one year in the ocean. Jacks use a sneaker strategy to spawn and often have relatively high reproductive success. While most populations have very low jacking rates, others can reach close to half of the male population. Previous research discovered that jacking is a heritable trait, but specific environmental effects also influence its prevalence. In Chinook salmon, genetic effects of age-at-maturity were associated with male-specific haplotypes. This suggests that this phenotype is a sex-linked trait, which is further supported by the rare occurrence of one-year ocean females that have much lower reproductive success than their male counterparts. In this study, we sequenced the whole genomes of individuals from three Alaskan sockeye salmon populations that have a high propensity for jacking, and jacks were compared to the older male age classes (normal males). We found a large genetic component to jacking that is present on both the sex chromosome and two autosomal chromosomes, with the genotype-phenotype association varying slightly by population. Interestingly, the chromosomal region near sdY does not show the same sex differentiation between females and jacks as it does for females and normal males, which may indicate a sexually antagonistic mechanism within the sex chromosome that influences jacking propensity.

Hoyt, Heather A.; ADF&G; "Three million and counting: Genetics Sample Archiving for the Alaska Department of Fish and Game"; *Thurs, 5/15, 11:40 AM*

Coauthor(s): Sara Gilk-Baumer, ADF&G

Alaska Department of Fish and Game's Gene Conservation Laboratory has maintained genetics tissue samples since the early 1990s. We have over 3 million samples in the archives with approximately 125,000 new samples added per year. Our archives include a multitude of managed species from various taxonomic groupings, including fish (primarily Pacific salmon but also herring, rockfish, and many others), invertebrates (crustaceans, shellfish), aquatic plants (primarily kelp), and wildlife (bears, ptarmigan, wolves, moose, etc.). Many changes have been implemented over the years, such as which tissues were sampled and retained and how tissues were stored from ethanol to scale envelopes to Whatman cards. We continue to struggle for space to store the samples, and as our archives continue to grow, space will become a premium. I will provide an overview of the archives, historical changes to management and methods, and share current successes and challenges.

Hsu, Bobby; ADF&G; "Using computer simulation to assess sample size for mixed stock analysis"; *Wed, 5/14, 8:30 AM*

Coauthor(s): Tyler Dann, ADF&G

It is easy to conflate different sources of errors in Mixed-stock analysis (MSA) due to the complicated nature of sampling design for mixed-stock fisheries. A MSA consists of two main components: obtaining a sample that represents the mixed-stock fisheries (i.e., mixture) and identifying the stock composition of the mixture. Each MSA component has its associated error. A sampling error occurs if only certain portions of the mixed-stock fisheries are included in the mixture. A measurement (or observational) error occurs if a mixture individual is allocated to the wrong population during stock identification. Traditionally, Alaska Department of Fish & Game determines MSA sample size based on multinomial variance. The sample size is often overestimated because determination is based on the worst scenario. However, in recent years, an abundant sample size has become difficult to obtain for some fisheries due to dwindling numbers in escapement and harvests. Therefore, we developed a cross-validation analysis that can be customized to meet the specific needs and determine appropriate sample sizes of a MSA program. Our study is motivated by Alaskan fishery programs, but the results from this study can inform MSA programs elsewhere.

Jalbert, Chase; ADF&G; "Alaska's Other Potential Eruption: Illuminating Fish Stocks with MAGMA"; *Wed, 5/14, 8:10 AM*

Accurate fishery stock assessments often require detailed age-by-stock composition estimates. We describe MAGMA, a Bayesian genetic stock identification model that builds upon the Pella-Masuda framework. MAGMA uniquely integrates genetic data with matched biological information (age and hatchery/wild origin) to enhance resolution in stock composition analyses. The model estimates two primary parameter sets: stratum-specific population proportions (including hatchery groups) and annual age proportions across populations. These are combined to generate detailed age-by-stock compositions for each stratum, which serve as critical inputs for run reconstruction models and stock-specific management decisions. MAGMA employs a Markov Chain Monte Carlo algorithm to estimate parameters and accommodates individuals with incomplete genotype or age data by assigning probabilistic memberships. This flexible framework supports robust estimation under a wide range of sampling and data quality conditions. By summarizing results into point estimates and credible intervals, MAGMA provides fisheries managers with interpretable, actionable information to evaluate mixed-stock harvests, assess hatchery contributions, and support sustainable harvest and conservation strategies.

King, Erika; ADF&G; "Updated status of Southeast Alaska coho salmon genetic baseline"; *Tues, 5/13, 4:10 PM*

Coauthor(s): Kyle Shedd, ADF&G; Matt Catterson, ADF&G; Chase Jalbert, ADF&G; Justin Priest, ADF&G; Andy Piston, ADF&G; Steve Heinl, ADF&G (retired)

Effective use of genetic stock identification (GSI) requires a baseline that adequately represents contributing populations and their structure. We present recent efforts to improve the Southeast Alaska (SEAK) coho salmon baseline, which lacked widespread coverage of spawning populations that contribute to fisheries. Over 10,000 fish from 145 collections across SEAK were genotyped using GT-seq for 350 SNP markers developed by the Washington Department of Fish and Wildlife in collaboration with Fisheries and Oceans Canada. After pooling collections and filtering SNPs, the current baseline includes 115 populations and 308 SNPs. Baseline evaluation tests showed that broad geographic regions within SEAK meet ADF&G standards for reporting group accuracy and precision. We observed genetic structure among populations based on run timing and geographic proximity, and shallow year-class structure within some streams as demonstrated by significant differences in allele frequencies among temporal collections. Future work will include collecting and genotyping additional samples to ensure the baseline reflects the production, geographic distribution, run timing, and life history diversity of coho salmon in SEAK. The long-term goal is to integrate the SEAK baseline with the existing baselines from Canada and Washington to improve understanding of genetic stock structure and support management in Pacific Salmon Treaty fisheries.

Klegarth, Amy; Element Biosciences; "Shift Your Science"; *Wed, 5/14, 12:00 PM*

Element Biosciences technologies have made genomics research more accessible through their scalable benchtop platform, AVITI and low-cost sequencing chemistry. Learn how the latest innovations to avidite base chemistry (ABC) make AVITI even more powerful and more flexible. The AVITI consistently produces some of the highest accuracy sequencing data in the industry. Exceptionally high accuracy, flexible scaling, compatibility across existing workflows, and affordable pricing enables labs to transition technologies with ease and allows room for growth. We will also discuss the new Trinity workflow, where we show how time-consuming and burdensome steps of the hyb-capture workflow have been automated onto the AVITI platform to increase efficiency and consistency. WGS libraries can also be spiked into Trinity runs to simultaneously collect low-pass WGS for population monitoring or breeding programs.

Larson, Wes; Salmon Enthusiast; "Understanding the genetic basis of run timing diversity in four species of Pacific salmon"; *Wed, 5/14, 1:20 PM*

Coauthor(s): Patrick Barry, NOAA; Natasha Howe, PSMFC; Gregory Owens, University of Victoria; Diana Baetscher, NOAA; Katie D'Amelio, NOAA; Scott Vulstek, NOAA; Josh Russell, NOAA; Elizabeth Lee, ADF&G; Tony Gharrett, UAF (emeritus); Dave Tallmon, UAS

Migration is an important component of the life cycles of many organisms and differences in migration timing can greatly influence fitness. Variation in migration timing (hereafter referred to as run timing) is found in many salmon species and contributes to the portfolio of life history diversity that is vital for maintaining healthy populations. Large effect loci that strongly influence run timing have been discovered in Chinook salmon and steelhead and these loci have been a major focus of research and conservation efforts over the last decade. However, the genetic basis of run timing variation has not been investigated in other Pacific salmon. Here, we use a combination of whole genome sequencing and targeted amplicon sequencing to identify loci associated with run timing variation in sockeye, pink, chum, and coho salmon. We find that two small genomic regions on homoeologous chromosomes that arose after an ancient whole genome duplication are strongly associated with run timing across the four species. The genes most closely associated with these regions are the Leucine Rich Repeat Containing 9 (LRRC9) gene and the Estrogen Receptor Beta (ESRB) gene. The LRRC9 region is associated with run timing in sockeye, chum, and pink salmon, and the ESRB region is associated with run timing in chum and coho salmon. Notably, the Six6 gene, which is associated with age-at-maturity in steelhead and Atlantic salmon, is also found near the regions we identified. Our results suggest that the two duplicated versions of this region are highly associated with variation at multiple phenotypes in salmon. We hypothesize that this may be a master regulatory region that influences gene expression at many genes involved in multiple physiological pathways.

Lee, Elizabeth; ADF&G; "Genetic Stock Identification from Gravel to Gravel: Use of Genetic Tools in Forecasting and Monitoring Yukon River Chinook Salmon Runs"; *Wed, 5/14, 8:50 AM*

Coauthor(s): Tyler Dann, ADF&G

Chinook salmon (*Oncorhynchus tshawytscha*) returns have decreased in the Yukon River within the last decade, creating economic, food security, and cultural preservation issues for fishing communities throughout the region. In addition to the societal challenges this poses to communities along the Yukon River, these declines present challenges to fishery managers, biologists, and other stakeholders. With low returns, it is important to minimize uncertainties around estimates of stock-specific harvest, escapement, run reconstruction, and forecasts of future returns used in management decisions. Genetic stock identification is an effective method for studying stock-specific trends across the salmon lifecycle, including marine-stage salmon maturing in the Bering Sea and adult salmon returning to tributaries of the Yukon River. Here, we present the utility of an updated genetic baseline for fisheries management and research projects that encompass the full lifecycle of Yukon River Chinook salmon. Genetic tools have proved to be an important component of efforts to forecast, monitor, and understand declines in Yukon River Chinook salmon runs in recent years.

Luzzio, Alana*; UC Davis Genomic Variation Lab; "Using parentage-based tagging to identify natal origins of Chinook salmon (*Oncorhynchus tshawytscha*) returning to a restored creek"; *Tues, 5/13, 11:20 AM*

Coauthor(s): Andrea Schreier, UCD; Mac Campbell, UCD; Nann A. Fangue, UCD; Dennis E. Cocherell, UCD; Anne Boyd, UCD; Alexandra Wampler, UCD; Andrew Rypel, UCD

Climate change and anthropogenic impacts are leading to species decline, resulting in loss of biodiversity and degraded ecosystems. California is the only location where all four different run types of Chinook salmon co-occur, however, all four are listed under the Endangered Species Act. Restoration of habitat is one of the most effective ways to address ecosystem degradation. Putah Creek, a stream in the Central Valley, has undergone 25 years of restoration resulting in reestablished perennial flows and native fish diversity. Recently, Chinook salmon have been observed spawning in Putah Creek. Previous research using otolith microchemistry found returning salmon are mostly hatchery origin with at least 11 individuals of Putah Creek origin. However, exact contributions of Putah Creek origin fish to the subsequent generations remains unknown. I will use the genetic method of parentage-based tagging (PBT) via a validated SNP panel to 1) elucidate the natal origin of Chinook salmon spawning in Putah Creek; and 2) explore factors influencing individual reproductive success. I first developed a novel parentage-based tagging genotyping assay to create a pedigree of the previous seven years of tissue collected from the creek, then I analyzed the constructed pedigree to understand the natal origins of the Chinook salmon in Putah Creek. Finally, I will analyze population dynamics by assessing reproductive success. Salmon are declining throughout California, however, confirmation of a new spawning run, initiated by hatchery strays, is interesting and may be a model for recovering Chinook salmon in other previously degraded and rehabilitated ecosystems. Further, this work provides a key demonstration of PBT towards Chinook salmon management in California streams.

Narum, Shawn; CRITFC; "Conservation of Neutral and Adaptive Genomic Variation in Anadromous Fishes of the Columbia River"; *Wed, 5/14, 11:40 AM*

Overall genomic variation is necessary to maintain in naturally occurring species for long-term persistence, especially in disturbed ecosystems. Genetic monitoring is ongoing for multiple anadromous species in the Columbia River to ensure variation is maintained across the genome, along with variation associated with critical life history diversity. Examples of genetic monitoring for both neutral and adaptive genetic variation will be presented in multiple species, and here I will focus on the importance of adaptive genomic variation that maintains life history types. Genes of major effect have been identified for critical life history traits in multiple species, and development of markers from these candidate genes has enabled monitoring of phenotypic and genetic variation in natural populations or hatchery-reared stocks. This is a promising approach to maintain a broad portfolio of phenotypic diversity that can buffer against changing environments and enable species persistence in disturbed ecosystems.

Phelps, Michael; Washington State University; "Tracking invasive and threatened salmonid species using real-time and automated systems"; *Thurs, 5/15, 10:40 AM*

Coauthor(s): Tholen Blasko†, WDFW; Evan Barnes, WSU; Shubhankar Sircar, WSU; Tyler Boies, WSU

Salmon resource management can benefit from reducing the time from sample collection to obtaining genetic information. This is especially important for invasive species management, which may require rapid identification and removal of individuals from a system. To facilitate the streamside identification of salmonid species, we have developed a range of technologies to empower field biologists with molecular tools to aid in combating invasive species or identifying systems with threatened stocks. These technologies combine rapid CRISPR detection technology with mechanical and electrical engineering devices to enable real-time genetic analysis of environmental DNA (eDNA) or tissue samples. We have employed these tools for eDNA tracking of Chinook salmon (*Oncorhynchus tshawytscha*) as well as the interaction between native Cutthroat trout (*O. clarkii*) and invasive brook trout (*Salvelinus fontinalis*). Current efforts are also using these technologies to examine bull trout (*Salvelinus confluentus*) and brook trout hybridization zones in Eastern Oregon and Idaho. Future research efforts are focused on expanding the methods to automated eDNA sampling devices that can remotely analyze water samples at preset intervals for unmanned monitoring of target species. These approaches seek to expand the capabilities of resource managers to enhance salmonid conservation efforts in the Pacific Northwest.

Robinson, Zachary; CRITFC; "Estimating Chinook Salmon Escapement Using Transgenerational Mark-Recapture (tgMR) in the Presence of Precocial Parr"; *Tues, 5/13, 10:40 AM*

Coauthor(s): Aidan Rigdon, CRITFC; Casey Baldwin, CRITFC; Shawn R. Narum, CRITFC

Accurate estimates of annual escapement are critical for the management of anadromous salmonids but are often challenging to obtain. Transgenerational mark-recapture (tgMR) is a promising approach for estimating escapement and calibrating index-based methods using genetic data. While tgMR is analogous to the traditional two-sample mark-recapture method (tradMR), it differs in that adult returns are marked through genotyping and then the proportion of marked and unmarked fish is estimated through genetic parentage assignment of their offspring. This parent-and-progeny sampling framework aligns with common sampling regimes (e.g., weirs and smolt traps) and can leverage existing genetic monitoring by providing annual escapement estimates using the same data used for mixed-stock and reproductive success analyses. In this study, we used known escapement data from a summer Chinook Salmon reintroduction program in the Sanpoil River, WA, to assess the accuracy of tgMR-based estimates. In the first year following reintroduction, tgMR estimates were concordant with known escapement. However, in subsequent years, estimates of adult escapement were inflated by up to 87.7% due to the putative presence of precocial male spawners. We identified a statistical correction for unsampled male spawners, resulting in highly accurate escapement estimates for the Sanpoil River. Our approach was further validated through simulations. While careful consideration of assumptions is critical, tgMR represents a powerful, and likely underutilized, method for estimating escapement and calibrating index-based methods in anadromous salmon populations.

Rondeau, Eric; DFO; "A SNP-based coastwide sockeye salmon baseline for genetic stock identification in British Columbia"; *Tues, 5/13, 3:10 PM*

Coauthor(s): Kim Jonsen, DFO; Carrie Gummer, DFO; Kelsey Dougan, DFO; Ashtin Duguid, DFO; Katherine Horst, DFO; Ben J.G. Sutherland, Sutherland Bioinformatics; William I. Atlas, WSC; Matthew Sloat, WSC; Scott Carlson, CRC; Kate A. McGivney, SFU; Jonathan W. Moore, SFU

Genetic stock identification (GSI) for sockeye salmon in British Columbia (BC) has been largely based on microsatellite genotyping for the past 30 years, which has provided a consistent method to evaluate mixed-stock proportions across a number of fisheries coastwide. However, increasing needs for improved resolution and support for more complex analyses including for conservation purposes have necessitated the transition to a more powerful toolset. To meet this need, a high throughput, 566 amplicon panel targeting single nucleotide polymorphisms (SNPs) for sockeye salmon has been developed for use on the IonTorrent platforms. To ensure compatibility and support international collaboration and standardization, a significant portion of SNPs in the panel were sourced from existing resources and panels currently in use. New markers, where added, have been designed to improve stock delineation specifically within the North and Central coast regions. The panel further incorporates markers for species and sex identification, as well as genomic regions that are associated with phenotypic effects. To put this panel into operation, baseline genotyping to cover all regions and populations that are anticipated to be encountered in fisheries resulted in approximately 24,000 individuals genotyped, representing 248 distinct spawning locations. Validation of the panel generally supports improved mixed-stock assignment accuracy over the microsatellite panel, although the most notable improvements are in individual assignment accuracy to conservation units (CUs) when baseline representation is sufficient. The SNP panel and baseline will replace the existing microsatellite baseline, and improve GSI accuracy, and enable parentage-based tagging (PBT) in coastal BC applications.

Rosenbaum, Samuel*; University of Montana; "Chromosome-level reference genome for male brook trout (*Salvelinus fontinalis*) from a long-term genetic rescue study"; *Wed, 5/14, 11:00 AM*

Coauthor(s): Devon E. Pearse, NOAA; Jeffrey M. Good, University of Montana; Samuel A. May, USDA; Andrew R. Whiteley, University of Montana

Reference genomes are advancing exploration of natural populations; however, few species possess multiple assemblies that capture the breadth of diversity distributed across their ranges. Furthermore, many references are assembled using homogametic specimens. Thus, decreased mapping success of resequenced samples, known as reference bias, is expected to obscure analysis of sex-linked regions and phylogeographically divergent specimens to an unknown extent when using assemblies from homogametic or evolutionarily distinct individuals. Generation of local reference genomes should advance region- and sex-specific discovery by mitigating reference bias. Brook trout are a salmonid native to North America that express locally adapted traits across their range, leading to opportunities for genetic variants to shift in frequency via neutral and adaptive processes. Until now, only a single, homogametic genome for brook trout has been developed from the northernmost extent of the species range. While this assembly can accurately anchor sequences from populations within close geographic and phylogenetic distances, reference bias may skew findings when studying less proximate or genetically diverged populations.

Here, we present the first heterogametic brook trout reference genome from the south-central portion of the species range. Notably, we are using a wild male specimen to ensure characterization of both sex chromosomes. To generate a nearly gapless assembly we are integrating HiFi, Omni-C, and ultra-long ONT data. Our reference genome will enable comparative and pangenomic analyses within and across salmonids, serving as a novel resource to improve characterization of structural variation and fitness-linked traits among brook trout populations and sexes across North America.

Seamons, Todd; WDFW; "Genetic discovery and description of a Nisqually River Chinook salmon population"; *Tues, 5/13, 1:20 PM*

Coauthor(s): Adrian Spidle, NWIFC; Seth Smith, WDFW; Garrett McKinney, WDFW; Matt Klungle, WDFW; Gabe Madel, WDFW; Adam Lindquist, WDFW; Riley Freeman, WDFW; Joseph Anderson, WDFW; Jim Scott, WDFW; Christopher Ellings, Nisqually Tribe; Sayre Hodgson, Nisqually Tribe; Craig Smith, Nisqually Tribe; Jedidiah Moore, Nisqually Tribe; G. Blair, Nisqually Tribe; David Troutt, Nisqually Tribe

The Nisqually River was once known to have spring and fall Chinook salmon populations. Chinook salmon were believed to have been extirpated after years of abuses of the habitat. Native Chinook salmon were replaced with a hatchery program using fall run Chinook salmon from the nearby Green River. All management and recovery efforts at this point were based on the understanding that any natural-origin Nisqually Chinook salmon were naturalized Green River origin salmon. Recent genetic analysis of Nisqually River Chinook salmon revealed what appears to be two separate populations. The first is genetically indistinguishable from the introduced Green River ancestry Chinook salmon currently spawning naturally and propagated in two tribal hatcheries. The second is clearly different from the Green River ancestry population, but its origins and relationships to extant Puget Sound and other range-wide Chinook salmon populations are unknown. I report on our efforts to genetically evaluate this second population, which we currently refer to as Local Nisqually Chinook salmon. Specifically, we evaluated genetic relationships with extant Chinook salmon populations across their range and within Puget Sound, providing insight into its origin, and evaluated genetic diversity of the population compared to other Washington populations, providing insight into the demographic history of the population. Population surveys, expanded since this discovery, have found Chinook salmon, likely the local Nisqually population, spawning in unexpected times and places in the Nisqually River.

Setzke, Christopher*; University of Washington; "Mechanisms of specialist-generalist tradeoffs for IHNV in salmonids"; *Wed, 5/14, 10:20 AM*

Coauthor(s): David Páez, USGS; Gael Kurath, USGS; Kerry Naish, UW

Viruses evolve specialist and generalist infection strategies, which have associated fitness tradeoffs. Evidence for specialist-generalist tradeoffs using viral replication as a measure of fitness has been demonstrated in Infectious Hematopoietic Necrosis Virus (IHNV)-salmonid systems. However, little is known about the extent to which specialist-generalist tradeoffs are mediated by host responses. Here, we use host transcriptomic data from Sockeye Salmon following exposure to viruses in specialist, generalist, or non-specialist subgroups of IHNV to quantify and characterize mechanisms of host response to different viral strategies. These responses were measured through RNA sequencing in entry (fin) and target (kidney) tissues of 93 Sockeye juveniles exposed to viruses in three IHNV subgroups at three different time points following exposure. We found minimal host response at any time or tissue resulting from exposure to the non-specialist virus. This result, coupled with little observed viral replication, suggests that non-specialist viruses may have difficulty entering and replicating within the host. In contrast, host responses were observed following exposure to generalist and specialist viruses. Early response in the kidney to the generalist, but not the specialist virus suggests that early host evasion may be a mechanism of increased fitness in specialized hosts. In addition, delayed response of pattern receptor recognition pathways to the generalist virus compared to the specialist may be explained by early host suppression of viral replication. These results may inform how the evolution of specialism and generalism in IHNV is mediated by host responses, which may play a role in determining the replicative tradeoffs observed in the different subgroups.

Shedd, Kyle; ADF&G; "A range-wide genetic baseline for Chinook salmon improves resolution for stock identification in Alaska and northern Canada"; *Tues, 5/13, 3:50 PM*

Coauthor(s): Andrew W. Barclay†, ADF&G; Natasha Howe, PSMFC; Pat Barry, NOAA; Elizabeth Lee, ADF&G; Tyler Dann, ADF&G; Eric Rondeau, DFO; Jon Hess, CRITFC; Sara Gilk-Baumer, ADF&G; Wes Larson, NOAA

Genetic stock identification (GSI) requires a comprehensive baseline of spawning populations genotyped with markers capable of reliably differentiating stocks (reporting groups). Over time, baseline development has advanced from allozymes to microsatellites, and more recently to panels with hundreds of single nucleotide polymorphisms (SNPs) and/or microhaplotypes. Building coastwide baselines that span the full range of Chinook salmon (*O. tshawytscha*) is challenging due to the extensive range and intermixing of populations, especially in feeding areas like Alaska, but remains critical for effective management. We present a multi-stage GSI approach that leverages existing SNP data based on the CRITFC-IDFG Chinook GT-seq v3.0 299-SNP panel. This framework combines a coastwide baseline (508 populations, 81 SNPs) with an Alaska-specific baseline (258 populations, 245 SNPs). The coastwide baseline unites GSI baselines from Alaska (ADF&G/NOAA), Canada (DFO), and the Columbia River (CRITFC). Together, these baselines and the multi-stage GSI approach enable the resolution of up to 82 fine-scale reporting groups, providing the precision needed for managing Alaska's mixed-stock fisheries. This new framework replaces previous baselines, including the 13-microsatellite, 357-population GAPS baseline for Southeast Alaska Chinook fisheries managed under the Pacific Salmon Treaty, and the 37-SNP, 172-population baseline used for Chinook bycatch monitoring in Gulf of Alaska and Bering Sea/Aleutian Islands federal groundfish fisheries.

Spidle, Adrian; Northwest Indian Fisheries Commission; "Rescue program for South Fork Nooksack Spring Chinook salmon"; *Tues, 5/13, 2:00 PM*

Coauthor(s): Todd Seamons, WDFW; Tom Chance, Lummi Nation; Ned Currence, Nooksack Indian Tribe

South Fork Nooksack spring Chinook salmon are required to recover for the Puget Sound ESU, listed as threatened under the US ESA, to be delisted. ~20,000 juvenile Chinook salmon were collected from 2007-2012. Genetic stock id verified approximately 4,000 were from the SF spring population targeted. Captive-reared fish were spawned from 2010-2017, with crosses chosen according to relatedness. Anadromous progeny of program fish were incorporated to the program beginning in 2014. In 2016 the first complete cohort of anadromous progeny had returned (ages 2-5 year olds). Since 2018 the program has been run exclusively with anadromous returns. The program has succeeded in greatly increasing abundance of SF Nooksack Chinook salmon in the river. Ne estimated by the method of temporal variance in allele frequencies increased 180% over the point between the baseline collections and the 1st anadromous cohort, and 380% between the captive-reared juveniles and their 1st anadromous cohort, indicating genetic diversity taken into the program was maintained through the point of anadromous returns. Production of hatchery returns remains stable while production of natural-origin fish continues to increase. Before the program began, approximately 10% of adult Chinook salmon in the South Fork Nooksack matched the South Fork spring Chinook genetic baseline, and in the present day over 95% of Chinook salmon in the South-Fork match the genetic baseline.

Tigano, Anna; DFO; "Fine-scale population genomics of chum from the southern Canada/USA border based on whole genome data"; *Wed, 5/14, 2:00 PM*

Coauthor(s): Kayla Long, DFO; Timothy M. Healy, DFO; Kyle W. Wellband, DFO; Eric B. Rondeau, DFO

Chum salmon is one of the Pacific salmon with the widest pan-Pacific distribution and is an ecologically and economically important species throughout their range. Despite the considerable efforts put in place for the management of their fishery in Canada, assessment of population structure and stock delineation are based on just a few hundred genetic markers. These in turn support the presence of a few large conservation units, grouping several spawning aggregates connected through straying. Whole genome data could help characterize finer population structure, identify SNPs for higher Genetic Stock Identification (GSI) resolution, and address a wealth of questions related to population differentiation and adaptation and genetic health. We started by focusing on a few geographic areas between the southern Canada/USA border and sequenced the whole genomes of >900 individuals from 45 collections from Puget Sound, the Fraser River, and the Strait of Georgia. As anticipated, we found strong differentiation between these three areas, but much weaker differentiation within each area. However, within sub-areas, we identified SNPs able to differentiate key management areas including 1) from the Chilliwack River versus the rest of the Fraser River, and 2) from east versus west Strait of Georgia. Within the Strait of Georgia we also identified a block of strong inter-individual differentiation that include LRRC9 and other genes that are often associated with spawning behaviour in other Pacific salmon; however, no clear phenotype can be associated to the sporadic pattern observed to date in chum. Our analyses will help increase GSI resolution in chum and understand the evolution and maintenance of a differentiated genomic area shared by many salmonids.

Wellband, Kyle; DFO; "Shared patterns of DNA Methylation variation in hatchery-origin Coho Salmon and implications for developing molecular monitoring tools"; *Wed, 5/14, 10:40 AM*

Coauthor(s): Dionne Sakhrani, DFO; Yukiko Graham, DFO; Carlo Biagi, DFO; Eric Rondeau, DFO; Timothy Healy, DFO

Salmon released from hatcheries to support fisheries and conservation objectives often differ from those originating in natural environments. In particular, hatchery-origin fish often have reduced reproductive output compared to natural-origin salmon. Enhancement of Pacific salmon in Canada is managed to minimize genetic differences from developing between hatchery and natural origin fish and thus differences are likely to represent plastic responses to the hatchery environment. Previous research has suggested that epigenetic variation in the form of DNA methylation may contribute to observed differences between hatchery and natural-origin fish. If hatchery-associated DNA methylation patterns are sufficiently conserved, they may be useful for the development of molecular tools that could be used to identify hatchery-origin fish and in the monitoring and management of hatchery rearing practices. We compiled existing and new whole genome methylation data for three enhanced Coho Salmon stocks in BC. We evaluated the strength of hatchery rearing signals in two tissues of adult fish as well as compare and contrast shared patterns of DNA methylation differences between systems. We discuss the feasibility of developing DNA methylation-based molecular tools for application to salmon hatchery management.

Willis, Stuart; CRITFC; "Heritability and genomic basis of age-at-maturity in Chinook Salmon"; *Thurs, 5/15, 8:50 AM*

Coauthor(s): Rebekah L. Horn, CRITFC; Jon E. Hess, CRITFC; Jeffrey K. Fryer, CRITFC; John M. Whiteaker, CRITFC; and Shawn R. Narum, CRITFC

Intra-population variation in the age at return and reproduction of Chinook Salmon (*Oncorhynchus tshawytscha*), or age-at-maturity, acts as a buffer against stochastic environmental variation. We investigated the genetic component of this trait by estimating heritability of age-at-maturity and the genomic basis of both sex and age-at-maturity in stocks representing the three major lineages of the Columbia River Basin. We found that heritability of age-at-maturity was generally stronger for fathers with male offspring (mean h^2 = 0.37, SD = 0.164) than mothers with female offspring or opposite sex offspring (mean h^2 = 0.25-0.29, SD = 0.077 – 0.155). We identified several regions of the genome that were consistently associated with sex across all three lineages that included expected sex-chromosomes (Chr17, 18), but also putative copies of sex-linked regions in several autosomal chromosomes. Further, large regions of the same two chromosomes (17 and 18) were associated with age-at-maturity in a lineage-specific manner. Patterns of genotype by phenotype with multi-marker haplotypes confirmed the association of SNPs on chromosome 17 with both size (fork length) in natural-origin males from the two interior lineages, and age-at-maturity (ocean-age) in interior ocean-type males, but not in females. Further studies will be necessary to verify other candidate regions and polygenic effects on size and age-at-maturity in this species. While rearing environment and growth play a major role in age-at-maturity, these results provided evidence for genetic heritability and candidate genes associated with this trait that will assist in monitoring genetic variation to maintain life history variation in Chinook Salmon.

Poster Presentation Abstracts

Americus, Benjamin; Chickaloon Village Traditional Council; "Using eDNA from soil to understand past salmon diversity"

Coauthor(s): Cody A. Henrikson, Chickaloon Village Traditional Council; Damian M. Menning, USGS; Jessica E.D. Winnestaffer, Chickaloon Village Traditional Council

Chickaloon Village Traditional Council (CVTC) employs fisheries staff to help protect, enhance, and restore culturally important salmon populations. Much of our work is focused at Tsidek'etna "Grandmothers' Stream", known presently as Moose Creek (near Palmer). Traditional knowledge tells of abundant populations of all five species of Pacific salmon. In the early 1900s, the habitat quality of Tsidek'etna was severely degraded by coal mining and railway development. Around 1910, a waterfall barrier to fish passage was introduced, blocking four of eight total miles of spawning habitat. This fish passage barrier was removed by CVTC in 2005 during river restoration. Coho and Chinook now spawn above the barrier. In 2024, we collected soil cores from nine biologically and culturally relevant sites above and below the former waterfall barrier. To understand past salmon diversity across space and time, we subdivided cores by "top" and "bottom" samples and are using primers for *Oncorhynchus* species to detect salmon sedDNA (sedimentary DNA). To understand past salmon abundance, we are testing the feasibility of quantifying marine-derived nitrogen (δ15). Preliminary results suggest soil from the top halves of the cores has more total DNA than samples from the bottom halves. Soil from higher in the watershed has more total DNA than samples from lower. Total DNA appears correlated with nitrogen content. Pending metabarcode sequencing will test for the presence/absence of *Oncorhynchus* species. For soil samples containing salmon DNA, we will also quantify marine-derived nitrogen.

Davis, Hayden; University of Washington; "Investigation into the genomic factors associated with IHNV resistance in rainbow trout."

Coauthor(s): Yniv Palti, USDA; Christopher Setzke, UW; Kyle Martin, Hendrix Genetics; Kerry A. Naish, UW

Infectious Hematopoietic Necrosis (IHN) is caused by a virus (IHNV) that can lead to morbidity and acute mortality in many salmonid species, especially within hatchery and aquaculture systems. Development of commercial lines of rainbow trout (*Oncorhynchus mykiss*) that have resistance to IHNV is a critical component of maintaining a productive industry. Previous research has shown that resistance to the disease is an oligogenic trait, but multiple QTLs have been identified with putative links to IHNV resistance using SNP genotyping. Here, we expanded this work to investigate the underlying biology of this architecture by generating over 1,800 low coverage whole genome sequences. With the expanded dataset, we aimed to identify novel SNPs closely linked to the causative loci characterizing the genetic interactions within and between loci, and to investigate the prevalence of disease-linked alleles within the population. To do so, we applied a genome wide association approach using a survival analysis based on a Cox regression with the time to death as the primary outcome variable, and we examined allelic interactions at each QTL. Further, our expanded dataset allowed us to assess the presence and importance of loci hypothesized to be linked to resistance in previous studies. Using our whole genome approach, we can more precisely identify loci and genomic regions that provide a deeper understanding of the genomic underpinning of IHNV resistance in rainbow trout.

Headley, Racheal; USFWS; "Use of genetic markers to inform and monitor reintroduction of an extirpated population of Chinook Salmon"

Coauthor(s): Jennifer Von Bargen, USFWS; Christian T. Smith, USFWS

The Sacramento River in central California is home to the greatest diversity of Chinook salmon ecotypes of any basin in their range, including the endemic winter run Chinook Salmon (WRCS). One of the requirements for recovery of endangered WRCS is re-establishment of a population in Battle Creek, where the species was previously extirpated. In 1911 construction of the Battle Creek Hydroelectric Project, which is now owned and operated by Pacific Gas & Electric, caused the extirpation of WRCS in the Battle Creek watershed. In 1945 and 1950, Shasta Dam and Keswick Dam, respectively, were built; cutting off migration of WRSC to their natal spawning habitat in the upper Sacramento River and its tributaries, the McCloud and Pit rivers. In 1994, WRCS were listed as endangered under the U.S. Endangered Species Act. In 1996, to help recover WRCS, Livingston Stone National Fish Hatchery (LSNFH) was built. Due to severe drought conditions in 2014-2015, a Captive Brood Program was re-initiated at LSNFH, to preserve the genetics of the population before another bottleneck. LSNFH captive brood were spawned, and their progeny were reintroduced into Battle Creek. The first out-planting of offspring (BY17) was in the spring of 2018, and additional spawning of captive brood and releases of their progeny has happened in each year since. The first returns to Battle Creek were jacks (age 2 males) in the spring of 2019. Here we will present a summary of WRCS returns to Battle Creek from 2019-2024 and their assignment back to LSNFH captive brood family groups.

Healy, Timothy; DFO; "Variation in DNA methylation associated with hatchery-origin in Chinook Salmon"

Coauthor(s): Braden J. Judson, DFO; Rose-Lynne F. Savage, DFO; Ellika M. Crichton, DFO; Kyle W. Wellband, DFO; Eric B. Rondeau, DFO

Hatchery production of salmonids is used throughout the northern Pacific to support or enhance wild salmon. Yet, hatchery-origin salmon typically exhibit lower performance and fitness in wild habitats than their natural-origin counterparts. Consequently, hatchery releases pose a potential long-term fitness risk for wild populations. However, the mechanisms through which hatcheries impact the productivity of wild salmon populations remain relatively poorly understood. In Canada, Chinook Salmon (*Oncorhynchus tshawytscha*) are a major focus of hatchery enhancement with objectives ranging from conservation to harvest, and all enhanced populations are managed as integrated systems with gene flow between the natural habitat and the hatchery. This results in limited contemporary genetic differentiation between hatchery- and natural-origin spawners. In contrast, there can be substantial variation in DNA methylation between hatchery- and natural-origin Pacific salmonids, although little is known for Chinook Salmon. We used parentage-based tagging to identify hatchery- and natural-origin Chinook adults among returns to hatcheries operated by Fisheries and Oceans Canada. DNA was isolated from females and males of each origin, and whole-genome DNA methylation patterns were assessed by enzymatic-methylation sequencing. We characterized differential methylation between hatchery- and natural-origin individuals generally and specifically for each hatchery assessed. Hatchery-origin returns were also stratified by age of return, allowing examination of age-associated DNA methylation. Our results not only improve understanding of hatchery-mediated epigenetic variation in Chinook Salmon, but also provide a foundation for epigenetic biomarker development in this iconic species.

Koch, Ilana; CRITFC; "An epigenetics pilot study to evaluate effects of rearing density on methylation patterns in Chinook salmon"

Coauthor(s): Hayley Nuetzel, CRITFC; Shawn Narum; CRITFC

Fitness differences between fish born in nature (natural-origin) versus in the hatchery setting (hatchery-origin) are well documented, yet strong genomic differences between these phenotypes have not been consistently found. On the contrary, parallel epigenetic differences between hatchery- and natural-origin salmonids have recently emerged from the literature. However, the specific environmental triggers that shape epigenetic differences remain largely unknown. We present plans for an upcoming experiment that is designed to test the hypothesis that hatchery rearing density influences methylation patterns in Chinook salmon. Offspring from 8 half-sib families will be divided in a controlled experiment into three different study groups including low density treatment, high density treatment, and a density level mimicking conservation hatchery targets. Multiple tissue types will be collected from parents and offspring (during parr and smolt life stages) from each family to further determine the heritability of epigenetic signals. Using whole genome bisulfite sequencing, we will explore the functional regions of the genome that are differentially methylated in response to density treatments. Results from this study are expected to provide insight into the relationship between environmental triggers, methylation patterns, and subsequent fitness differences between hatchery- and natural-origin fish that could ideally be incorporated into future hatchery management protocols.

Lewis, Devayne Marcel; CRITFC; "Utility of Parentage Based Tagging for Research, Monitoring, and Evaluation of Hatchery Programs within the Columbia River Basin"

Coauthor(s): Jon Hess†, CRITFC; Matthew Campbell, IDFG; Jesse McCane, IDFG; Forrest Bohlen, IDFG; Audrey C. Harris, IDFG; Shawn Narum, CRITFC; Rebekah Horn, CRITFC; Jeff Stephenson, CRITFC

Salmon and steelhead hatchery programs in the Columbia River Basin (CRB) are essential for supporting healthy populations and mitigating hydrosystem impacts. Hatchery managers need effective methods for research monitoring and evaluation (RME) of these programs. Parentage-based Tagging (PBT), a modern genetic tool, offers advantages over traditional tagging methods (e.g., coded wire tags, marks, and PIT tags), including being cost-effective, achieving nearly 100% tag rates, no tagshedding, and non-lethal tag recovery from any life stage. PBT Baselines for Chinook Salmon and Steelhead were initiated in 2008 in the Snake River Basin and expanded by 2012 to cover hatcheries above Bonneville Dam.

Combining PBT-based RME data from adult returns with other RME efforts can provide hatchery managers with comprehensive insights into stock abundances, run timing, and harvest utilization across the CRB. This study aimed to demonstrate PBT's utility for comprehensive RME by comparing observed values for percent PBT-assigned, age and stock composition, and stock abundances at Bonneville Dam to expected values. The expected percent PBT-assigned for 52 Chinook Salmon collections (N=57,095) was 85.2% (range: 53.5–100%), and for 15 Steelhead collections (N=5,951), it was 93.6% (range: 66.9–100%). These values largely aligned with observed PBT-assigned percentages, except for rare cases, such as intentional integration of natural-origin fish in broodstocks. The study also identified rare deviations in age, stock composition, and stock-specific abundances, which, if monitored regularly, could be useful for hatchery management.

Masingale, Jonathan*; University of Idaho; "The heart of the matter: disentangling genetic and environmental influences on thermal performance in redband trout"

Coauthor(s): Zhongqi Chen, University of Idaho; Christopher Caudill, University of Idaho; Brian Small, University of Idaho

Temperature governs physiology in ectotherms and limits the distribution of coldwater fishes such as trout. We are evaluating how genetic and plastic traits influence the adaptive capacity of redband trout (*Oncorhynchus mykiss gairdneri*, RBT) to changing thermal regimes, including how diel variation in stream temperature affects traits. Cardiac function is a limiting factor in thermal performance and tolerance because higher temperatures elevate metabolic demand for O2 and decrease O2 solubility. To understand the genetic and plastic components of cardiac performance, we collected RBT fry from two desert and two montane forest streams in Idaho. We reared fish in a common garden setting using two constant temperature regimes (15 and 21°C) and two matching diel fluctuating temperature regimes (±3°C). To evaluate how cardiac function differed across populations, acclimation temperatures, and diel thermal regimes, we measured heart rate in response to acute warming and calculated cardiac performance metrics (N = 240). We generated low-coverage whole genome sequencing data for each individual to identify genomic regions associated with cardiac performance. Because performance is influenced by both genetics and environment, we hypothesized that desert populations exhibit optimum cardiac performance at higher temperatures than montane populations, and that the physiological optimum window shifts with acclimation temperature. We also hypothesized that diel fluctuating temperatures will widen the scope of thermal tolerance, increasing the upper thermal range of optimum physiological performance. These data will help us understand the relative contribution and interactions among genetic and plastic components to predict adaptive capacity of RBT at watershed scales.

McPhee, Megan; University of Alaska Fairbanks; "Variation in smolts sampled per spawner by parental sex and origin (hatchery/wild) in Auke Lake sockeye salmon, brood years 2016-2018"

Evaluating the demographic and evolutionary impacts of hatchery supplementation is key to optimizing the enhancement of harvest opportunities without jeopardizing wild populations. We have been evaluating the first- and second-generation consequences of three consecutive brood years (2011-2013) of a short-term, experimental, and integrated sockeye salmon program in Auke Lake, Juneau, Alaska using complete genetic sampling of all adults returning to the Auke Creek weir since 2008. Opportunistic smolt sampling at the Auke Creek weir allowed us to ask: does reproductive success, in terms of number of smolts produced per spawner, differ between hatchery- and wild-born individuals when spawning in the wild? We genotyped smolts sampled 2018-2021, which includes years when the grand-offspring of the original hatchery broodstock could be emigrating out of Auke Lake. Genotypes at 340 SNPs were compared between 1,064 smolts and 1,566 hatchery-born and ~11,000 wild-born adults to identify parentage. We calculated RSS, or the 'relative number of smolts sampled' per hatchery- and wild-born parents over the three brood years (2016-2018) when smolts of both parental origin were detected. In 2016, RSS was not statistically distinguishable from unity, suggesting no difference in adult-smolt survival rates by parental origin. In contrast, the relative number of smolts sampled was lower for hatchery- than wild-origin females in 2017 and lower for hatchery- than wild-origin males in 2018. These findings largely track results based on adult-to-adult success rates, but not entirely. How parental age, uncertainty in parental sex identification, and the age and emigration timing of smolts might affect the RSS estimates is currently being explored.

O'Malley, Kathleen; State Fisheries Genomics Lab, Coastal Oregon Marine Experiment Station, Department of Fisheries, Wildlife and Conservation Sciences, Hatfield Marine Science Center, Oregon State University, Newport, Oregon; "The distribution of *Oncorhynchus mykiss* genetic diversity in the Klamath Basin before dam removal"

Coauthor(s): Mark E. Hereford, ODFW; Kevin C. Olsen, OSU; Devon E. Pearse, NOAA; Jonathan B. Armstrong, OSU; William R. Tinniswood, ODFW; Benji S. Ramirez, ODFW; Stanley Piotrowski, OSU

Genetic assessments can serve as powerful tools to evaluate the effects of anthropogenic habitat fragmentation on natural populations. In the Klamath Basin, construction of Copco No. 1 Dam beginning in 1912 had a profound impact on the distribution of anadromous fishes, blocking access to over 960 river kilometers of spawning, incubation, and rearing habitat. The limit of upstream migration for anadromous fishes in the basin was established in 1962 with the completion of Iron Gate Dam, which divided the Lower and Upper Klamath Basins. To evaluate the genetic diversity and connectivity among *Oncorhynchus mykiss* in the upper and lower basins prior to dam removal, we genotyped 2,466 samples collected from 74 collections at 298 genetic markers, comprised of 193 presumably neutral markers and 105 putatively adaptive markers. Broadly, we detected an apparent divide in the genetic composition of *O. mykiss* downstream and upstream of the outlet of Upper Klamath Lake. The results of our population genetic analyses highlight the genetic diversity and structure of *O. mykiss* in the Klamath Basin and will serve as an important baseline for future assessments post dam removal.

Strickland, Garret; CRITFC; "Streamlined Primer Design Pipeline Improves Success Rates in Amplicon Sequencing Panels"

Coauthor(s): Zachary L. Robinson, CRITFC; Jeff J. Stephenson, CRITFC; Shawn R. Narum, CRITFC

Effective primer design is critical for the success of amplicon sequencing panels, yet many commonly used tools fail to account for primer specificity and performance in highly multiplexed contexts. This often results in higher costs and inefficient optimization. We present a Python-based primer design pipeline, optimized for GTseq applications, that streamlines design and incorporates multiple in silico checks for primer dimers and specificity using MFEprimer3. To test our pipeline, we employed a post hoc approach analyzing a novel set of primer pairs, designed using Primer3 and limited filtering, that were incorporated into a pre-existing primer panel for Chinook Salmon. A substantial proportion of these new markers failed during optimization due to non-specific amplification or dimerization. We found that integrating MFEprimer3 into our pipeline would have predicted and excluded approximately ½ of non-performing primers while providing few false positives. This illustrated that our new pipeline is expected to provide a more reliable and efficient strategy for GTseq marker development compared to more limited "design and optimize" strategies. The pipeline requires only a variant file and reference genome and automates interactions with external programs (e.g., Primer3 and MFEprimer3). It designs allele-specific search strings, retains positional information, and supports microhaplotype markers. Additionally, the workflow is suitable for expanding pre-existing primer panels with new markers. Here, we offer a conceptual diagram of the primer design pipeline, discuss implementation details, and highlight the benefits of adoption. We also outline improvements to our genotyping pipeline that further illustrate the efficiency and effectiveness of GT-seq.

Von Bargen, Jennifer; USFWS; "Parentage based tagging to track survival of Chinook salmon fry"

Coauthor(s): Christian T. Smith†, USFWS; Steve Mussmann, USFWS; Brice Adams, USFWS

Coleman National Fish Hatchery was built on Battle Creek, an upper Sacramento River tributary, in 1942 to mitigate for loss of salmon spawning and rearing habitat with the construction of Shasta Dam. The fall Chinook Salmon program at Coleman is one of largest operated by the US Fish and Wildlife Service, with the annual release target and rearing capacity of the hatchery at 12 M smolts. Poor returns of salmon to the upper Sacramento River in recent years have led to demands that production at Coleman be increased to 20-22 M fish per year, with the additional 8-10 M fish being released as fry. Fish released as fry cannot be marked using traditional methods, and parentage-based tagging (PBT) has been proposed as a tool to monitor the fry releases. Several laboratories analyze genetic samples from Sacramento River Chinook Salmon to answer various management questions, and the use of a common set of markers and data sharing protocols would thus greatly improve the efficiency of a PBT program at Coleman. Here we describe an effort underway to develop shared resources among state, federal and private laboratories working on Sacramento River Chinook Salmon, and to deploy those tools to implement PBT at Coleman and other hatcheries.

Notes

Tuesday 5/13				
Time	**Category**	**Session**	**Speaker**	**Title**
6:30 AM	Breakfast			
8:00 AM	Welcome		Sara Gilk-Baumer	
8:15 AM	Keynote		Jim and Lisa Seeb	Synergies among ADF&G Genetics, AFS Genetics Section, and "Coastwides"
9:00 AM	Break			
9:10 AM	Talk	CKMR/Parentage	Matthew Campbell	Evaluating genetic introgression from hatchery-origin steelhead in the Snake River Basin using advanced grandparentage inference
9:30 AM	Talk	CKMR/Parentage	Audrey Harris	Clearing the hurdle: How arrival timing and size influence reproductive success in steelhead returning to Fish Creek, Idaho
9:50 AM	Sponsor	Illumina	Sandi Calhoun	Introducing the Illumina MiSeq i100
10:00 AM	Break			
10:20 AM	Talk	CKMR/Parentage	Mary Commins	Evaluating the second-generation effects of hatchery supplementation in Auke Lake sockeye salmon
10:40 AM	Talk	CKMR/Parentage	Zachary Robinson	Estimating Chinook salmon escapement using transgenerational mark-recapture (tgMR) in the presence of precocial parr
11:00 AM	Talk	CKMR/Parentage	Scott Blankenship	Estimating abundance of *Oncorhynchus mykiss* in anadromous waters using CKMR approach
11:20 AM	Talk	CKMR/Parentage	Alana Luzzio	Using parentage-based tagging to identify natal origins of Chinook salmon (*Oncorhynchus tshawytscha*) returning to a restored creek
11:40 AM	Talk	CKMR/Parentage	Brice Adams	Migratory form bull trout parentage in the Clark Fork River, Montana
12:00 PM	Sponsor	GTseek	Nathan Campbell	Salmonid genome structure and implications for GT-seq marker selection
12:10 PM	Lunch			
1:20 PM	Talk	GSI/Popgen	Todd Seamons	Genetic discovery and description of a Nisqually River Chinook salmon population
1:40 PM	Talk	GSI/Popgen	John Hargrove	Temporal trends in hybridization between native and non-native salmonids in the Clearwater and Lochsa Rivers, Idaho
2:00 PM	Talk	GSI/Popgen	Adrian Spidle	Rescue program for South Fork Nooksack Spring Chinook salmon
2:20 PM	Talk	GSI/Popgen	Rebecca Cheek	Scaling up: Harnessing the power of an updated regional baseline for broad scale genetic stock identification of chum salmon (*Oncorhynchus keta*)
2:40 PM	Sponsor	Student Travel Grant Awards	Sara Gilk-Baumer	
2:50 PM	Break			
3:10 PM	Talk	GSI/Popgen	Eric Rondeau	A SNP-based coastwide sockeye salmon baseline for genetic stock identification in British Columbia
3:30 PM	Talk	GSI/Popgen	Andy Barclay	An updated coastwide baseline for genetic stock identification of chum salmon: a resource for examining stock-specific marine migration and harvest
3:50 PM	Talk	GSI/Popgen	Kyle Shedd	A range-wide genetic baseline for Chinook salmon improves resolution for stock identification in Alaska and Northern Canada
4:10 PM	Talk	GSI/Popgen	Erika King	Updated status of Southeast Alaska coho salmon genetic baseline
4:30 PM	Closing		Sara Gilk-Baumer	
6:00 PM	Poster			

Wednesday 5/14				
Time	Category	Session	Speaker	Title
6:30 AM	Breakfast			
8:00 AM	Welcome		Sara Gilk-Baumer	
8:10 AM	Talk	GSI/Popgen	Chase Jalbert	Alaska's other potential eruption: Illuminating fish stocks with MAGMA
8:30 AM	Talk	GSI/Popgen	Bobby Hsu	Using computer simulation to assess sample size for mixed stock analysis
8:50 AM	Talk	GSI/Popgen	Elizabeth Lee	Genetic stock Identification from gravel to gravel: Use of genetic tools in forecasting and monitoring Yukon River Chinook salmon runs
9:10 AM	Talk	GSI/Popgen	Tyler Dann	GSI of South Alaska Peninsula chum salmon harvests: Genetic tools inform management of fisheries that connect stakeholders amid conservation crises
9:30 AM	Talk	GSI/Popgen	Jon Hess	Genetic identification of lamprey genera and anadromous ecotypes in watersheds of the Northeastern Pacific Ocean
9:50 AM	Sponsor	open timeslot		
10:00 AM	Break			
10:20 AM	Talk	Genomics	Christopher Setzke	Mechanisms of specialist-generalist tradeoffs for IHNV in salmonids
10:40 AM	Talk	Genomics	Kyle Wellband	Shared patterns of DNA Methylation variation in hatchery-origin Coho Salmon and implications for developing molecular monitoring tools
11:00 AM	Talk	Genomics	Sam Rosenbaum	Chromosome-level reference genome for male brook trout (*Salvelinus fontinalis*) from a long-term genetic rescue study
11:20 AM	Talk	Genomics	Timothy Healy	Genomic estimates of climate change vulnerability in sockeye salmon
11:40 AM	Talk	Genomics	Shawn Narum	Conservation of neutral and adaptive genomic variation in anadromous fishes of the Columbia River
12:00 PM	Sponsor	Element Biosciences	Amy Klegarth	Shift Your Science
12:10 PM	Lunch			
1:20 PM	Talk	Genomics	Wes Larson	Understanding the genetic basis of run timing diversity in four species of Pacific salmon
1:40 PM	Talk	Genomics	Kristen Gruenthal	Genomic signatures of natural and domestication selection in wild and hatchery pink salmon
2:00 PM	Talk	Genomics	Anna Tigano	Fine-scale population genomics of chum from the southern Canada/USA border based on whole genome data
2:20 PM	Sponsor	Twist Biosciences	Paul Doran	Twist's FlexPrepTM: Accelerating the Transition from Microarrays to Next-Generation Sequencing in Agrogenomic Application
2:30 PM	Break			
2:50 PM	Breakouts			(1) Pacific Salmon Commission Fraser sockeye, (2) Revised Chinook SNP baseline
4:30 PM	Closing		Sara Gilk-Baumer	
6:00 PM	Social			

Thursday 5/15				
Time	**Category**	**Session**	**Speaker**	**Title**
6:45 AM	Breakfast			
8:20 AM	Welcome		Sara Gilk-Baumer	
8:30 AM	Talk	Genomics	Rebekah Horn	Genomic insights into local adaptation and migration success in reintroduced coho salmon of the Wenatchee River Basin
8:50 AM	Talk	Genomics	Stuart Willis	Heritability and genomic basis of age-at-maturity in Chinook salmon
9:10 AM	Talk	Genomics	Natasha Howe	Age at maturity in sockeye salmon has a strong genetic component found on both sex and autosomal chromosomes
9:30 AM	Talk	Straying	Nancy Hillstrand	What are acceptable hatchery stray proportions in Alaska's anadromous waters
9:50 AM	Sponsor	Standard Biotools	Zach Farrow	Fast answers for fast fish (Standard Biotools)
10:00 AM	Break			
10:20 AM	Talk	eDNA	Nate Cathcart	Fish surveys, salmon population genetics, and eDNA detection in Bering Land Bridge National Preserve
10:40 AM	Talk	eDNA	Michael Phelps	Tracking invasive and threatened salmonid species using real-time and automated systems
11:00 AM	Talk	Lab/Infastructure	Lanie Galland	Mobile DNA sequencing laboratory for real-time assessment of Columbia River basin fisheries: Genotyping in a van down by the river
11:20 AM	Talk	Lab/Infastructure	Jodi Estrada	Non-destructive high-throughput DNA extractions from pink salmon otoliths
11:40 AM	Talk	Lab/Infastructure	Heather Hoyt	Three million and counting: Genetics sample archiving for the Alaska Department of Fish and Game
12:00 PM	Closing		Sara Gilk-Baumer	