Coastwide Salmonid Genetics Meeting 2010:

Genetic Adaptation of Salmonids

June 1-4, 2010

The Grove Hotel, Boise, Idaho

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Coastwide Salmonid Genetics Meeting 2010: Genetic Adaptation of Salmonids

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Walking Maps

Meeting Agenda

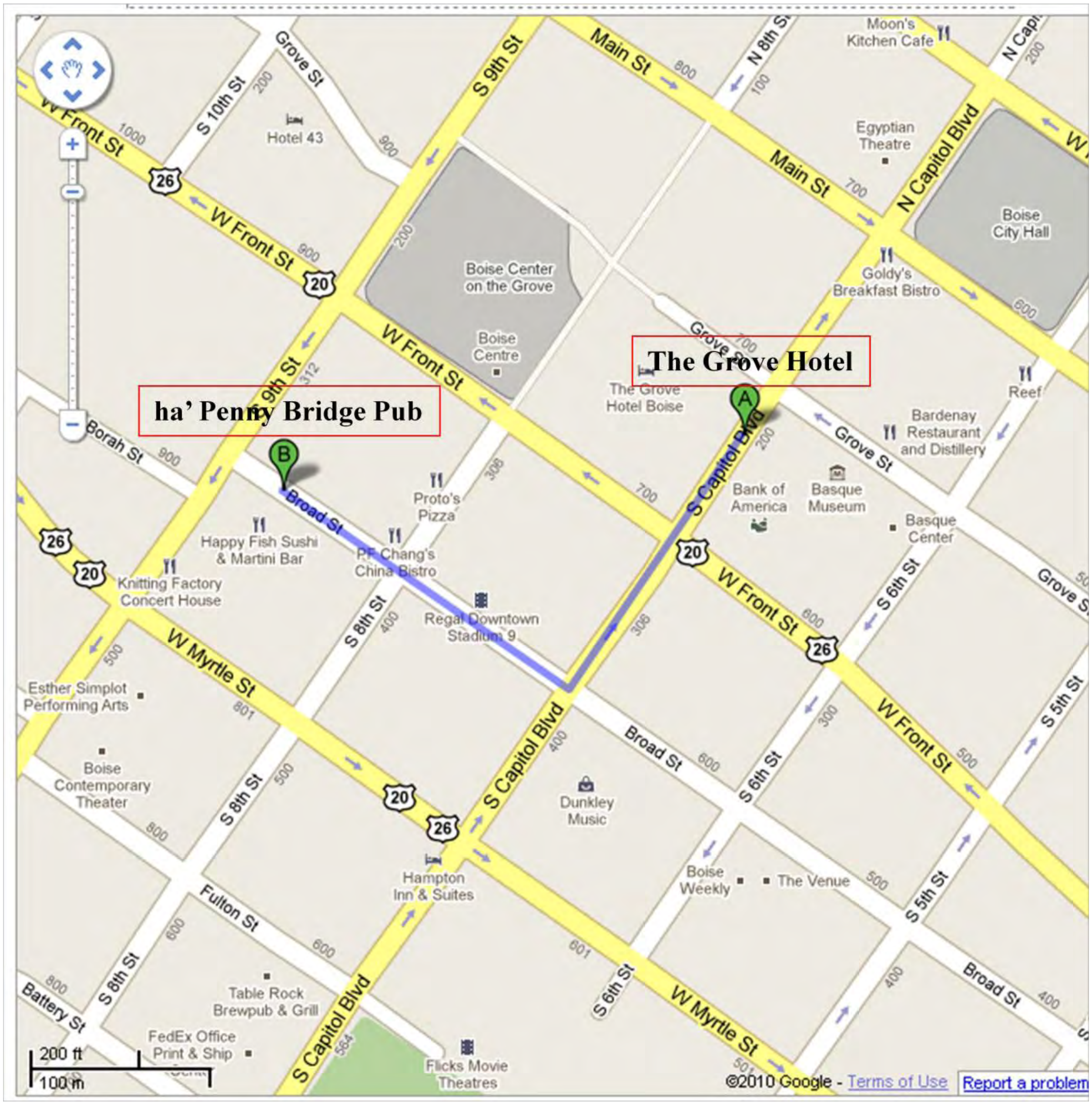
Walking directions from the Grove Hotel to ha' Penny Bridge Pub (Tuesday night social)

Distance = 0.2 miles

1. Head southwest on S Capitol Blvd toward W Front St

2. Turn right at Broad St

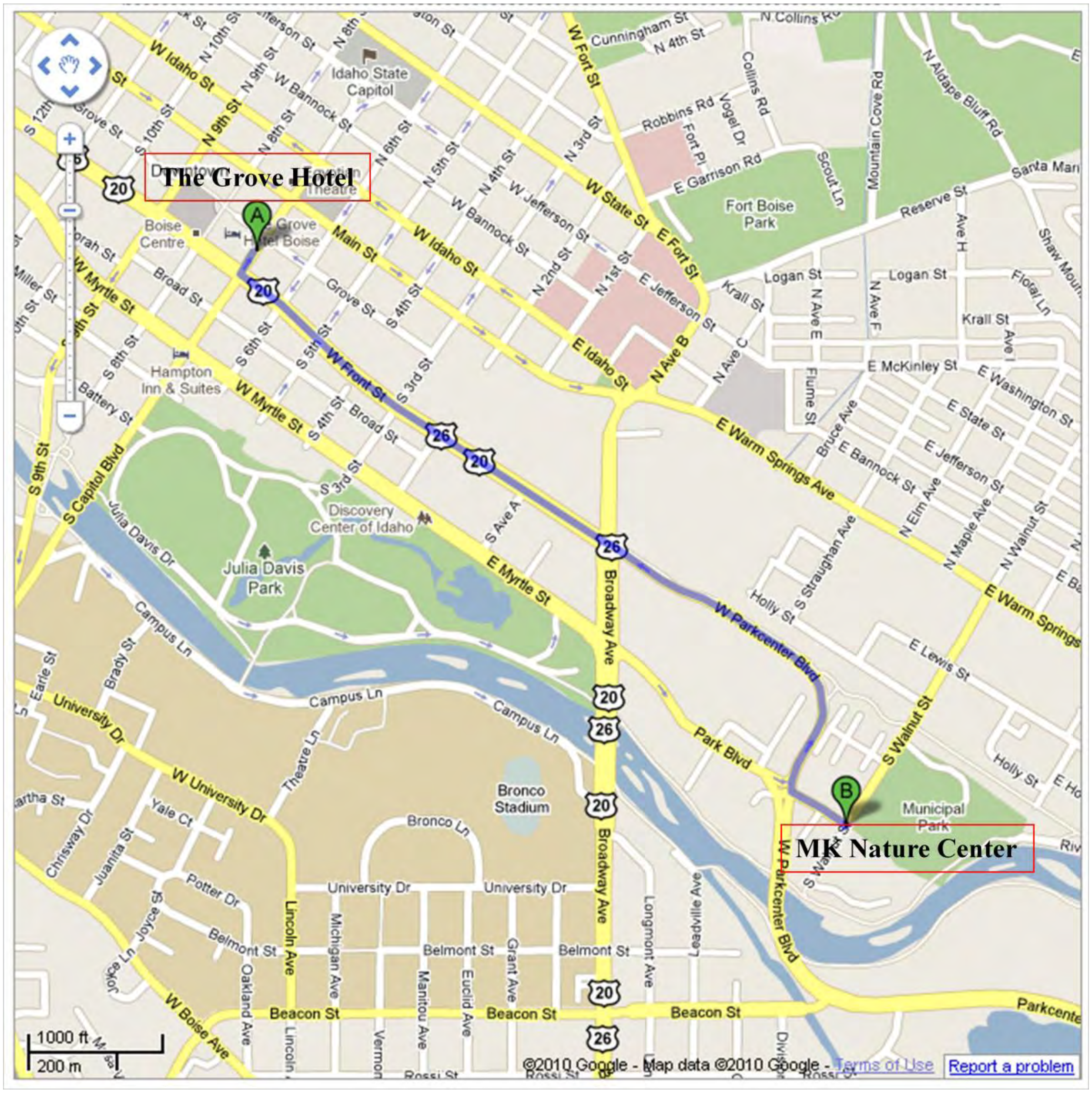
3. ha„Penny will be on your left



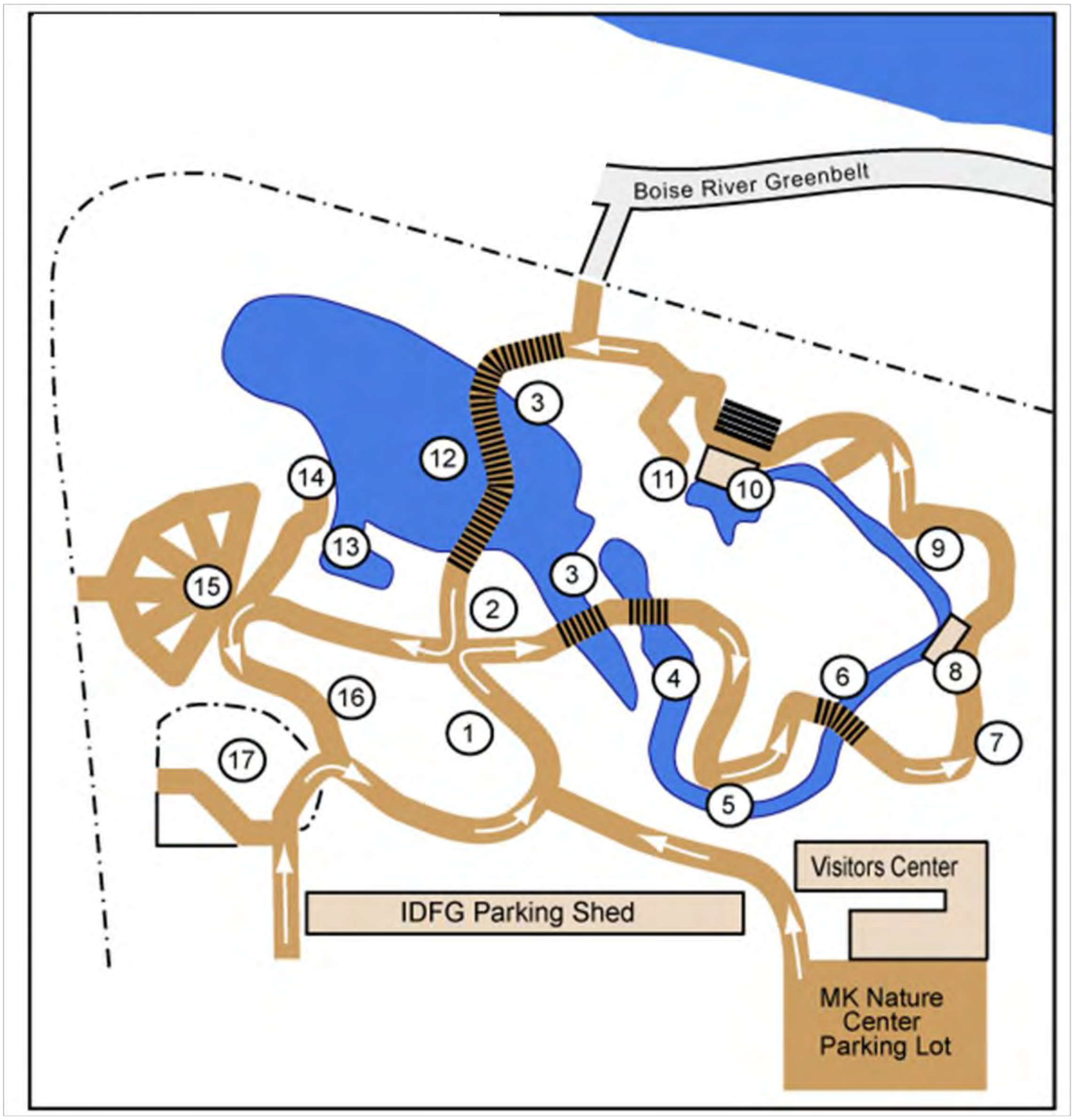
Walking directions from the Grove Hotel to the MK Nature Center (Wednesday banquet)

Distance = ~1 mile
1. Head southwest on S Capitol Blvd toward W Front St
2. Turn left at W Front St
3. Continue onto W Parkcenter Blvd
4. Turn left at Park Blvd
5. MK Center is at the intersection of Park Blvd and Walnut St. (600 S Walnut St.)

For a longer, but more scenic walk (~2 miles), head toward Julia Davis Park and follow the Greenbelt along the Boise River



MK Nature Center Stream Walk



①	HIP
②	Snags
③	Wetlands
④	Logjam
⑤	Shelter Window
⑥	Lava Rocks
⑦	High Desert
⑧	Riffle Window
⑨	Egg Window
⑩	Alpine Lake Window
⑪	Waterfall Overlook
⑫	Pond
⑬	Beaver Dam
⑭	Viewing Blind
⑮	Butterfly Garden
⑯	Compost
⑰	Formal Backyard

Tuesday, June 1

Welcome

3:00 – 6:00 p.m. **Registration, The Grove Hotel**

7:00 p.m. **Ice breaker social at ha' Penny Bridge Pub**

Wednesday, June 2

Plenary Session – Salmonid Adaptation

7 – 8:30 a.m.	**Breakfast**
7:00 a.m.	**Registration**
Moderator:	**Jon Hess**
8:45 a.m.	Welcome and Introduction
9:00 a.m.	**Mike Ackerman**; SNP markers under diversifying selection provide increased accuracy and precision in mixed stock analyses of sockeye salmon (*Oncorhynchus nerka*)
9:20 a.m.	**Jon Hess**; SNP loci correlated with run-timing in Chinook salmon from the Columbia River Basin
9:40 a.m.	**Lisa Seeb**; Patterns of nearshore juvenile migration of sockeye salmon in the eastern Bering Sea
10:00 a.m.	**Scott Pavey**; Ecological transcriptomics in muscle tissue of lake-type and riverine sockeye salmon (*Oncorhynchus nerka*).
10:20 a.m.	Break
10:50 a.m.	**Lisa Creelman**; Temporal and geographic genetic divergence: Characterizing sockeye salmon populations in the Chignik watershed, Alaska using single nucleotide polymorphisms
11:10 a.m.	**Molly McGlauflin;** Influences of spawning habitat and geography: genetic structure and juvenile migration timing of sockeye salmon in the Wood River Lakes, Alaska
11:30 a.m.	**Eric Iwamoto**; Retention of historical genetic structure of sockeye salmon in the Wenatchee Basin despite homogenization by the Grand Coulee Fish Maintenance Project
12:00 p.m.	Lunch

Moderator: **Shawn Narum**

1:15 p.m. **Scott Blankenship**; Genetic structure and adaptation of Columbia River Basin steelhead and rainbow trout

1:35 p.m. **Devon Pearse**; Population Genomics of Coastal California Resident and Anadromous *Oncorhynchus mykiss* in Scott Creek, CA

1:55 p.m. **Megan McPhee**; Candidate loci fail to find differentiation between sympatric steelhead and rainbow trout *Oncorhynchus mykiss*

2:15 p.m. **Shawn Narum**; Candidate genetic markers associated with anadromy in *Oncorhynchus mykiss* of the Klickitat River

2:35 p.m. **Ewann Berntson**; Pushing hatchery fish uphill: Diminished reproductive success complicates the use of supportive breeding in Snake River steelhead recovery

2:55 p.m. Break

3:15 p.m. **Andrew Matala**; Using SNPs to Compare and Resolve Adaptive and Demographic Divergence Among Chinook Salmon in the Columbia River Basin

3:35 p.m. **Paul Moran**; Studies of connectivity and life history adaptation in West Coast Chinook salmon populations: Size matters.

3:55 p.m. **Maureen Small**; Does Lower Crab Creek in the Eastern WA desert have a native population of Chinook salmon?

4:15 p.m. **Kathleen O'Malley**; *Clock* Polymorphism in Pacific Salmon: Evidence for Variable Selection along a Latitudinal Gradient

4:35 p.m. **Christian Smith**; Persistent reproductive isolation between sympatric lineages of fall Chinook salmon in White Salmon River, Washington

5:30 p.m. Social & Banquet at the Morrison Knudsen Nature Center - A shuttle will be available from 5:30-9:30 p.m. for transportation between The Grove and the MK Center.

Thursday, June 3

General Session

7 – 8:30 a.m. **Breakfast**

Moderator: **Sara Gilk**

9:00 a.m. **Eleni Leto Petrou**; The phylogeography of chum salmon from the Alaska Peninsula, the contact zone between distinct genetic lineage

9:20 a.m. **Don VanDoornik**; Genetic monitoring reveals genetic stability within and among Chinook salmon populations in the Salmon River, Idaho

9:40 a.m. **Victoria Pritchard**; Genetic Population Structure of Rio Grande Cutthroat Trout

10:00 a.m. **Michael Young**; Broad-scale genetic and compositional monitoring of fish populations: a proof of concept in the interior Columbia River and upper Missouri River basins

10:20 a.m. Break

10:40 a.m. **Sammy Matsaw**; Barriers to movement and genetic population structure of westslope cutthroat trout (*Oncorhynchus clarkii lewisi*) in the Salmon River Basin, Idaho

11:00 a.m. **Pat DeHaan**; Genetic Population Structure of Olympic Peninsula Bull Trout and Implications for Elwha Dam Removal

11:20 a.m. **Carlos Garza**; Are coho salmon native to coastal California streams south of the Golden Gate?

11:40 a.m. **Sara Gilk**; Adrift in a complex landscape: Sockeye salmon in Southeast Alaska

12:00 p.m. Lunch

1-5 p.m. Fluidigm Demonstration & Breakout Groups

6:00 p.m. Poster Session & Social

Friday, June 4

General Session

7 – 8:30 a.m.	**Breakfast**
Moderator:	**Matt Campbell**
9:00 a.m.	**John Candy**; Measuring –compactness” and –connectedness” a new method for quantifying genetic diversity within species
9:20 a.m.	**Steven Kalinowski**; Improving estimates of allele frequencies for genetic stock identification by using data from multiple populations at once
9:40 a.m.	**Bill Templin**; Estimating run timing in the presence of small samples: Reverend Bayes saves the day
10:00 a.m.	**Ruth Phillips**; Assignment of Chinook salmon (*Oncorhynchus tshawytscha*) linkage groups to chromosomes
10:20 a.m.	Break
10:40 a.m.	**Anna Elz**; Anthropogenic influences on life history traits in the Snake River fall Chinook
11:00 a.m.	**Matt Campbell**; Genetic stock identification of wild Snake River steelhead mixtures at Lower Granite Dam
11:20 a.m.	**Tyler Dann**; Selection of 96 SNPs to represent coastwide sockeye salmon genetic variation for mixed-stock analysis applications
11:40 p.m.	**Tyler McCraney**; Genetic stock identification of chum salmon in the North Pacific Ocean and Bering Sea using microsatellites
1pm-8:00pm	Rafting Trip

Poster Session – Thursday, June 3, 6:00 p.m.

Kristy L. Bellinger; Differences in burst swimming performance among 5 genetically differentiated clonal rainbow trout lines, varying in domestication levels

Janet Campbell; Neurobiology and aggressive behavior in domesticated and wild rainbow trout.

Nate Campbell; Relative Genetic Diversity Estimates amongst Four Pacific Salmonids.

Kris Christensen; Antipredator behavior changes between wild-type and hatchery-derived rainbow trout clonal lines

Josh Faber-Hammond; The Sockeye Salmon Neo-Y Chromosome is a fusion between the Coho Y Chromosome and an Autosome

Peter Galbreath; Are Hatchery Effects Forever? - Use of Hatchery Stocks to Reintroduce Extirpated Coho Salmon to the Mid-Columbia and Snake River Basins

Chuck Guthrie; Sockeye Salmon Genetic Stock Identification using Single Nucleotide Polymorphisms (SNPS) for the Southeast Alaska 2006 and 2007 District 101 Gillnet and District 104 Purse Seine Fisheries.

Andrew Harwood; 12 new linked and sex-specific SNP markers, and associated TaqMan assays, for genotyping various subspecies of cutthroat trout, rainbow trout, and their hybrids.

Maureen Hess; Evaluating adaptation of reintroduced spring-run Chinook salmon in the Hood River, Oregon

Christine Kondzela; Genetic analysis of immature chum salmon from the eastern Bering Sea

David Kuligowski; Genetic stock identification of juvenile steelhead (*Oncorhynchus mykiss)* tissues collected from the stomachs of double-crested cormorants (*Phalacrocorax auritus*) in the Columbia River Basin

Eric LaHood; Molecular departures from neutrality related to run timing in Chinook salmon: toward the goal of understanding adaptation in natural populations.

Orlay W. Johnson; Genetics and life history of chum salmon in the southern portion of their range (California, Oregon, and Washington) -- impacts of climate and habitat changes

Ken Livak; High-throughput melt curve analysis for verification and genotyping of SNPs in 4 Alaska populations of chum salmon

Megan McPhee; Genetic and ecotypic variation within and among sockeye salmon (*Oncorhynchus nerka*) populations in the Kuskokwim River drainage of western Alaska.

Kathleen Neely; Feeding Ration and Reproductive Traits in Coho Salmon: Is Bigger Better?

Jeff Stephenson; Using the program Structure to define reporting units for Genetic Stock Identification in mixed collections.

Sharon VillageCenter; Factors influencing the relative fitness of hatchery and wild spring Chinook salmon in the Wenatchee River, Washington

Gary Winans; Population genetic structure and life history variability in *Oncorhynchus nerka* from the Snake River Basin

Abstracts

Organized alphabetically by presenting author

Coastwide Salmonid Genetics Meeting 2010: Genetic Adaptation of Salmonids

SNP markers under diversifying selection provide increased accuracy and precision in mixed stock analyses of sockeye salmon (*Oncorhynchus nerka*)

Michael W. Ackerman[1], Christopher Habicht[2], and Lisa W. Seeb[1]
[1]School of Aquatic and Fishery Sciences, University of Washington
[2]Department of Fish and Game, Gene Conservation Laboratory, Alaska

Presenter: Michael W. Ackerman, (206) 897-1871, mwa44@uw.edu

Oral Presentation, Student

Genetic markers are rapidly replacing traditional physical tags as the markers of choice for ascertaining the population of origin of individuals or mixtures of individuals of Pacific salmon. With increased use of genetic stock identification technologies has come a rapid evolution in the choice of genetic marker types involved. Allele frequencies of earlier marker types (i.e. microsatellites) were assumed to be determined primarily by stochastic processes (migration and drift). Conversely, SNP markers are increasingly being discovered in coding regions of the genome, and therefore, diversifying selection may influence their allele frequencies. Incorporating SNPs influenced by diversifying selection may provide a greater ability to differentiate Pacific salmon populations than by using neutral markers alone. While this makes non-neutral SNPs highly informative for studies of mixed stock analysis, the stability of allele frequencies must be evaluated, requiring more frequent sampling of reference populations. Here, we identify four SNP markers from a panel of 45 as candidates for diversifying selection in sockeye salmon populations from the Copper River and adjacent coastal drainages in Southcentral Alaska. We assess the ability of these four markers to improve the accuracy and precision of stock composition estimates using 41 reference populations (n = 6,224). The average F_{ST} was 0.089 for neutral loci and 0.262 for loci under diversifying selection. We also conducted leave-one-out tests to assess our ability to assign individuals to population of origin. Using the neutral marker panel, 42.9% and 69.7% of individuals assigned back to the correct population and reporting region, respectively. Adding the four markers under diversifying selection increased the correct assignment of individuals back to populations (47.7%) and reporting groups (79.6%). Our results indicate that markers under diversifying selection will increase our ability to track the homing and straying of individual fish and identify the composition of mixed populations.

Differences in burst swimming performance among 5 genetically differentiated clonal rainbow trout lines, varying in domestication levels

Kristy L. Bellinger and Patrick A. Carter
Washington State University

Presenter: Kristy L. Bellinger, (402)–960–1370, klbellin@gmail.com

Poster Presentation, Student

Purposeful and inadvertent selection on high growth rates and large body size in hatchery salmonids is common. However, theory predicts likely evolutionary trade-offs between other components of fitness with body size. My research project explores potential trade-offs between growth and burst swim performance among 5 genetically

differentiated clonal lines of rainbow trout (*Oncorhynchus mykiss*), varying in origin from AK to CA and varying in time under domestication. Individuals from each of the 5 lines were repeatedly measured for body size and swum over 15 weeks. The preliminary findings indicate significant differences in body mass and burst swimming performances between the semi-wild lines and the more domestication lines, with domesticated lines being larger but poor swimmers. Implications for the survival and reproduction of hatchery trout released into the wild are explored.

Pushing hatchery fish uphill: Diminished reproductive success complicates the use of supportive breeding in Snake River steelhead recovery

Ewann A. Berntson[1], Eric Ward[2], Richard W. Carmichael[3], Michael W. Flesher[3], and Paul Moran[2]
[1] Manchester Field Station, Northwest Fisheries Science Center, Port Orchard, U.S.A.
[2]Conservation Biology Division, Northwest Fisheries Science Center, Seattle, Washington U.S.A.
[3]Oregon Department of Fish and Wildlife, Eastern Oregon University, LaGrande, Oregon U.S.A.

Oral Presentation, Professional

Hatchery supplementation programs are designed to boost natural production; however, it can be difficult to evaluate the success of these programs. This study investigated relative reproductive success of steelhead spawning in nature by creating pedigrees for hatchery-reared and natural steelhead. We genotyped adult steelhead that returned to the weir and were released upstream to spawn naturally on Little Sheep Creek, as well as adult rainbow trout from upstream of the weir, and determined the parentage of sampled progeny at various life history stages, including returning adults from later years. Initial results from progeny at juvenile life stages suggested the relative reproductive success of hatchery fish was significantly less than that of their natural counterparts (30-60%). These supplementation hatchery fish are genetically similar to wild, yet they exhibit a substantial decrease in fitness based on parentage analysis that uses presumably neutral gene loci. We used generalized linear models to address the importance of various factors associated with reduced reproductive success, and found class (hatchery vs. wild), length, and the number of same-sex competitors to have the greatest effects on relative reproductive success. Differential survival of juveniles, and behavior of offspring and/or spawning adults may all contribute to diminished fitness in hatchery-reared salmon. Patterns of differential reproductive success are becoming clear, but understanding the processes that drive those patterns remain problematic. However, with the continued analysis of adult returns as they become available (we present here the initial five years of data from a ten-year study), we can close the life history loop in this system and take a step closer to understanding why natural origin *O. mykiss* typically out-perform their hatchery counterparts.

Genetic structure and adaptation of Columbia River Basin steelhead and rainbow trout

Scott M. Blankenship[1], Matt Campbell[2], Jon Hess[3], Maureen Hess[3], Todd Kassler[1], Christine Kozfkay[2], Andrew Matala[3], Paul Moran[4], Shawn Narum[3], Melanie Paquin[4], Maureen Small[1], Jeff Stephenson[3], and Ken Warheit[1]

[1]Washington Department Fish and Wildlife
[2]Idaho Department Fish and Game
[3]Columbia River Inter-Tribal Fish Commission
[4]NOAA – Northwest Fisheries Science Center

Presenter: Scott M. Blankenship, (360) 902-2783, scott.blankenship@dfw.wa.gov

Oral Presentation, Professional

Standardized microsatellite data (13 SPAN loci; see Stephenson et al. 2008) were compiled for 226 collections (N=15,658 individuals) of *Oncorhynchus mykiss* from throughout the Columbia and Snake River Basins by a collaboration of Pacific Northwest genetics laboratories. The genetic dataset was composed primarily of the anadromous life-history form of *O. mykiss*, although some collections were classified as non-anadromous (i.e., redband trout). Standard population genetic metrics were estimated for each collection. Allelic diversity was high, with an average unbiased gene diversity of 0.766 calculated over all collections. Observations of statistical associations among alleles within loci were infrequent, with single-locus genotype frequencies for 219 of 226 collections consistent with random mating of individuals. In contrast, statistical associations among alleles between different genetic loci (linkage disequilibrium) were commonly observed. The observed linkage disequilibrium may reflect that collections are composed of groups differentiated at the population, brood year, or family level. While genetic differentiation was observed at multiple hierarchical levels (i.e., region, river system, or tributary), the predominant genetic division was defined at the Cascade Mountains, with ―coastal” winter and summer steelhead present in the lower Columbia River and ―inland” summer steelhead present east of the divide. Within the geographic interior, the middle and upper Columbia River collections appeared a more complex conglomeration of genetic diversity than the Snake River collections. Genetic data were partitioned among three aggregates 1) lower Columbia, 2) middle/upper Columbia, 3) Snake River and the magnitude of genetic divergence relative to genetic diversity was analyzed (per locus) to test for evidence of selection and subsequent signals of adaptation. These data provide a foundation for future investigations on the molecular ecology and conservation genetics of *O. mykiss*.

Neurobiology and aggressive behavior in domesticated and wild rainbow trout.

Janet M.Campbell and Gary Thorgaard
Washington State University

Presenter: Janet M.Campbell, 509-335-1526, campbell9@wsu.edu

Poster Presentation, Student

We are investigating several neurobiological questions that will help elucidate mechanisms underlying changes in behavior associated with the domestication process in the rainbow trout (*Oncorhynchus mykiss*). The first question is: what is the relationship between brain morphology, aggressive behavior and domestication in rainbow trout? Six male rainbow trout clonal lines with varying degrees of domestication will be raised in a barren, hatchery style environment. Baseline measurements of 5 brain regions (i.e. telencephalon, olfactory bulb, optic

tectum, hypothalamus and cerebellum) will be taken using ellipsoid model with length, width and height as inputs. Initial results for three lines (one wild, two domesticated) are presented. A mirror aggression protocol will be used to identify aggression responses. Initial results for two lines (one wild, one domestic) are presented. Our hypotheses predict that the wilder lines will have larger relative brain measurements while the more-domesticated lines will show more aggression. Our second question is: how do the concentration of the major brain neurotransmitters (serotonin (5-HT), dopamine (DA), and norephinephrine (NE)) differ among clonal lines raised in different environments? We hypothesize that enriched environments will result in changes in all lines. Our third question will examine the genetic and epigenetic components that might be underlying any morphological or chemical brain changes seen. Quantitative Trait Loci (QTL) mapping of differences between lines and DNA methylation studies will be used to address this question.

Genetic stock identification of wild Snake River steelhead mixtures at Lower Granite Dam

Matthew R. Campbell[1], Christine C. Kozfkay[1], Timothy Copeland[1], William C. Schrader[1], and Shawn R. Narum[2]

[1]Idaho Department of Fish and Game
[2]Columbia River Inter-Tribal Fish Commission

Presenter: Matthew R. Campbell, 208-939-6713, matthew.campbell@idfg.idaho.gov

Oral Presentation, Professional

We identified the stock composition of adult wild steelhead (*Oncorhynchus mykiss*) passing Lower Granite Dam on the Snake River by sex, length, age, and run-timing. A total of 1,087 samples collected at Lower Granite Dam August 24 - November 25, 2008 were genotyped with 13 standardized steelhead microsatellite loci and a new modified Y-specific genetic assay that differentiates sex in *O. mykiss*. A genetic baseline of 66 populations was utilized to complete genetic stock identification (GSI) of unknown-origin samples from Lower Granite Dam. Large differences in reporting group (stock) contributions were observed for the run as a whole, with the Snake/Lower Clearwater reporting group having the largest single contribution (36.1%). Other large contributors included the Upper Clearwater reporting group (15.4%) and the Lower Salmon reporting group (13.9%). Smaller contributions came from the other 6 reporting groups: Imnaha (9.5%), Upper Salmon (9.2%), South Fork Clearwater (7.6%), Middle Fork Salmon (5.1%), South Fork Salmon (2.7%), and Elk Creek (0.5%). Significant differences in reporting group contributions were observed when samples were grouped by length, age, and run-timing. Of the samples analyzed, 339 were identified as males (34.3%) and 650 were identified as females (65.7%). There were no significant differences in reporting group contributions between males and females. This is the first study to use genetic stock identification mixture analyses to estimate individual stock contribution of Snake River steelhead over Lower Granite Dam. These results demonstrate that this approach should greatly assist managers with the task of assessing the viability of the Snake River steelhead ESU by providing information to estimate Viable Salmonid Population parameters involving abundance, population productivity, spatial structure and diversity.

Relative Genetic Diversity Estimates amongst Four Pacific Salmonids

Nathan Campbell and Shawn Narum
Columbia River Inter-Tribal Fish Commission

Presenter: Nathan Campbell, 208-837-9096 x1128, camn@critfc.org

Poster Presentation, Professional

Genetic diversity within a species is a reflection of its evolutionary past and ongoing mutation, drift, and adaptation. Species that occupy a diverse range of habitats and have adapted for generations under selective pressures will carry a genetic imprint of that adaptation within specific genes. Alternatively, genetic diversity may be reduced within a species due to historical bottlenecks and genetic drift. For this study, genetic diversity was estimated in four species of Pacific salmon (*Oncorhynchus mykiss*, *Oncorhynchus tshawytscha*, *Oncorhynchus kisuch*, and *Oncorhynchus nerka*) using 208-573 kilobases of DNA sequence data from thirty-two individuals per species. Individual samples were chosen to represent the major lineages of each species across their natural range. Results show the highest genetic diversity estimates for *O. mykiss* while the lowest were in *O. nerka*. Statistically significant differences were observed between the two species displaying the highest genetic diversity (*O. mykiss* and *O. tshawytscha*) and the two least diverse (*O. kisuch* and *O. nerka*). Loci displaying the highest genetic diversity within each species are listed as potentially influenced by directional selection.

Measuring “compactness” and “connectedness” a new method for quantifying genetic diversity within species

John Candy, Colin Wallace, and Terry Beacham
Molecular Genetics Lab, Pacific Biological Station, Department of Fisheries and Oceans, Nanaimo, British Columbia

Presenter: John Candy, 250-756-7224, john.candy@dfo-mpo.gc.ca

Oral Presentation, Professional

Under a number of national and international treaties Canada has committed to maintaining biodiversity. One approach to conserving fundamental units of biodiversity is to classify populations into genetically similar groups. A number of methods have been developed to determine these groups. Typically genetic data is used to estimate genetic distances (i.e. F_{st} metric) between populations for distance-based methods. Agglomerative or ―bottom-up” tree-building algorithms (i.e. neighbor-joining) display groupings as dendrograms. However, boundaries between genetic groups are often not very clear and rely on understanding of geographical and biological differences between populations before being drawn. A new divisive or ―top down” method of clustering considers all pairwise distances between populations at once. Populations are optimally clustered by minimizing intracluster distances using a mean-field annealing heuristic. Using Chinook salmon populations from the Fraser (n = 58) and West Coast of Vancouver Island (n = 19) as an example, quantitative measure of ―compactness” (mean intracluster distance) and ―connectedness” (mean intercluster distance) may help direct conservation efforts when managing for genetic diversity. The mean-field annealing software PORGS-MFA is available as free download from http://www.pac.dfo-mpo.gc.ca/sci/mgl/applications_e.htm

Antipredator behavior changes between wild-type and hatchery-derived rainbow trout clonal lines

Kris Christensen and Gary Thorgaard
Washington State University

Presenter: Kris Christensen, 509-335-1526, kchriste2006@wsu.edu

Poster Presentation, Student

Antipredator behavior was studied in order to understand how genetic alterations of behavior can occur and how they may affect survival rates. Selective regimes imposed by hatcheries likely cause genetic alterations in salmonids raised in them. These alterations have negative effects on survival once hatchery fish are released into wild environments and could potentially impact wild fish populations through introgression. A novel program for quantitative analysis of behavior was developed and used to analyze behavior of juveniles from two rainbow trout clonal lines. Preliminary data suggests that a hatchery-derived clonal line of rainbow trout moves more often in a new environment than a wild-type clonal line.

Temporal and geographic genetic divergence: Characterizing sockeye salmon populations in the Chignik watershed, Alaska using single nucleotide polymorphisms

Lisa Creelman[1], Lisa Seeb[1], Lorenz Hauser[1], William Templin[2], and Ryan Simmons[3]

[1]University of Washington
[2]Alaska Department of Fish and Game
[3]Forest and Chanel Metrics

Presenter: Lisa Creelman, 206-897-1871, lisakc@u.washington.edu

Oral Presentation, Student

The high fidelity of Pacific salmon to their natal spawning habitat results in isolated populations that are highly divergent, both genetically and phenotypically. Although both types of variation have been described extensively, the relative effects of demographic and selective forces in shaping molecular genetic variation are still relatively unknown. The Chignik watershed, Alaska supports highly productive sockeye salmon *(Oncorhynchus nerka)* populations which vary in return timing and spawning locations among breeding populations. Here, we describe the genetic structure of these using 45 single nucleotide polymorphisms in 19 collections of spawning adults. From these data we estimated within population statistics and among population divergence, detected loci in linkage disequilibrium and loci under selection, and tested the baseline for potential for use in mixed stock assessments. Results indicate significant genetic structure exists across sockeye salmon populations in the Chignik watershed on both spatial and temporal scales. This structuring can largely be explained by the evidence of selection at two non-neutral markers and differences in spawn timing between collections. Genetic structure determined at geographical and temporal levels provides a basis for application in the conservation of this resource and management of commercial and subsistence fisheries.

Selection of 96 SNPs to represent coastwide sockeye salmon genetic variation for mixed-stock analysis applications

Tyler H. Dann[1], Jim Jasper[1], Chris Habicht[1], Heather A. Hoyt[1], Heather L. Hildebrand [1], Jim E. Seeb[2], Lisa W. Seeb[2], and William D. Templin[1]

[1]Alaska Department of Fish and Game, Gene Conservation Laboratory
[2]International Program for Salmon Ecological Genetics, School of Aquatic and Fisheries Sciences, University of Washington

Presenter: Tyler H. Dann, (907) 267-2201, tyler.dann@alaska.gov

Oral presentation, Professional

Genetic markers potentially useful to determine stock compositions of salmonid fishery harvests are being discovered at increasingly rapid rates. Often, incorporating all available markers is inefficient for most laboratories so choosing the subset of markers that best meet the varied requirements of each project becomes increasingly important both to reduce costs within laboratories and to enable data sharing across laboratories. We screened 36 populations of sockeye salmon (*Oncorhynchus nerka*) from across the Pacific Rim for 123 single nucleotide polymorphism markers (SNPs) to choose the 96 that best meet our needs while incorporating the needs of other laboratories. Our methods for choosing the best subset of SNPs included measures of laboratory performance using a microfluidic chip, within population analyses of Hardy-Weinberg equilibrium and linkage, among population variation within and among regions, and tests for natural selection. In addition, we evaluated the contribution to successful mixed stock analysis within regions important to laboratories using sockeye salmon SNPs. The final set of 96 SNPs defines the most comprehensive SNP baseline available for sockeye salmon.

Genetic Population Structure of Olympic Peninsula Bull Trout and Implications for Elwha Dam Removal

Patrick DeHaan[1], Brice Adams[1], Sam Brenkman[2], and Pat Crain[2]

[1]U.S. Fish and Wildlife Service, Abernathy Fish Technology Center
[2]Olympic National Park

Presenter: Patrick DeHaan, 360-425-6072 x331, patrick_dehaan@fws.gov

Oral Presentation, Professional

The Olympic Peninsula of Washington represents one of the unique areas where bull trout inhabit freshwater and marine habitats. In the Elwha River, two dams constructed nearly a century ago limit anadromous bull trout to 7.9 km below Elwha dam and have also isolated fish above the dams. Removal of the two dams is scheduled for 2011, and represents one of the largest dam removal projects in the U.S. Following dam removal, large-scale disturbance is expected downstream of the dams as accumulated sediments erode from the reservoirs. Presently little information exists regarding the genetic relationship among Olympic Peninsula bull trout populations and among bull trout separated by the Elwha Dams. This information is critical for planning bull trout restoration activities following dam removal. Our objectives were to: 1) determine levels of genetic variation among Olympic Peninsula bull trout populations; 2) to determine the relationship among bull trout separated by the Elwha dams and; 3) determine the population of origin of bull trout collected below Elwha dam. Analysis of 16 microsatellite

markers revealed a high degree of variation among bull trout from six Olympic Peninsula rivers (global F_{ST} = 0.241). Using genetic assignment tests, we determined that unknown origin bull trout collected in the lower Elwha River originated above the dams and were not migrants from other nearby rivers. We observed no significant genetic variation among bull trout collections separated by the Elwha dams; however, fish collected above a presumed seasonal velocity barrier near the Elwha headwaters appear to be a distinct population. Our data indicate that bull trout do move downstream through the Elwha dams and suggest that Elwha bull trout will resume anadromy following dam removal. Results from this work will be useful for developing protection and restoration strategies for bull trout during future dam removal projects.

Anthropogenic influences on life history traits in Snake River fall Chinook

Anna Elz, Emma Timmins-Schiffman, Linda Park, and Robin Waples
NOAA, National Marine Fisheries Service, Northwest Fisheries Science Center

Presenter: Anna Elz, 206-860-3278, anna.elz@noaa.gov

Oral Presentation, Professional

Snake River fall Chinook salmon have experienced a wide range of anthropogenic influences to their ecosystem that could elicit an evolutionary response. Virtually all juveniles historically migrated to sea as sub-yearling smolts, but more recently an increasing proportion of the run overwinters in the reservoirs and migrate to sea as yearlings. Evidence suggests current conditions selectively favor survival of yearling smolts, which could drive evolution of a novel life history strategy for this population. This ongoing research evaluates the extent to which the observed changes in juvenile life history have a genetic basis. We have genotyped all adults spawned in 2007-2009 at the Nez Perce Tribal Hatchery and recorded their age at smolting based on scale analysis. In subsequent years, returning adults will be sampled and genetically matched to their parents to determine whether smolt age of parents predicts smolt age of their offspring. In the meantime, we have conducted parentage analysis on juvenile offspring sampled at the time of PIT-tagging and will report results of analyses that evaluate whether growth rate or juvenile migration patterns are related to the juvenile life history of parents.

Alternately, phenotypic plasticity could be responsible for the observed shift in juvenile life history traits, possibly related to a developmental threshold expressed in different environmental conditions. Conservation and management of these ESA listed fish would be aided by information regarding the processes underlying these changes.

The Sockeye Salmon Neo-Y Chromosome is a fusion between the Coho Y Chromosome and an Autosome

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Poster Presentation, Student

Previous work showed that the sex chromosomes are not conserved in Pacific salmon and trout. There is a conserved male-specific region, but it maps to different linkage groups and chromosomes in rainbow trout, chinook salmon, coho salmon, chum salmon and pink salmon (Brunelli et al., 2008; Phillips et al., 2007; See Figure 1). A difference in chromosome number between male and female sockeye salmon has been found in all populations examined with 2N=58 in females, and 2N=57 in males (Thorgaard, 1978). These results suggest that there has been a Y-autosome fusion giving rise to a X1X2Y sex determination system in sockeye salmon. Because the sister species of coho and chinook salmon have completely different sex chromosomes and sex linkage groups, it was assumed that the sex linkage group would be different in the more distantly related sockeye salmon. To confirm this, we mapped several sex-linked microsatellite loci from rainbow trout, chinook salmon and coho salmon in male and female progeny from several crosses of kokanee (land-locked sockeye salmon) from Lake Whatcom, Washington. Results showed that two microsatellite loci closely linked to sex in coho salmon are also closely linked to sex in the kokanee crosses. Using fluorescence in situ hybridization (FISH), we mapped a BAC clone containing a microsatellite locus sex linked in coho to a location near the centromere of an acrocentric (X1) and metacentric (neo Y) chromosome in male sockeye and to one pair of acrocentrics (X1X1) in females. The X2 linkage group is unknown.

Are Hatchery Effects Forever? - Use of Hatchery Stocks to Reintroduce Extirpated Coho Salmon to the Mid-Columbia and Snake River Basins

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Poster Presentation, Professional

The Columbia River treaty tribes are actively involved in efforts to reestablish coho salmon populations within their ceded areas in the Mid-Columbia and Snake River basins – the native populations having been extirpated from the river system above McNary Dam. The Yakama Nation has ongoing reintroduction programs in the Yakima, Wenatchee and Methow rivers, as has the Nez Perce Tribe in the Clearwater River. These programs were initiated by stocking juveniles from a lower Columbia River (LCR) hatchery stock, followed by annual supplementation with progressive integration of in-basin adult returns into the programs' broodstock. The presumption is that over generations, fish from the LCR hatchery stock will readapt to the natural environments to which they have been introduced. Is this presumption reasonable? Not only was the founder stock of out-of-basin origin, it had also been in a segregated hatchery program for over 15 generations and could be considered as being highly domesticated. Given the concerns associated with deleterious effects of hatchery rearing on the natural fitness potential of a salmon stock, has this LCR stock retained the genotypic and phenotypic capacity to reestablish a naturally productive population? Results from the tribal programs show that a portion of the reintroduced hatchery smolts not only return as mature adults to these rivers, but they also successfully spawn and their natural progeny are returning in generally increasing numbers. There have been dramatic increases in both annual escapement and in redd counts in each of these subbasins. Evidence for increased out-migration survival of smolts produced from in-basin broodstock versus LCR broodstock has also been observed. It would appear that accumulated domestication effects within the LCR hatchery stock are being reduced through appropriate juvenile acclimation and broodstock management strategies, and by natural selective forces, and that new populations of increasing natural productivity are indeed being developed.

Are coho salmon native to coastal California streams south of the Golden Gate?

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Oral Presentation, Professional

Coho salmon inhabit streams and rivers in coastal North America as far south as Santa Cruz County, California. Recently, a question has been raised about whether coho salmon in the southernmost part of the range, specifically those south of the Golden Gate (the entrance to San Francisco Bay), are native or are a —game fish” that exist there only because they were imported at the turn of the 20th century. This hypothesis is based primarily upon the lack of coho salmon bones found in excavations of native American middens from the area, historical documents which are interpreted as supporting absence of salmon prior to stocking, and purported habitat and ecological differences distinguishing these streams from those immediately to the north. These claims are the basis for an ESA petition by a large timberland owner to delist coho salmon in the area south of the entrance to San Francisco Bay. NMFS is currently evaluating the petition and will announce its findings by the end of 2010.

We present analyses of population genetic structure from two datasets of 18 microsatellite loci typed in ~8000 coho salmon, primarily in California. The first, and larger, dataset is from a compilation of samples that were collected over more than a decade and include data from different cohorts, broodyears and life stages. The second is from a —snapshot” of population structure in California coho salmon obtained by sampling the entire range of the species in a single year and for a single cohort. We show how these data clearly demonstrate that coho salmon at the southern extent of their range are part of the larger Central California Coast Coho Salmon ESU and how the genetic patterns correspond nicely with current management boundaries. We also discuss the conservation status of the species in California.

Adrift in a complex landscape: Sockeye salmon in Southeast Alaska

Sara Gilk[1], Jim Jasper[1], Tyler Dann[1], Charles Guthrie[2], Chris Habicht[1], and William Templin[1]

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Oral Presentation, Professional

Southeast Alaska is a complex landscape, consisting of both short coastal streams linked to lakes and large rivers that traverse the coastal mountain range. Sockeye salmon are found throughout this landscape, utilizing a variety of life history patterns in numerous small and large populations. A survey of 80 populations in Southeast Alaska and British Columbia at 45 single nucleotide polymorphism (SNP) markers reveals very high F_{ST} values among coastal populations (e.g. F_{ST}=0.163 in Southern Southeast Alaska) compared to large transboundary rivers in Alaska (e.g. F_{ST}=0.081 in the Taku and Stikine rivers). These populations tend to show little isolation by distance when compared to populations found in the larger rivers. The varied landscape in coastal Southeast Alaska has resulted in smaller, more isolated populations with large genetic differences due to genetic drift and subsequent isolation. This isolation and complex landscape promote differences in life history types due to different selection pressures. The high degree of variability seen in these populations is particularly useful for management of mixed stock fisheries such as those in the Northern Boundary Area.

Sockeye Salmon Genetic Stock Identification using Single Nucleotide Polymorphisms (SNPS) for the Southeast Alaska 2006 and 2007 District 101 Gillnet and District 104 Purse Seine Fisheries

Chuck Guthrie[1], Michele Masuda[1], Hanhvan Nguyen[1], Wei Cheng[1], Glen Oliver[2], Richard L. Wilmot[1], and Jeffrey R. Guyon[1]

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Poster Presentation, Professional

The purpose of this study was to genetically analyze axillary process samples from ~6000 sockeye salmon harvested in the 2006 & 2007 Alaskan Districts 101 gillnet and 104 purse seine sockeye fisheries to determine proportions of Canadian and U.S. fish. A SNP genetic baseline of 45 SNPs (41 markers as 3 groups of SNPs are linked) assayed in 84 sockeye populations from southeast Alaska and British Columbia was developed by the ADFG. The 84 populations were grouped into 14 regions. Genetic samples from approximately 380 fish were collected each statistical week of the District 101 and 104 fisheries. Stock proportions were estimated using a Bayesian mixture analysis. Analysis of the stock proportions of sockeye caught in Districts 101 and 104 over varying weeks shows interesting trends. The district 101 fishery predominantly harvests Nass Region fish early in the season, but over 10 weeks, this stock group decreases. These fish were replaced with Skeena and Hugh Smith fish. In the District 104 fishery, Skeena region stocks predominated throughout the entire fishery. Our results indicate that a majority of sockeye salmon caught in the ADF&G District 101 gillnet and 104 purse seine fisheries originate from Canadian stocks. Our results are in general agreement with the mark-recapture studies completed in the early 1980's, scale pattern analyses completed since 1982, and allozyme/freshwater age/parasitism analyses completed in the late 1980's. These correlations strongly suggest that all stock assessment methods have produced accurate and meaningful results in the management of these Northern Boundary fisheries.

12 new linked and sex-specific SNP markers, and associated TaqMan assays, for genotyping various subspecies of cutthroat trout, rainbow trout, and their hybrids

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Poster Presentation, Student

A suite of 12 species-specific single nucleotide polymorphism (SNP) markers was developed which distinguish rainbow trout ((RT) Oncorhycus mykiss) from four subspecies of cutthroat trout: Westslope cutthroat trout ((WCT) Oncorhynchus clarki lewisi), Yellowstone cutthroat trout ((YCT) Oncorhynchus clarki bouvieri), Coastal cutthroat trout ((CCT) Oncorhynchus clarki clarki), Lahontan cutthroat trout ((LCT) Oncorhynchus clarki henshawi), as well as their hybrids. TaqMan assays have been developed to genotype these SNPs. Several of the markers were linked and sex-specific assays were also developed. These included species-specific SNPs from the male specific OMY1 region in RT and mtDNA markers from the cytochrome oxidase 1 region used in barcoding. Hybrid trajectories can be examined with this suite of markers.

SNP loci correlated with run-timing in Chinook salmon from the Columbia River Basin

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Oral Presentation, Professional

Run-timing in Chinook salmon is a life-history trait that varies among populations throughout the Columbia River Basin and has a demonstrated genetic basis. This genetic basis has largely been observed through direct correlation of run-timing with allelic variation at functional genes involved in the molecular architecture of circadian rhythms. It is likely there are a number of other groups of genes under selection for this complex trait. In this study, we used 92 SNP markers linked to at least 75 different functional genes (including *OtsClock1a*) to test for correlations with run-timing. We obtained samples of Chinook salmon on a weekly basis as they passed a fixed point (Bonneville Dam) on the lower Columbia River mainstem during the majority of the migratory run from April to October. These fish represent unknown mixtures of the three major genetic lineages in the Columbia River Basin. We used genetic stock identification to assign individuals to their likely stock of origin. We then determined whether allelic variation at any SNP loci was correlated with the date of passage of fish within groups of individuals that had been assigned to a particular stock of origin. Significant correlations were examined for concordance across three sequential years of data from 2007-2009 (mixture n=2731, 3504, and 3022 respectively). We also examined whether any SNP loci shown to be correlated with date-of-passage (across Chinook salmon stocks) were similarly identified as candidates for positive selection using outlier methods. Future work will test candidate SNPs using run-timing information of fish of known-origin within particular Columbia River subbasins to help validate the potential role of these genetic linkage groups in this important life-history trait.

Evaluating adaptation of reintroduced spring-run Chinook salmon in the Hood River, Oregon

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Poster Presentation, Student

Supplementing declining salmonid populations with hatchery-reared individuals is an important fishery management tool used to increase abundance for conservation and/or harvest objectives. Integrating locally-derived natural origin individuals into supplementation broodstock can help offset negative effects on fitness such as inbreeding and domestication selection. However, when entire populations have been extirpated from historically occupied areas, no indigenous stock remains to initiate a re-introduction program, necessitating use of an out-of-basin stock. We are currently examining how a reintroduced stock in the Hood River, Oregon, may be adapting to its new environment, as reflected by differences in reproductive success between hatchery and natural origin individuals. Spring-run (stream-type) Chinook salmon were deemed extirpated from the Hood River basin following seven consecutive years (1965-1971) of essentially zero escapement to the fish ladder at Powerdale Dam. A re-introduction program was initiated in 1986 with annual releases of juveniles from Carson NFH, then beginning in 1993 with releases from the adjacent Deschutes River stock. To create a localized Hood River stock, an increasing proportion of in-basin adult returns have been incorporated into the hatchery broodstock. Here we report preliminary results from the study, involving genotyping of ~6,300 individuals across 16 years (1992-2007) using 15 microsatellite loci, followed by parentage analysis for hatchery and natural origin individuals spawning above Powerdale Dam. Our results showed that fish returning to the Hood River during this period were mixtures of the reintroduced stream-type genetic lineage as well as an unexpected proportion of stray fish from the Lower Columbia lineage. The stream-type and Lower Columbia lineages are evolutionarily distinct in the Columbia River Basin, and their sympatry in the Hood River affords a rare opportunity to study their relative reproductive success, in addition to the planned comparisons between the hatchery and natural origin fish derived from the Carson then Deschutes supplementation stocks.

Retention of historical genetic structure of sockeye salmon in the Wenatchee Basin despite homogenization by the Grand Coulee Fish Maintenance Project

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Oral Presentation, Professional

To compensate for fish runs affected by Grand Coulee Dam, the Grand Coulee Fish Maintenance Project (GCFMP) trapped all sockeye salmon migrating upstream at Rock Island Dam from 1939 through 1943 and planted the adults or their hatchery-reared offspring randomly into the Okanogan (Lake Osoyoos) and Wenatchee (Lake Wenatchee) river basins. The genetic effects of the subsequent mixing of sockeye stocks from these two basins together with those from the headwaters of the Columbia River in Canada by the GCFMP are poorly understood, as few samples are available from this era. Using 12 microsatellite loci, genetic analysis of archived scales from approximately 300 adults returning to the Wenatchee basin in 1943 confirms that the GCFMP was successful in homogenizing the populations of the Columbia River basin. Despite the homogenization, however, genetic differences are observed between the contemporary Okanagan and Wenatchee populations. We believe these differences are a result of selection for locally adapted individuals, as contemporary Wenatchee sockeye are genetically similar to their counterparts that inhabited Lake Wenatchee in the 1920's.

Genetics and life history of chum salmon in the southern portion of their range (California, Oregon, and Washington) -- impacts of climate and habitat changes

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Oral Presentation, Professional

Spawning populations of chum salmon historically extended as far south as the San Lorenzo River in California and 322 km upstream in the Sacramento River. In 1905-06 chum salmon juveniles were the most abundant salmon species in streams surveyed between the Sacramento and Columbia rivers. Today, these populations have greatly declined with the most southern established population being in mid-Oregon. Chum salmon in the Columbia River are now listed under the ESA as a threatened species. Little life history, genetic, or other biological information has been developed on these fish. This information is important as southern runs may represent remnants of historical populations with characteristics essential to the successful restoration of depleted present day populations. In cooperation with ODFW, WDFW, USFWS, we collected life history, genetic, and demographic data (such as presence or absence of spawning populations, age structure, and timing of migrations) from 2003 through 2009. Preliminary microsatellite genetic data indicate population structure among coastal populations is different from interior and Puget Sound runs. Run timing and some life history traits are also different between these southern populations and others. These runs may contain unique genotypes and adaptations of importance as increasingly rapid changes in climate and development expose salmonids to pressures beyond their ability to adapt, forcing further declines and even extinction.

Improving estimates of allele frequencies for genetic stock identification by using data from multiple populations at once

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Oral presentation, Professional

Genetic data are frequently used to estimate the composition of mixed stock fisheries. We show that a major source of error for genetic stock identification is estimation error for allele frequencies in contributing populations, and present a novel statistical method for improving estimates of allele frequencies by using samples from neighboring populations to improve allele frequency estimates. The method uses Dirichlet-multinomial local regression (DMLR) to "shrink" observed allele frequencies towards expectations obtained from allele frequencies of populations in a local cluster Although the DMLR is based on a somewhat complex state-space model parameter estimation under this method is much faster than other methods currently used and achieves substantial reduction in MSE. The usefulness of this for genetic stock identification will be discussed.

Genetic analysis of immature chum salmon from the eastern Bering Sea

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Poster Presentation, Professional

The increased incidental catch (bycatch) of chum salmon in the eastern Bering Sea groundfish fisheries during the last decade has sparked renewed interest in determining the origin of the bycatch, particularly in light of the simultaneous lower spawning runs in some western Alaska rivers that have triggered closures of subsistence and commercial fisheries in some years. Through an Arctic-Yukon-Kuskokwim Sustainable Salmon Initiative (AYKSSI) funded project, we are examining the spatial and temporal marine distribution of chum salmon populations in the eastern Bering Sea with genetic stock identification analyses of samples collected from the Bering Sea bycatch and from several U.S. and Russian Bering Aleutian Salmon International Survey (BASIS) research surveys between 1988 and 2005. The project includes a baseline development component of SNP and microsatellite markers that builds on previous work. Analysis of a temporally stratified subset of the 2005 samples indicated that overall, approximately half of the chum salmon were of Asian origin and most of the North American contribution was from western Alaska, British Columbia, and Washington State. The regional contributions shifted over time, with the western Alaska component more dominant in the early sampling period (mid-June to early July) and the Asian component more dominant in the later sampling period (mid-July to late September). Additional analyses will take into account the age of the fish, and comparisons of stock compositions will be made across four spatial areas within years, across time periods within years, and within areas across years.

Genetic stock identification of juvenile steelhead (*Oncorhynchus mykiss)* tissues collected from the stomachs of double-crested cormorants (*Phalacrocorax auritus*) in the Columbia River Basin

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Poster Presentation, Professional

A multi-agency study begun in the late 1990's has documented the substantial impact of fish-eating birds on the survival of juvenile salmonids (*Oncorhynchus* spp.) in the Columbia River Basin. Two main areas of study are East Sand Island near the mouth of the Columbia River and Foundation Island located near the confluence of the Snake and Columbia rivers. East Sand Island is inhabited by the largest colony of double-crested cormorants (*Phalacrocorax auritus*) in western North America (ca. 12,000 breeding pairs). The Foundation Island colony of double-crested cormorants is the largest on the mid-Columbia River, but is much smaller at ca. 300 breeding pairs. Double-crested cormorants prey on a broad diversity of fish species and consume millions of juvenile salmonids in the Columbia River Basin annually. Genomic DNA was isolated from frozen samples of salmonid tissues collected from the fore-guts (stomach and esophagus) of double-crested cormorants during the 2006 through 2009 nesting seasons. Species identification using the mitochondrial DNA fragment COIII/ND3 was successful for 332 of 400 samples collected from 64 cormorants. Steelhead (*O. mykiss)* was the most frequent salmonid in stomach samples (46%) followed by coho salmon (*O. kisutch*; 28%) and Chinook salmon (*O.*

tshawytscha; 26%). Four sockeye salmon (*O. nerka*) and two cutthroat trout (*O. clarki*) were also identified. We used 13 standardized SPAN microsatellite loci to examine the stock origins of fish identified as steelhead. Of 151 individuals, 144 were successfully genotyped at 8 or more loci. Genetic stock identification analysis indicated that our samples contained individuals from summer and winter runs and included fish from 6 different genetic stock groups. We identified *O. mykiss* from the Lower Columbia River distinct population segments (DPS), as well as from the Upper Columbia River and Snake River Basin DPSs, suggesting that predation by double-crested cormorants potentially impacts *O. mykiss* populations from throughout the Columbia River Basin.

Molecular departures from neutrality related to run timing in Chinook salmon: toward the goal of understanding adaptation in natural populations

Eric LaHood
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Poster Presentation, Professional

In highly migratory anadromous species, selection and local adaptation can vary in space and time. One important temporal adaptation for salmonids is their migration timing, both the age of juvenile migration to the ocean and the return time of adults to natal breeding sites. Chinook salmon (*Oncorhynchus tshawytscha*) provide an excellent study system to explore the genetic basis for migratory adaptation because this species demonstrates high intra-annual variability in spawning time, with individuals belonging to one of several seasonal runs that represent both similar and highly diverged lineages. Recent studies suggest that Expressed Sequence Tag (EST)-linked micro satellite loci can provide potentially meaningful information, not only to augment genetic stock identification and mixture allocation, but also to explore the genetic basis of adaptive variation. In this study we surveyed 15 GAPS reporting-group populations at 13 anonymous and 22 EST-linked micro satellite loci, and used the software program LOSITAN, which provides an estimate of Fest based on the Method of Beaumont and Nichols (1996), to ascertain putative outlier loci that might indicate departures from neutral expectation. We sought to capture differences between life-history types, which included a genetic and geographic breadth that spans the interior Fraser, Columbia, and Sacramento River basins. We explore the meaning of these departures in the context of population structure and demography to more fully characterize them in natural populations. This study aims to provide the molecular and analytical foundation that might better elucidate both the patterns and the processes of molecular and phenotypic adaptation in this culturally important species.

High-throughput melt curve analysis for verification and genotyping of SNPs in 4 Alaska populations of chum salmon

Ken Livak, Lisa Seeb, Jim Seeb, Jun Wang, Krishna Datta, Carita Pascal

Presenter: Ken Livak

Poster Presentation, Professional

Next generation sequencing has dramatically increased the availability of SNPs for studies of population genetics. Cost effective laboratory procedures at sufficient throughput for SNP verification and genotyping have not kept pace. At the same time, the use of SNPs for tackling very difficult population problems has become very appealing for fish management and conservation. North Pacific Anadromous Fish Commission nations are currently faced with the daunting task of identifying populations of chum salmon as they migrate through a changing and patchy marine environment. We describe newly developed melt curve analyses used to rapidly and inexpensively verify putative SNPs identified through next generation sequencing. Using the power of ascertainment bias, we focus these efforts on four major and very closely related sets of populations inhabiting the eastern Bering Sea: Norton Sound, Yukon River, Kuskokwim River, and Bristol Bay. For initial verification, heteroduplex analysis of PCR products is performed to estimate the minor allele frequency for putative SNPs in each of the four populations using 96 fish from each population. This is done to eliminate putative SNPs that either failed PCR or have a low minor allele frequency. For the reduced number of SNPs, genotyping is performed on the same set of individuals using a T_m shift method that combines allele-specific PCR and melt curve analysis. This eliminates putative SNPs derived from sequencing results of homeologous loci. The result is a set of verified SNPs that can now be tested across all chum populations to assemble a robust set of identification SNPs.

Using SNPs to Compare and Resolve Adaptive and Demographic Divergence Among Chinook Salmon in the Columbia River Basin

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Oral Presentation, Professional

Chinook salmon (*Oncorhynchus tshawytscha*) in the Columbia River Basin (CRB) include three primary lineages; one form occupying the lower Columbia River, and two sympatric interior forms (ocean-type and stream-type) with distinct biological attributes. Significant divergence between lineages and differentiation within the stream-type lineage has been described in depth based on neutral microsatellite loci (uSAT). We genotyped 52 Chinook salmon populations sampled among lineages, ranging in location from the upper Salmon River to near the Columbia River estuary, using a panel of 96 single nucleotide polymorphism (SNP) assays. Our goal is to better understand processes shaping population structure by investigating the basis of genetic variation beyond the limit of inference possible with neutral marker data. Because SNPs occur throughout the genome, including regions within coding regions or functional genes, they retain an advantage as candidate markers for detecting positive selection; a feature providing an added evolutionary perspective based on local adaptation. Differences in the distribution of SNP allele frequencies across landscapes may help delineate patterns of local and regional adaptation that influence genetic differentiation. In our analyses, population structure of Chinook salmon throughout the CRB was generally concordant between uSAT and SNPs. Using regression analysis and outlier methods we have identified at least 18, 3 and 4 candidate SNP loci for positive selection among stream-type, ocean-type, and lower-type Chinook salmon respectively. Candidate SNP allele frequencies appear most highly correlated with temperature and elevation among stream-type. We did not observe a significant association of isolation by distance for any lineage with our SNP panel, however there was a significant relationship between F_{st} and mean annual temperature. Associations between candidate loci and environment remain less clear for the less divergent ocean-type and lower-type Chinook populations. In all cases, the apparent adaptive variation complemented the results of demographic genetic structure but with higher resolution of population differentiation.

Barriers to movement and genetic population structure of westslope cutthroat trout (*Oncorhynchus clarkii lewisi*) in the Salmon River Basin, Idaho

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Oral Presentation, Student

Barriers to movement in aquatic ecosystems can impede gene flow or connectivity between fish populations leading to changes in gene frequencies between populations. Although historic isolation of fish populations was caused by natural geologic events such as land up-lifting leading to canyons, mountains, and islands; more recent human activities (roads, dams, urban and agricultural expansion) are rapidly fragmenting native fish populations. In this study, we assess genetic differentiation and diversity of westslope cutthroat trout (*Oncorhynchus clarkii lewisi*) populations to examine the effects of habitat fragmentation isolated by natural and artificial barriers. Our study was conducted in the Salmon River Basin of central Idaho within the traditional-use area of the Shoshone-Bannock Tribes. Currently, we are genotyping individual fish and our results should be mostly complete to verify effects of natural and artificial barriers on the genetic population structure of cutthroat trout. Also, we are assessing the differentiation and diversity for future management and conservation of westslope cutthroat trout populations in the Salmon River Basin.

Genetic stock identification of chum salmon in the North Pacific Ocean and Bering Sea using microsatellites

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Oral Presentation, Professional

Understanding the stock and age-specific distributions of chum salmon during ocean residence is essential to both the conservation and management of this important resource. Using 11 microsatellites and a publicly available genetic baseline of 381 populations on 1,963 mixture samples collected onboard international research surveys during the fall of 2006 and 2007 and the winter of 2009, we found spatial and temporal differences in the age and origin of chum salmon in the North Pacific Ocean and Eastern Bering Sea. Japanese and Russian stocks dominated mixtures in the northernmost surveys of the Bering Sea in 2006 and 2007 and in all surveys of the North Pacific Ocean in 2009. In contrast, the stock composition of mixtures from the southern study area of the Bering Sea differed significantly between years and ocean habitats, with Japanese and Russian stocks predominate in the continental slope surveys of 2006 and shelf surveys of 2007, while North American stocks prevailed in the continental slope surveys of 2007. These results contribute to the growing knowledge of how changing climate and ocean conditions affect salmon ecology. Further, by relating these findings to the spatial and temporal patterns of chum salmon taken as bycatch in the walleye pollock fishery, we can advance our understanding of bycatch stock composition, and use these data to improve fisheries management.

Influences of spawning habitat and geography: genetic structure and juvenile migration timing of sockeye salmon in the Wood River Lakes, Alaska

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Oral Presentation, Student

The strict homing of sockeye salmon results in reproductively isolated populations that may spawn in close proximity and share common rearing habitat. High spawning fidelity enables these populations to adapt to local conditions, resulting in a wide range of life history characteristics and genetic variation within a lake or drainage. Differences in adult traits such as body size, age at maturity, and timing of spawning are directly affected by the spawning habitat and vary greatly between populations. Juvenile characteristics, such as body size and emigration timing, likely also exhibit local adaptation. The Wood River System in southwestern Alaska provides a pristine, well-studied system in which to examine the connections between ecology and genetics. Adult sockeye salmon spawn in lake beaches, rivers and small tributaries throughout this watershed, and juveniles from all populations rear together in five nursery lakes. We use forty-five single nucleotide polymorphisms to examine the genetic structure of thirty populations of sockeye salmon from these three ecotypes and investigate the timing and duration of smolt migration from populations throughout the watershed using mixed stock analysis.

Candidate loci fail to find differentiation between sympatric steelhead and rainbow trout *Oncorhynchus mykiss*

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Presenter: Megan V. McPhee, 907-796-5464, mvmcphee@alaska.edu

Oral Presentation, Professional

Although anadromous (―steelhead”) and nonanadromous (―rainbow trout”) forms of *Oncorhynchus mykiss* historically were viewed as distinct groups, genetic data suggests that partial anadromy, where both types arise from a single interbreeding population, is typical of this species. However, the genetic basis for life-history determination in *O. mykiss* is not well understood. We used three classes of loci to test for allele frequency differences between sympatric steelhead and rainbow trout: 1) microsatellites linked to genes involved in growth and maturation; 2) microsatellites potentially linked to loci under sexually antagonistic selection; and 3) microsatellites linked to a QTL for smolting in out-crossed lines. We were unable to detect differentiation between sympatric steelhead and rainbow trout with these three classes of markers, adding further support for the importance of phenotypic plasticity in the origin of life-history types within, if not necessarily among, *O. mykiss* populations.

Genetic and ecotypic variation within and among sockeye salmon (*Oncorhynchus nerka*) populations in the Kuskokwim River drainage of western Alaska

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Poster Presentation, Professional

Ecotypic variation is thought to be an essential component of the success and resilience of the Bristol Bay sockeye salmon fishery, where ecotypically distinct populations respond differently to environmental variation, leading to enhanced stability at the regional scale via the portfolio effect. This ―biocomplexity” arises in part from the variety of discrete spawning biotopes found within the Bristol Bay region, mostly associated with large and stable glacial-origin lake systems. The Kuskokwim drainage, on the other hand, is dominated by dynamic floodplain systems, but supports an increasingly important sockeye salmon fishery. We sought to quantify genetic and ecotypic (morphological, life-history) variation within and among sockeye salmon populations in two important sockeye producing regions of the Kuskokwim: the Holitna River and Telaquana Lake. As expected, body depth variation was associated with spawning biotope (creek, lake, and river). However, using geometric morphometrics, we also detected morphological variation that was correlated with neutral population genetic structure regardless of spawning biotope. Genetic differentiation was greater among spawning aggregations in Telaquana Lake than in the Holitna River, and we found substantial differentiation between outlet and inlet/lake spawners in Telaquana Lake. We discuss our findings in the context of sockeye salmon resilience at 1) contemporary/human time scales; and 2) long-term/geologic time scales.

Studies of connectivity and life history adaptation in West Coast Chinook salmon populations: Size matters

Paul Moran and the GAPS Consortium
NOAA-Fisheries
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Oral presentation, Professional

Life history variation in Chinook salmon has undoubtedly been shaped by powerful forces in earth history, including repeated formation and subsidence of continental and grounded marine ice sheets, sea level change and isostatic rebound, volcanism, and tectonics. Moreover, human activities have further altered habitats and patterns of genetic connectivity. Despite a great deal of study of population genetics and life history variation—indeed, more than for any other Pacific salmon species—there remains a great deal of confusion over key aspects of juvenile and adults life history variation in Chinook salmon. Specifically, there is a persistent notion that genetic relationships in Chinook salmon are characterized by two evolutionary lineages that exhibit different ancestral and predominant life history types (so called ―ocean-type” and ―stream-type”). It is thought that these lineages diverged in isolated refugia during the last glacial maximum. The goal of this study was to revisit this and other questions through examination of a large, coast-wide, shared, microsatellite data set. River basins and sub-basins were strongly diverged genetically, but relationships among those regions were poorly resolved—essentially a star phylogeny. We found an isolation-by-distance pattern between northern and southern ―lineages” (clusters) but no deep bifurcation. Only in the interior Columbia River basin do life history types show the distinctiveness that is often attributed to the species in general. The elucidation of these relationships is intended to better explain the processes of Chinook life history evolution and ultimately to provide insight into effective conservation and restoration of critically depressed and imperiled populations.

Candidate genetic markers associated with anadromy in *Oncorhynchus mykiss* of the Klickitat River

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Oral Presentation, Professional

Both environmental and genetic factors influence anadromy in *O. mykiss*, but genetic mechanisms that contribute to migratory selection are not well understood. In this study, we used a limited genome scan approach to identify candidate genetic markers associated with anadromy in 10 populations of *O. mykiss* from the Klickitat River, Washington USA. From an initial panel of 96 single nucleotide polymorphism (SNP) markers, we identified 3 SNPs that were significantly associated with anadromy ($p < 0.01$) after accounting for underlying population structure and selective environmental conditions. Univariate logistic regression of allele frequencies and residency/anadromy were also significant ($p < 0.05$) and thus three SNPs were considered candidate markers associated with anadromy (Omy_IL6-320, Omy_LDHB-2_i6, and Omy_ndk-152). A multivariate logistic model was developed from allele frequencies of these three markers to predict the potential of anadromy in natural populations. This model was applied to eight additional populations of *O. mykiss* to evaluate the utility of this model. Results of this study indicate that these markers are strong candidates associated with anadromy in *O. mykiss* of the Klickitat River, but further testing is needed to evaluate this association across a broader distribution of this species' range. Common garden experiments may also help clarify the association of genotype of these candidate markers with smoltification phenotypes of individual fish.

Feeding Ration and Reproductive Traits in Coho Salmon: Is Bigger Better?

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Poster Presentation, Professional

Aquaculture research relating to feeding and nutrient allocation has primarily focused on the maximization of body growth without regard to the associated effects on reproductive traits. In this study, we assessed the effects of different feeding rates on reproductive traits in coho salmon (Oncorhynchus kisutch). Ration treatments were established to subject fish to different energetic levels during oocyte proliferation (year one) and oocyte maturation (year two). Fish were fed at either a restricted ration or excess ration (twice the restricted ration amount) during each time interval. Overall, the fish fed the excess ration during both treatment periods grew the fastest, had the highest fecundity and the largest eggs; however, the group fed a restricted ration during the first year and to excess during the second year had the highest egg yield (number of eggs per unit body weight), although this difference was not statistically significant. Egg yield appeared to be highly conserved across all of the ration treatments. Family effects were significant for nearly all of the traits measured. The relative performance of families within each ration treatment was not affected by family by ration (G x E) interactions. Although ration modification did produce significant changes in reproductive trait expression, especially fecundity, family effects had a much stronger influence than did ration on egg yield (eggs per gram female body weight) and egg weight. Estimates of broad-sense heritability for all reproductive traits were significantly different from zero, a somewhat surprising result given the 20 generations of selection that this closed population has been subjected to. These results suggest that reproductive traits are under substantial genetic influence and are likely to respond to selective breeding.

Clock Polymorphism in Pacific Salmon: Evidence for Variable Selection along a Latitudinal Gradient

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Oral presentation, Professional

Seasonal timing of life history events is often under strong natural selection. The *Clock* gene is a central component of an endogenous circadian clock that senses changes in photoperiod (day length) and mediates seasonal behaviors. Among Pacific salmonids (*Oncorhynchus* spp.), seasonal timing of migration and breeding is influenced by photoperiod. A previous study of 42 Chinook salmon (*O. tshawytscha*) populations ranging from Alaska to California found evidence for a latitudinal cline in the *OtsClock1b* gene based on length polymorphisms in the polyglutamine domain (PolyQ). These results contrast sharply with those obtained for presumed selectively neutral microsatellite markers suggesting that the observed variation may be maintained by selection and reflect an adaptation to ecological factors correlated with latitude, such as the seasonally changing day length. To expand on this study, we tested whether duplicated *Clock* genes contribute to population differences in reproductive timing. Specifically, we examined geographic variation along a similar latitudinal gradient in the PolyQ domain of *OtsClock1a* and *OtsClock1b* among 53 populations of three species: chum (O. *keta*), coho (*O. kisutch*), and pink salmon (*O. gorbuscha*). We found evidence for variable selection on *OtsClock1b* that corresponds to latitudinal variation in reproductive timing among these species. We then evaluated the contribution of day length and a freshwater migration index to *OtsClock1b* PolyQ domain variation using regression trees and found that day length on the date of peak spawning explains much of the variation in *OtsClock1b* allele frequency among chum and Chinook but not coho and pink salmon populations. Our findings suggest that *OtsClock1b* mediates seasonal adaptation and influences geographic variation in reproductive timing in some of these highly migratory species.

Ecological transcriptomics in muscle tissue of lake-type and riverine sockeye salmon (*Oncorhynchus nerka*)

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Oral Presentation, Professional

Many genomes are now sequenced with tentative functions assigned to many of the individual genes. Model organisms in laboratory settings are the basis for most of these assignments and the ecological context of gene function is lacking. Here we provide an ecological context to expressed genes of sockeye salmon muscle tissue. We sampled natural juvenile sockeye salmon populations in distinct habitats (rivers and lakes) that characterize a major life-history division (riverine and lake-type). Based on morphology, feeding strategy and predation, we predicted genes related to burst swimming would be favored in riverine sockeye and genes related to aerobic metabolism would be favored in lake-type sockeye. We compared mRNA abundance with the cGRASP 16k

microarray chip. We found 141 genes significantly differentially expressed after correcting for multiple tests. Overall, these genes agreed with our predictions. In addition, we performed a gene ontology (GO) enrichment analysis with a larger set of differentially expressed genes and found the ―biosynthesis” category enriched for the riverine population and the ―metabolism” category enriched for the lake-type population. We provide a starting point for more extensive, targeted studies for the ecological function of genes in sockeye salmon.

Population Genomics of Coastal California Resident and Anadromous *Oncorhynchus mykiss* in Scott Creek, CA

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Oral Presentation, Professional

In central California, variation in life history patterns in a key characteristic of steelhead biology. Anadromous forms occupy a range of habitats from large river systems to small coastal streams. Resident populations above barrier falls, whether natural or stocked, can add an additional dimension to the variation present within a single drainage, and both forms can co-exist, even within small streams. Genetic data from Scott Creek *O. mykiss* has shown that resident rainbow trout above Big Creek Falls are derived from the anadromous population present in Scott Creek and that above-barrier trout are moving over Big Creek Falls into the population below. With the large number of salmonid microsatellite markers available and the rapid development of linkage maps, the effects of natural selection on specific regions of the genome can be identified. Natural selection typically affects a specific locus, but regions of the genome linked to genes affected by natural selection can be identified by identifying marker loci with greater differentiation between populations than expected by purely neutral genomic processes. We are using a combination of hatchery rearing experiments and genome-wide SNP and microsatellite data to identify genes under differential selection and determine the developmental differentiation and extent of hybridization between resident and anadromous fish below the falls. Identification of regions in the genome that are potential areas for selection will provide valuable information about the genetic basis of selection in novel habitats.

The phylogeography of chum salmon from the Alaska Peninsula, the contact zone between distinct genetic lineages

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Oral Presentation, Student

Environmental conditions during the Last Glacial Maximum 21 kyr ago had a large impact on the distribution of species in the northern latitudes. This period was characterized by colder global temperatures, lower sea levels, and the presence of massive ice sheets. The fossil record suggests that many species experienced latitudinal and altitudinal range shifts, which led to considerable demographic changes and provided opportunities for adaptation to occur. During this period, salmonid populations in the North Pacific Ocean and Bering Sea were separated from each other by the Cordilleran Ice Sheets. Previous studies suggest that as the glaciers receded, salmon from the north and south repopulated the Alaska Peninsula. The region now contains a hybrid zone between two genetically distinct lineages of chum salmon. The study of differential patterns of gene flow among loci is one of the exciting topics that can be addressed in hybrid zones using multilocus data, and these types of studies can provide insight into the dynamics of genes under selection in natural populations. Here, we describe the dynamics of neutral and non-neutral loci across a hybrid zone for chum salmon along the North Alaskan Peninsula.

Assignment of Chinook salmon (*Oncorhynchus tshawytscha*) linkage groups to chromosomes

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Oral Presentation, Professional

We have assigned the Chinook salmon (*Oncorhynchus tshawytscha*) genetic linkage groups to chromosomes and correlated the resulting chromosome map with the rainbow trout (*O. mykiss*) chromosome map. This has been done by mapping microsatellite loci from the rainbow trout genetic map in a chinook cross and hybridizing BAC clones containing markers on the genetic map to chinook chromosomes. Although theoretically a few centric fissions could convert the karyotype of rainbow trout (2N=58-60) into that of Chinook salmon (2N=68), our data suggest that whole chromosome arms are conserved but they underwent multiple centric fissions and subsequent new centric fusions to form the current Chinook salmon karyotype. Only one third of the chromosomes have been conserved between the two species. In previous work we correlated the rainbow trout chromosome map with that of Atlantic salmon (*Salmo salar*), so our research will allow investigators to better utilize the rainbow trout and Atlantic salmon genomic resources for Chinook salmon.

Genetic Population Structure of Rio Grande Cutthroat Trout

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Oral presentation, Professional.

The cutthroat trout (*Oncorhynchus clarkii*) of western North America have been heavily impacted by human activity over the past two centuries, causing many subspecies to decline to a small fraction of their historic range. I present results of a study using microsatellites to investigate the population genetic structure of Rio Grande cutthroat trout (*O. c. virginalis*) in New Mexico. Several populations contained substantial amounts of genetic material from other taxa, and others appeared to have originated via anthropogenic transfer. Native populations exhibited high inter-population differentiation, which may be attributed in part to recent severe fragmentation. However, a partial signature of long-term evolutionary independence between drainages persisted. Finally, I discuss current work developing novel SNP markers for use in addressing multiple management questions for all *O. clarkii* subspecies.

Patterns of nearshore juvenile migration of sockeye salmon in the eastern Bering Sea

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Oral Presentation, Professional

We estimate patterns of nearshore migration of outmigrating (age .1) Bristol Bay sockeye salmon in the eastern Bering Sea. Over 3,000 juveniles were collected during the late summers of 2005-2007 as part of the Bering-Aleutian Salmon International Survey (BASIS) and tested with a regional genetic baseline of 45 single nucleotide polymorphism (SNP) markers. Population specific and westward migrations from natal rivers were evident. A southern route was followed by Ugashik and Egegik fish, and respective routes to the north were predominated by Naknek and Kvichak, Wood River and Igushik, and finally Kuskokwim Bay populations. These patterns are consistent with post-Pleistocene adaptations that maximize early marine survival and growth. As monitoring continues, these juvenile surveys promise to refine predictions of the magnitude of adult returns to their respective rivers of origin, and thereby assist in the management of this valuable resource.

Does Lower Crab Creek in the Eastern WA desert have a native population of Chinook salmon?

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Oral presentation, Professional

Chinook salmon juveniles and spawner carcasses collected over three years in Lower Crab Cr., WA, were genetically characterized with the GAPS Chinook salmon microsatellite DNA locus suite and compared to proximate and distant Chinook salmon collections from throughout the greater Columbia basin. Lower Crab Cr. Chinook salmon collections were temporally stable and significantly different from other Chinook salmon collections. Lower Crab Cr. Chinook salmon individuals assigned with high confidence back to the Lower Crab Cr. collection in a baseline that included Chinook salmon collections from the greater Columbia basin. The data suggests that there is a genetically distinct, native population of Chinook salmon in the Lower Crab Cr. This population is surprising since the groundwater-fed tributary traverses desert habitat and in several portions the water quality is poor, summer water temperatures are lethal and stream habitat is degraded. The creek was thus thought to be unsuitable for Chinook salmon.

Persistent reproductive isolation between sympatric lineages of fall Chinook salmon in White Salmon River, Washington

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Oral presentation, Professional

Populations of fall Chinook salmon in the Columbia River are divided among two Evolutionary Significant Units: ESA-listed Lower Columbia River fall Chinook salmon or ―Tules" in the lower portion of the river, and Mid-Columbia River Upriver Brights (URBs) in the upper portion of the river. The two lineages migrate together through portions of the Lower Columbia River, but spawn allopatrically. Broad scale analyses of allozyme and microsatellite variation have indicated that these two lineages are nearest neighbors to one another. Little White Salmon National Fish Hatchery (NFH) has been releasing URB salmon adjacent to what was historically exclusively Tule spawning habitat in the White Salmon River for approximately 22 years. Hatchery and wild Tule and URB salmon now spawn in sympatry in the adjacent White Salmon River, and a recent evaluation of the URB program at Little White Salmon NFH identified introgression among the lineages as a Genetic Risk posed by this program. In order to assess the extent of introgression, we applied thirteen microsatellite markers to smolts migrating out of White Salmon River for three consecutive years. Comparison of smolts to a baseline of Columbia River fish revealed that smolts leaving White Salmon River in March – early May strongly resembled Tule populations, while those leaving in late May-June strongly resembled URB populations. Model based assignment to parental and hybrid classes identified the early and late emigrating groups as parental taxa, and further identified between 4 and 15 percent of individuals as hybrids between the two lineages. Following identification and removal of full sibships, divergence between the two lineages in White Salmon River was comparable to that between these lineages in other parts of their natural ranges. We speculate that slight differences in peak spawning time and in migratory patterns contribute to persistent reproductive isolation between the two lineages.

Using the program Structure to define reporting units for Genetic Stock Identification in mixed collections

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Poster Presentation, Professional

We reviewed the use of the program Structure to define reporting units for Genetic Stock Identification in Shitike Creek, a tributary to the Deschutes River. Shitike Creek is known to have migratory runs of both resident rainbow trout and anadromous steelhead populations. To eliminate admixture from the baseline population, Structure was first tested to determine its ability to separate the two populations. These results were then used to create two reporting units to determine if assignment success was improved.

Estimating run timing in the presence of small samples: Reverend Bayes saves the day

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Oral presentation, Professional

Pacific salmon returning to their natal streams to spawn often exhibit differences in the timing of their return. Fishery managers often take advantage of this run timing to direct human activities affecting these fish to meet resource management objectives. In situations where genetic distinctions exist between early- and late-returning fish, genetic stock identification of periodic samples can be used to estimate characteristics of the run timing (e.g. transition date between runs). However, sufficient samples are not always available to estimate separate periodic stock proportions with adequate accuracy and precision. Hierarchical Bayesian methods can be used to analyze all the available samples simultaneously which improves the precision of each of the periodic estimates by allowing adjacent samples to influence the estimation for each individual sample. In addition to improving the periodic estimates, the method also estimates the distribution of curves which describe the run-timing behavior of the returning salmon. We present application of this method to estimate the timing of early and late runs of Chinook salmon into the Kenai River, Alaska based on weekly samples from the sport fishery, 2003-2009. Samples from this fishery are difficult to obtain and usually fewer than 50 are available for a weekly estimate. By using all the samples available across weeks without pooling them into larger groups, the information used for each weekly estimate was increased with a corresponding improvement in accuracy and precision.

Genetic monitoring reveals genetic stability within and among Chinook salmon populations in the Salmon River, Idaho

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Oral Presentation, Professional

Identifying and understanding temporal genetic changes within fish populations has important implications for their management, especially those with conservation concerns. Such changes are often the result of genetic drift, which can be exacerbated when the size of a population decreases. Using molecular genetics techniques, we monitored Chinook salmon populations in the Salmon River, Idaho, to determine how the genetic characteristics within and among the populations have changed over time. We found little evidence of change in the population's levels of heterozygosity or allelic richness over a 3-4 generation time span, most likely because the populations all maintained a stable and large enough effective population size. We did find that populations that had not been supplemented with hatchery-reared fish had a wider range of genetic variability over time than those that had been supplemented. The genetic structure among the populations also did not change appreciably over time. Temporal variation within each non-supplemented population was less than the amount of variation among populations. In contrast, the supplemented and hatchery populations within a sub-basin showed genetic similarity to each other, seemingly due to the extensive use of native fish for hatchery brood stocks, and minimal influence from out of basin stock transfers. The lack of a detectable decline in these population's levels of genetic diversity and effective size is encouraging, given their status as a threatened species under the Endangered Species Act.

Factors influencing the relative fitness of hatchery and wild spring Chinook salmon in the Wenatchee River, Washington

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Poster Presentation, Professional

Understanding the relative fitness of naturally spawning hatchery fish and the causes of any fitness differences compared to wild fish has become an important issue in the management and conservation of salmonids throughout their range. We used a DNA-based parentage analysis to measure the relative reproductive success of hatchery- and natural-origin spring Chinook salmon in the natural environment. Size and age had a large influence on male fitness, with larger and older males producing more offspring than smaller or younger individuals. Size had a significant effect on female fitness, but the effect was smaller than the effect of size on male fitness. For both sexes, run time had a smaller but still significant effect on fitness, with earlier returning fish favored. Spawning location within the river had a significant effect on fitness for both males and females. On average hatchery-origin fish of both sexes produced about half the juvenile progeny per parent when spawning naturally than did natural origin fish. Hatchery fish tended to be younger and return to lower areas of the watershed than wild fish, and these factors explained some of their lower fitness compared to wild fish.

Population genetic structure and life history variability in *Oncorhynchus nerka* from the Snake River Basin

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Poster Presentation, Professional

We used variation at 64 allozyme loci to examine genetic relationships among 32 samples of sockeye salmon and kokanee (/Oncorhynchus nerka/) from the Snake River basin. Average heterozygosities were relatively low (0.006-0.041), but genetic differentiation among populations was pronounced: the value of Wright's /F_ST / (0.244) is higher than has been reported in any other study of Pacific salmon.
A detailed examination of /O. nerka/ from lakes in the Sawtooth Valley of Idaho was undertaken to help guide recovery planning for the endangered Redfish Lake population and to help resolve relationships between resident and anadromous forms. In Redfish Lake, sockeye salmon were genetically distinct from Fishhook Creek kokanee but similar to a small population of "residual" sockeye salmon. This result is consistent with the hypothesis that the original sockeye salmon population was not extirpated by Sunbeam Dam early in this century. Populations of /O. nerka/ that appear to be native were also found in Alturas and Stanley Lakes. Collectively, the native /O. nerka/ from the Sawtooth Valley lakes form a coherent group that is well-separated genetically from all other populations of /O. nerka/ in the Pacific Northwest. In contrast, the kokanee population sampled from Pettit Lake appears to be the result of an introduction of late-spawning kokanee from northern Idaho (Lake Pend Oreille). In addition to a population of presumably native /O. nerka/, Stanley Lake also supports a population of kokanee that appears to be the result of an introduction from Wizard Falls Hatchery in Oregon. We found no evidence of permanent genetic effects from the 1980s releases into Stanley and Alturas Lakes of several million sockeye salmon eggs from the Babine Lake area in British Columbia.

Broad-scale genetic and compositional monitoring of fish populations: a proof of concept in the interior Columbia River and upper Missouri River basins

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Oral presentation, Professional

Monitoring fish populations is essential to gauge the success of conservation efforts and the status and trends of individual species, but obtaining abundance estimates is time-consuming and problematic because of spatial and temporal variation in abundance. Also, relations between fish populations and their surrogates, such as habitat characteristics, are often obscure. As an alternative, genetic assessment and monitoring offers promise as an indicator of population status and trends by providing information on effective population size, genetic diversity, connectivity among populations, and the prevalence of hybridization with non-native species. We have undertaken intensive sampling of native and nonnative fishes and amphibians with lotic life histories on a subset of streams currently monitored by the Pacfish/Infish Biological Opinion Monitoring Program. These streams represent a spatially comprehensive, random sample of subbasins in the interior Columbia River Basin and upper Missouri River Basin. In concert with the field sampling, we are developing a new panel of ~100 single nucleotide polymorphism markers for cutthroat trout, redband trout, and rainbow trout to describe patterns of hybridization and landscape genetic structure. If fully realized, analyses of tissues sampled from over 1500 streams in Montana, Idaho, eastern Oregon, and eastern Washington on federal lands should permit broad-scale evaluations of the status and distribution of much of the aquatic vertebrate fauna and enable detection of responses to climate change. Although many aspects of this project are in developmental stages, preliminary sampling at over 400 sites on 175 Montana streams indicates that brook trout are more widely distributed than previously recognized, the taxonomic diversity of sculpins is underappreciated, and that westslope cutthroat trout occupy headwater sites in most of their historical range except in the Kootenai and Missouri River basins.

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Coastwide Salmonid Genetics Meeting 2010: Genetic Adaptation of Salmonids

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