ABSTRACTS: ORAL PRESENTATIONS (alphabetical order by presenter)

Pedigree inference with SNPs: a novel, fast, Bayesian method

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I present novel software for Bayesian pedigree inference with SNP markers. The method provides a principled method for jointly performing single-parent and parent-pair parentage inference as well as sibship reconstruction. It is implemented in the R language with calls to compiled code (written in C++) for speed. The program makes substantial use of precomputed and stored quantities, and applies some (very accurate) approximations to enable the method to be applied quickly to data sets with thousands of individuals. The computational and inferential framework provides a principled approach to estimating the sampling fraction of parents, even in the presence of nonparental relatives, and can be extended to simultaneously and jointly perform parentage based tagging (PBT) and genetic stock identification (GSI). This software should be of interest to those conducting PBT or those using intergenerational tagging and sampling of outmigrating juveniles to estimate spawner abundances.

Parallel evolution of the summer steelhead ecotype in multiple populations of *Oncorhynchus mykiss* from Oregon and Northern California.

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[Student]

Adaptive divergence may result in differences in migratory and reproductive behavior in multiple populations when selection is acting similarly on these traits. Timing of migration, sexual maturity, and reproduction can have major impacts on the dynamics and viability of a population. Understanding the patterns of these traits is important for the management and conservation of a species. Life-history variation in steelhead trout, including variation in anadromous run timing, reproductive maturity, and spawn timing, are important aspects of their biology and adaptation to local habitats. Here we present genetic analysis of naturally spawning coastal steelhead to evaluate genetic relationships and ancestry of sympatric Summer and Winter reproductive ecotypes in Northern California and Oregon. Adult and juvenile fish from both Summer and Winter reproductive ecotypes were evaluated using 12 microsatellite loci and 90 single nucleotide polymorphisms (SNPs). Phylogenetic trees and molecular analysis of genetic variance revealed that sympatric reproductive ecotypes within a river were generally each other's closest relatives. Isolation by distance (IBD) confirmed that genetic relatedness was strongly associated with genetic distance, with limited migration or gene flow among river basins regardless of ecotype. These patterns suggest that the summer ecotype has repeatedly evolved through parallel evolution. We also examine the adaptive basis of the two ecotypes based on an Fst outlier analysis and demonstrate a strong association of specific loci with each of these ecotypes in multiple river basins. Further investigation of the underlying molecular mechanisms for the divergence of winter and summer steelhead trout life history traits will inform management and conservation efforts.

Potential for parental based tagging of Chinook salmon in British Columbia

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The Molecular Genetics Laboratory (MGL) at the Pacific Biological Station is undertaking an evaluation of the feasibility of implementing parental based tagging (PBT) as a potential replacement for the current coded-wire tag (CWT) program for Chinook salmon in British Columbia. In 2013, samples were collected from all Chinook salmon broodstock used in hatcheries where CWTs are currently applied, and similar collections are planned for 2014. Work is underway to use a next generation sequencing (NGS) platform (Ion Torrent Proton) to genotype Chinook salmon at approximately 350 SNPs by direct DNA sequencing. It is anticipated that costs for genotyping 350 SNPs on the NGS platform will be less than current MGL costs for genotyping 15 microsatellites. Accuracy of identification of individuals to specific families, thus providing age and location of release, will be verified by sampling of returns of jacks in 2015 in hatcheries where CWTs are applied. The sampling, logistical, and analytical requirements for PBT that are necessary to provide data of equivalent quality to that available from CWTs for Chinook salmon in British Columbia are outlined. If PBT can be demonstrated to be more cost-effective than the existing CWT program for Chinook salmon in British Columbia, the potential advantages of PBT application will be discussed.

Genomics of magnetic reception in salmonids

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[Student]

Highly magnetic receptor cells of trout that contain biogenic crystals of magnetite are hypothesized to transduce geomagnetic information into neural signals utilized by fish as orientation cues during migration. However, because these cells are extremely difficult to find and study, whether these cells are capable of magnetic signal transduction is not yet confirmed. Moreover, virtually nothing is known about the genetic underpinnings of magnetite crystal formation in eukaryotes. Here, from Chinook salmon olfactory epithelium tissue, magnetic and non-magnetic cell mRNA transcripts were isolated and sequenced using RNA-Seq. Approximately 500 genes were differentially expressed in the magnetic-cell sample, with annotation of the full olfactory rosette transcriptome in-progress. The genes most plausibly involved in magnetic sensory transduction are being developed into fluorescent probes and tested for hybridization to target cells. If successful, a probe can then be used for rapid and efficient cell location to conduct in situ tests of response to magnetic field treatments. Findings have relevance to resolving if salmon and other marine organisms imprint on magnetic fields and contributing to our understanding of how magnetic sense, genetic programming, and memory are involved in migratory distributions.

Population dynamics of natural-origin steelhead in the John Day River (Oregon)

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The John Day River is one of four Major Population Groups (MPGs) within the Middle Columbia River steelhead Distinct Population Segment (DPS) listed as "threatened" under the US Endangered Species Act (ESA). The John Day steelhead MPG is comprised of five populations (Upper and Lower Mainstem, and North, Middle, and South Forks) identified by the Interior Columbia Technical Recovery Team (ICTRT) in 2003, based on a combination of demographic, habitat, and genetic data. At the time these populations were identified, however, in-basin genetic information was limited, and the South Fork was the only population identified based on genetics. The John Day steelhead MPG is distinctive in that it is one of the few summer steelhead MPGs in the Interior Columbia Basin that has had no intentional influence from hatchery steelhead. although introgression has likely occurred from out-of-basin strays. Observations of fin-clipped fish on spawning grounds, PIT tag interrogations, and coded-wire tag recoveries suggest that out-of-basin strays may comprise a significant component of the John Day steelhead spawning population. Our goal was to determine the degree of genetic support for the five-population scenario set out by the ICTRT. We also sought to determine if a genetic signal was evident from the out-of-basin straying. Genetic data did not support the five-population system of the ICTRT. While genetic structure was evident, the relationships did not correspond to those hypothesized by the ICTRT. When compared to the Columbia Basin steelhead baseline, we found concordance with other John Day populations included in the baseline; however, they exhibited close affinities with Upper Columbia and Snake River populations (not only out-of-basin, but out-of-DPS). These associations are likely the result of strays from Upper Columbia and Snake River successfully spawning in the John Day. Our findings have significant implications for conservation and restoration of these ESA-listed populations.

An analysis of studies of relative reproductive success of early-generation hatchery salmon

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We review studies on the reproductive success of fish in populations supplemented with hatchery-reared fish produced by local and predominantly wild-origin parents. Combining 49 estimates from six studies on four species, we found: (1) first-generation hatchery fish averaged only half the reproductive success of their wild-origin counterparts when spawning in the wild, and (2) all species show similar effects. If this reduced fitness is heritable, then even first-generation hatchery fish could decrease the fitness of wild populations. We review evidence for genetic versus environmental effects, and insights into possible mechanisms for the fitness decline. Finally, we also show that statistical power to detect differences in fitness is very low for sample sizes typical of these studies. These data suggest that reduced fitness of even first-generation hatchery fish is a general phenomenon. Future research should focus on determining the causes of those fitness reductions.

Quantifying incidence of predation on salmonids and other species of interest using high-throughput qPCR

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In California's Central Valley watershed, predation has been implicated in the decline of several native species including *Oncorhynchus tshawytscha* and *Oncorhynchus mykiss*. Visual evidence of this predation has been scant, possibly because predators often target larval fish and identifying fish via visual analysis is limited to bony or undigested specimens. We have created highly sensitive Taqman assays to detect predation by non-native bass and the native Sacramento pikeminnow on these and eight other local species. The specificity of the Taqman assay provides positive identification of prey without cloning or sequencing and when implemented on a high-throughput platform, the possibility for using Taqman for large-scale ecological monitoring of predation becomes possible. The data on incidence of predation will be used to identify locations and environmental parameters associated with unwanted predation on at-risk species. With this data, habitat restoration efforts can be fine-tuned to minimize danger to at-risk species. Preliminary data will be presented.

FishGen.Net: a final repository for salmon and steelhead genetic data as part of GSI and PBT projects in the Columbia River basin and throughout the Pacific Coast of North America

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FishGen.Net is a final repository for salmon and steelhead genetic data as part of Genetic Stock Identification and Parentage Based Tagging projects in the Columbia River basin and throughout the Pacific Coast of North America. FishGen.net was developed by Resource Data, Inc. (RDI) with funding from the Pacific Coast Salmon Recovery Fund. Fish.Gen.net is web-based, GIS interfaced, and freely available to the public. With a very user-friendly interface and protocol for submitting and storing standardized genetic and sample metadata, it should be an excellent tool for supporting genetic research and monitoring projects throughout the region.

Genotyping in Thousands (GTseq): A cost effective SNP genotyping method based on custom amplicon sequencing

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GTseq is a method that uses massively parallel sequencing of multiplex amplified PCR products to generate genotypes from small to moderate panels (50-500) of targeted SNPs for thousands of individuals in a single Illumina HiSeq lane. This method uses only unlabeled oligos and PCR master mix in two thermal cycling steps for amplification of targeted SNP loci, addition of sequencing adapters, and dual barcode tagging, enabling thousands of individuals to be pooled in a single library. Post sequencing, reads from individual samples are split into individual files using their unique combination of barcode sequences. Then, a simple perl script counts amplicon specific sequences for each allele and genotypes are generated using ratios of allele counts. Testing of this method showed greater than 99% concordance between genotypes generated with the GTseq method relative to existing Taqman™ assays with call rates >97% for GTseq. This novel amplicon sequencing method greatly reduces the cost of small panel SNP genotyping relative to other methods by utilizing a simple library preparation method and a massive efficiency of scale.

Pacific Eulachon (*Thaleichthys pacificus*, Osmeridae) genetic stock structure from Single Nucleotide Polymorphism variation determined through RAD-sequencing

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Twelve eulachon (*Thaleichthys pacificus*, Osmeridae) populations from the northern Gulf of Alaska to the Columbia River in the south where examined by RAD sequencing. A total of 4,104 useful SNPs (Single Nucleotide Polymorphisms) where discovered across the eulachon genome, of which 193 were found to have a highly significant F_{ST} values used to determine regional stock structure. Three main regional groups of eulachon populations where identified by the SNPs consisted of: Fraser-Columbia group, SE Alaska-BC group, and northern Gulf of Alaska (GOA) group. A gradient of increasing genetic diversity (A_R and H_E) exists from south to north with the north and south extreme populations being significantly different from one another ($p<0.05$). A marked genetic boundary between Columbia-Fraser and more northerly populations within British Columbia is consistent with differences in eulachon vertebrae counts determined by early morphometric work from the 1940's and 1960's. Within the SE Alaska-BC stock group, differentiation was low, six of the seven populations had at non-significant pair-wise F_{ST} value with at least one other population in the group. Simulated mixture analysis, used as an indication of genetic stock identification (GSI) accuracy for mixed stock fisheries, found the set of 193 SNPs to be on average 2.6 times more accurate to population and 1.2 times more accurate to region (74.8% vs 28.0% to population and 100.0% vs 85.4% to region), compared to 14 microsatellite loci. This study identifies the first set of eulachon SNPs which should help provide higher resolution estimates of eulachon stock composition in marine fisheries.

Spatially explicit models of Chinook salmon in the California Current reveal distinct marine distributions among stocks

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Information about the stock distributions of coastal and pelagic marine fishes is important for successful management of fisheries, as well as for illuminating the ecology and evolution of these organisms. Because their anadromous life-history and natal-homing create stocks that are genetically distinct, salmon of the genus *Oncorhynchus* provide an opportunity to use genetic assignment methods to understand their distributions on a stock-specific basis. Over the 2010 - 2012 fishing seasons, we obtained GPS coordinates together with SNP or microsatellite genotypes for 26,250 adult Chinook salmon (*Oncorhynchus tshawytscha*), and assigned each fish to their stock of origin. Maximum-entropy stock distribution models for 12 stocks reveal significant differences in the spatial distribution of most Chinook stocks (as measured by Warren's I). Four stocks originating between Cape Mendocino and Cape Blanco have probability maxima to the south of their natal river mouth. Moreover, these stocks, together with most stocks from the Columbia River, show distinct responses to bathymetry, with clear probability maxima for bottom depths between 200-500 meters. Reasons for these distinctive spatial patterns are unclear, but might reflect different feeding strategies. Our results imply that Chinook stocks may be fished selectively, decreasing pressure on weak stocks by restricting fishing to certain depths.

Improved understanding of migration patterns of Bristol Bay sockeye salmon benefits management and harvest

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The river systems that drain into Bristol Bay support the world's largest return of sockeye salmon and one of the most valuable salmon fisheries in the world. The duration of the migration of returning adults to nine major rivers of origin is tightly compressed, with the majority of fish migrating into Bristol Bay and through the commercial fishery within two weeks. The combination of a large magnitude of fish, temporally compressed migration, and variable relative abundances among rivers makes management of the fishery difficult. Consequently, any data informing relative abundance and timing of the individual stocks is highly valuable. To address this need, we fit a model to stock-specific abundances in a distant test fishery and in commercial fishing districts to characterize stock-specific migration speeds and examine the influence of environmental variables on migration speeds. These results provide valuable estimates of stock-specific abundances and travel times between these important waypoints in the spawning migration to improve sustainable management of the fishery.

Genomic regions under selection in a hybridized population of westslope cutthroat trout (*Oncorhynchus clarkii lewisi*)

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Hybridization among taxa is increasingly influenced by anthropogenic activities. This outcome is especially true in fish populations where stocking and external fertilization often encourage hybridization among previously isolated populations and species. Our knowledge of the effect of the introgressed genome on physiological function and population fitness and dynamics is largely unknown. In the North Fork Flathead River, Montana, introduced rainbow trout (*Oncorhynchus mykiss*) have readily hybridized with native westslope cutthroat trout (*O. clarkia lewisi*). Previous work has suggested that hybridization between the two species could have negative effects on population dynamics of cutthroat trout through a reduction of fitness in the hybrid genome. Here, we investigated the genomic mechanisms explaining this response using approaches based on genotyping by sequencing. We assayed the previously studied adult spawning fish (rainbow, westslope cutthroat, and hybrid trout) from the North Fork Flathead River, and determined the degree of admixture at the genomic level within individuals, using reference genome maps (>4000 SNPs). Using this information, we describe the genomic architecture of hybridization between these two species, the invasion history in the population, and the relationship between genomic ancestry and individual fitness. Our results indicate that invasion is likely ongoing, with new non-native rainbow trout entering the system each year, possibly swamping native taxa. Introgression was observed to have a non-uniform distribution across the genome, with significant deviations (in both directions) from background admixture levels at multiple genomic regions. Lastly, multiple genomic regions were significantly correlated with reproductive success and may influence long-term fitness in wild populations. These results serve as a framework for further investigations of the genomic effect of admixture on native populations.

Evaluating a multi-generational reintroduction program for threatened spring Chinook salmon using genetic parentage analysis

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Presenter: Melissa Evans, melissa.evans@oregonstate.edu

Upper Willamette River spring Chinook salmon (*Oncorhynchus tshawytscha*) are listed as threatened under the U.S. Endangered Species Act. On the South Santiam River, a tributary of the Willamette, recovery of spring Chinook salmon is limited by the effects of Foster Dam, which inundates or blocks access to ~85% of the population's historical spawning grounds. In recent years, a trap and release-based reintroduction program has been implemented on the South Santiam to facilitate passage and natural spawning above Foster Dam. Tissue samples have been collected from released salmon since 2007. Using genetic parentage analysis of adult salmon returning to the South Santiam during 2010-2013, we estimated the fitness of salmon released above the dam in previous years and the contribution of the reintroduction program to population productivity. Our results indicated that most salmon released above the dam during 2012 (74%) and 2013 (66%), the cohorts for which we had near complete genetic sampling of potential parents, were the progeny of salmon previously released above Foster Dam as part of the reintroduction program. Furthermore, upwards of 15% of salmon sampled as carcasses from below Foster Dam were identified as the progeny of salmon released above the dam during 2007-2011. Females produced a greater number of adult progeny returning to the South Santiam compared to males, and salmon released above Foster Dam later in the spawning migration produced a greater number of progeny, a result that may be driven by higher apparent pre-spawn mortality of salmon released earlier in the spawning migration. Cohort replacement rates, calculated for the 2007 and 2008 adult spawners, were 0.96 and 1.15, respectively, suggesting that the reintroduction program is meeting/achieving population replacement.

Estimating rates of straying of wild salmon using parentage based tagging

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Understanding patterns of dispersal and gene flow among populations is important for understanding how evolution works in natural populations and for informing conservation and population management. Most studies of straying in salmon have been based on recovery of physical tags, and largely focused on hatchery released fish. Parentage analysis is a potentially powerful tool for studying patterns of fidelity and dispersal in wild salmon populations. In this study, we used parentage analysis, combined with detailed spawning location for both parents and adult offspring, to estimate rates of straying by natural origin Chinook salmon among major spawning areas within the Wenatchee River. As a point of comparison, rates of gene flow were also estimated using more traditional population genetic methods. The parentage and model-fitting methods agreed surprisingly well, and indicated relatively low rates of straying by wild fish within the Wenatchee River Basin.

Marker-Assisted Marker Development with RAD-sequencing (MAD-RAD) To Identify Potential Genomic Regions Linked to a Locus Under Selection in Summer-Run Chum Salmon (*Oncorhynchus keta*)

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Next-generation sequencing methods are providing tens of thousands of single nucleotide polymorphisms (SNPs) in non-model organisms at ever decreasing costs. Restriction-Associated DNA (RAD) sequenced with next generation technologies (RAD-Seq) improves upon earlier methods because it facilitates sequence alignment in the absence of a reference genome and it reduces genome complexity. Nuclear genetic markers that can differentiate among salmon populations in western Alaska - especially summer-run chum salmon - have proven to be elusive despite these new technologies and have made management efforts that use mixed stock analysis (MSA) difficult. We used Eco-TILLING in earlier work to identify mitochondrial haplotypes from sequences in the ND5 gene that differ among these chum salmon populations, but because they are physically linked, they behave as a single locus for MSA. The ND5 protein is a structurally important subunit of mitochondrial complex I that generates the proton gradient used to synthesize ATP and was shown to be the target of positive selection during the evolution of Pacific salmon. We hypothesized that nuclear encoded proteins must co-evolve with mitochondrial complex I function and will show similar levels of divergence among these populations. In order test this hypothesis we assembled an ascertainment panel of individuals based on the ND5 markers for RAD-seq on the Illumina platform. The RAD-seq identified nearly 20,000 potential SNPs from an ascertainment panel of 50 individuals representing 5 populations. We developed a series of methods to eliminate duplicated loci and identify these potentially informative SNP markers.

Hatcheries as Habit, Integrated vs. Segregated Programs, and Rehab for Hatchery Fish

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The primary mitigation for the negative effects of dams and associated water operations on anadromous salmon and steelhead has historically been the establishment of hatchery programs that "replace" the production from lost spawning and rearing habitat. As the evidence accumulates that hatchery salmonids are less fit when spawning in natural areas, and can have other negative effects on natural populations, many questions have arisen about how to manage these programs. One of the primary questions is whether gene flow between hatchery stocks and natural populations should be eliminated (segregated), or allowed but perhaps limited (integrated). I argue that segregated programs don't exist and, as with most such complicated situations, the "devil is in the details" and the ways in which domestication selection has produced differences in life history and fitness first need to be elucidated before appropriate strategies can be formulated. Genetic tagging and careful monitoring and evaluation are the only feasible way to do this. In addition, for many salmonid lineages, a large portion, or even the majority, of the ancestral genetic variation is now present partially or entirely in hatchery stocks, albeit in non-optimal combinations. Once the fitness landscape in that lineage is understood, the process of rehabilitating hatchery stocks can be undertaken, and their invaluable genetic legacy reintegrated into natural populations to advance recovery and restoration goals.

A graphical application demonstrating population effects and impacts on genetic diversity

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A graphical application was written to help visualize the effects of limited reproduction potentials on small simulated populations. Potential genetic impacts can often best be explained using simulated examples, but such applications can also provide insight into mechanisms guiding conservation measures. A graphical application was written in C++ using the Qt framework enabling the user to identify and evaluate impacts regarding the numbers of fish in the simulation, their swimming speeds, reproduction potential, generation times, and the numbers of generations between the beginning and end of the experiment. The placement of the fish on the screen, their swimming patterns, and sex are randomly determined. In addition, an option was included to subdivide the population into distinct populations so that impacts on genetic diversity could be monitored. Experimental results can be exported to a file for later statistical analysis. This application is intended to be an educational tool allowing users to explore genetic population effects through a visual application. This program is modeled on the "Colliding Mice Example" example available in Qt Creator (Digia, Inc).

Monitoring Stock-Specific Abundance, Run Timing, and Straying of Chinook Salmon in the Columbia River Using Genetic Stock Identification (GSI)

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Genetic stock identification (GSI) provides a method of characterizing stock-specific abundance, run timing, and straying as they pertain to the population demographics and behavior of both hatchery and wild fish and thus assists with fisheries management. In this study, tissues were collected and genotyped at 13 microsatellite loci from adult Chinook Salmon *Oncorhynchus tshawytscha* that passed Bonneville Dam during four consecutive migration years (2004–2007). GSI methods were used to estimate the proportions of stocks in a broad genetic baseline, with high-density coverage of Chinook Salmon across the eastern Pacific Rim. The estimates of abundance for interior Columbia River stocks showed widespread decline consistent with a shift to poor ocean conditions during the years when the fish in this study were at sea, but divergent stock- and age-specific patterns were also observed. For example, the upper Columbia River spring-run stock experienced a unique net gain in abundance during this period, and the interior Columbia River summer–fall-run stock experienced a delayed decline of 4-year-olds. Stocks with early run timing shifted to later migrations. However, run timing distributions did not shift unidirectionally for all stocks across years, and stock membership in three major run timing categories was maintained. Of 9,215 total adults sampled, 27 (0.3%) were out-of-basin strays and a quarter of the strays were putatively of wild origin. The general concordance of GSI results with those based on more traditional methods supports the effectiveness of GSI as a tool for fisheries management.

Signals of heterogeneous selection at an MHC locus in geographically proximate ecotypes of sockeye salmon (*Oncorhynchus nerka*)

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Parasites and pathogens exert considerable selective pressure on wild populations, creating a constant arms race. The genes of the major histocompatibility complex (MHC) are an important component of this arms race and have been found to be under strong natural selection in many vertebrates. Here, we sequenced a 350 base pair region of the MHC class II peptide binding region to quantify MHC diversity in 27 populations of sockeye salmon spawning in the Wood River system in southwest Alaska. We found that MHC variation is partitioned by spawning ecotype with fish that spawn in streams, rivers and beaches displaying markedly different MHC genotypes. Additionally, tests for selection indicated that beach populations are generally undergoing directional selection whereas stream populations show signatures of balancing selection. These data suggest that fine-scale variation in parasite communities has resulted in strong genetic differentiation at the MHC in populations that are separated by < 1 km.

Species ID for Free: Identifying Non-Target Species During Mixed Stock Assessment

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The Alaska Department of Fish and Game Gene Conservation Laboratory (GCL) uses species-specific analyses to describe population structure and estimate stock compositions in fishery mixtures. GCL has also established a species-identification protocol to identify species for samples of Pacific and Atlantic salmon where species is unclear. However, when non-target species are sampled in the field, they are detected as a wrong-species sample in the species-specific analysis, but the species-identification protocol is needed to identify the species of the sample. Analyzing samples with both methods is expensive and time-consuming. We performed experiments analyzing all 5 Pacific and Atlantic salmon through 3 species-specific analyses (sockeye, chum, and Chinook salmon) and examined the resulting scatter plots for species-specific patterns. Sockeye, chum, pink, coho, Atlantic and Chinook salmon exhibited patterns across all species-specific marker panels, allowing us to accurately identify non-target species using these panels, thereby eliminating the cost and time of performing a separate species-identification protocol. This gleaned information may prove useful to project managers by providing feedback on the species-identification errors in the field. Accurate species identification in the field results in higher numbers of correct-species samples run and therefore better allele frequency estimates for population structure and tighter confidence intervals for stock-composition estimates.

Relative contributions of neutral and non-neutral genetic differentiation to inform conservation of steelhead trout across highly variable landscapes

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Presenter: Andrew P. Matala, 208-837-4413 x1132, mata@critfc.org

Mounting evidence of climatic effects on riverine environments, and adaptive responses of fishes has elicited growing conservation concerns. Measures to rectify population declines include assessment of local extinction risk, population ecology, viability, and genetic differentiation. While conservation planning has been largely informed by neutral genetic structure, there has been a dearth of critical information regarding the role of non-neutral variation (e.g., adaptation). We evaluated genetic variation among steelhead trout of the Columbia River Basin, which supports diverse populations distributed among dynamic landscapes. We categorized 180 SNP loci as either putatively neutral or candidates for divergent selection (non-neutral) using a multi-test association approach. Neutral variation distinguished lineages and defined broad-scale population structure consistent with previous studies, but fine-scale resolution was also detected at levels not previously observed. Within distinct coastal and inland lineages, we identified 9 and 22 candidate loci (respectively) commonly associated with precipitation or temperature variables, and putatively under divergent selection. Observed patterns of non-neutral variation suggest overall climate is likely to shape local adaptation (e.g., potential rapid evolution) of steelhead trout in the Columbia River region. Broad geographic patterns of neutral and non-neutral variation demonstrated here can be used to accommodate priorities for regional management and inform long-term conservation of this species.

Use of genetic data to infer population-specific ecological and phenotypic traits from mixed aggregations

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Many applications in ecological genetics involve sampling individuals from a mixture of multiple populations and subsequently associating those individuals with the populations from which they arose. Analytical methods that assign individuals to their putative population of origin have utility in both basic and applied research, providing information about population-specific life history and habitat use, ecotoxins, pathogen and parasite loads, and many other non-genetic ecological, or phenotypic traits. Although the question is initially directed at the origin of individuals, in most cases the ultimate desire is to investigate the distribution of some trait among populations. Current practice is to assign individuals to a population of origin and study properties of the trait among individuals within population strata as if they constituted independent samples. It seemed that approach might bias population-specific trait inference. In this study we made trait inferences directly through modeling, bypassing individual assignment. We extended a Bayesian model for population mixture analysis to incorporate parameters for the phenotypic trait and compared its performance to that of individual assignment with a minimum probability threshold for assignment. The Bayesian mixture model outperformed individual assignment under some conditions. However, by discarding individuals whose origins are most uncertain, the individual assignment method provided a less complex analytical technique whose performance may be adequate for some common mixture problems. Our results provide specific guidance for method selection under various genetic relationships among populations with different trait distributions.

Mechanisms of thermal adaptation: transcriptional response to heat stress among desert and montane populations of redband trout

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Presenter: Shawn R. Narum, 208-837-9096, nars@critfc.org

As ectothermic organisms have evolved to differing aquatic climates, the molecular basis of thermal adaptation is a key area of research. In this study, we tested for intraspecific transcriptional response of natural populations of redband trout (*Oncorhynchus mykiss gairdneri*) that have evolved to warm and cool climates. Fish were reared in a common garden environment and exposed over four weeks to diel water temperatures that were similar to those experienced in desert climates within the species' range. Tissues were collected from gill arches of three strains of fish (desert, montane, F1 crosses) at the peak of heat stress and tested for mRNA expression differences across the transcriptome with RNA-seq methods. Strong differences in transcriptional response to heat stress was observed across strains confirming that fish from desert environments have evolved diverse mechanisms to cope with stressful environments. Each strain had both shared and unique contigs that were differentially expressed, but the desert population had more than double the number of unique differentially expressed genes than the montane population (4339 versus 2112 genes respectively) or F1 strain intermediate (2490 unique differently expressed genes). Key stress response genes such as molecular chaperones (i.e., heat shock proteins) had adaptive patterns of gene expression among strains, but also a much higher number of metabolic and cellular process genes were differentially expressed in the desert strain demonstrating these biological pathways are critical for thermal adaptation to warm aquatic climates. The results of this study further elucidate the molecular basis for thermal adaptation in aquatic ecosystems and extend the potential for identifying regions in the transcriptome and genome that may be critical for adaptation to changing climates.

Genomic Signatures of Adaptive Divergence Between Migratory and Non-migratory Population Pairs of *Oncorhynchus nerka*

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Presenter: Krista M. Nichols, 206-302-2470, krista.nichols@noaa.gov

Sockeye and kokanee salmon represent migratory and non-migratory life history forms of O. nerka, respectively, that further exhibit differences in spawning location and timing within the lakes and inlet streams in which they rear and spawn. In this study, we examine genomic signatures of natural selection in two population pairs of sockeye and kokanee salmon in central Idaho from two different lake systems: Redfish Lake (n=150) and Alturas Lake (n=63). RAD sequencing yielded 2593 genome-wide SNP markers that collectively suggest there are very different demographic histories for these populations. The resident-migratory pair in Alturas Lake shows no significant population differentiation (F_{ST} = 0.005), while the population pair in Redfish Lake shows a strong signal of population differentiation (F_{ST}=0.15). Despite no population differentiation in a global analysis in the Alturas Lake pair, 71 loci showed signatures consistent with divergent natural selection. In Redfish Lake, outlier analysis revealed 104 loci consistent with divergent natural selection. Only two loci showing divergent natural selection were in common, and may represent markers linked to genes influencing the migratory life histories of these population pairs. One of these loci was identified as both a candidate locus under divergent natural selection, and associated with migration vs. residency in a genome wide association analysis. Overall, our results suggest very different population histories, while providing important information to inform management and possible supplementation strategies in each system.

Influence of immune-relevant genotype on the reproductive success of a salmonid alternative mating strategy

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Presenter: Kathleen G. O'Malley, 541-961-3311, Kathleen.OMalley@oregonstate.edu

Major Histocompatibility Complex (MHC) and immune-relevant gene markers were used to evaluate differences in reproductive success (RS) among naturally spawning coho salmon *Oncorhynchus kisutch* mate pairs involving an alternative male reproductive phenotype, known as jacks. These mate pairs included both hatchery-reared and wild origin fish such that three classes were evaluated in two consecutive years (2005 and 2006) using a previously constructed multi-generational genetic pedigree: wild x wild (W x W), hatchery x hatchery (H x H), and wild x hatchery (W x H). Coho jack mate pairs mated randomly based on immune-relevant genotype in both years; a result consistent with the opportunistic mating strategy of jacks. An association between greater number of alleles shared at three immune-relevant gene markers and increased RS was found for: W x H mate pairs in 2005 (*BHMS429*), W x H pairs in 2006 (*SsalR016TKU*) and W x W pairs in 2006 (*OMM3085*). No correlation between immune gene diversity and RS was found for H x H pairs in either year. The results suggest that the influence of immune-relevant genotype on mating success may be different for jacks when compared to previous studies of large adult male salmon.

Single Genomic Basis for Rapid Parallel Evolution of Life-History Expression in Steelhead/Rainbow Trout

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Animal migration is a spectacular and widespread phenotype, and propensity towards migration varies among individuals in many animal populations. Among anadromous fishes, expression of the migratory phenotype is influenced by a combination of environmental, genetic, and developmental effects, and adaptation to novel environments may be accompanied by changes in specific genomic regions or co-adapted gene complexes affecting selected trait(s). In addition, phenotypic plasticity in trait expression has been shown to involve changes in norms of reaction relative to environmental cues. Both plastic and adaptive changes may be population-specific or, alternatively, may involve parallel evolution of the same genomic region(s) in multiple populations. Numerous studies have identified associations between specific genomic regions and the anadromous (steelhead) and resident (rainbow trout) life-history strategies of *Oncorhynchus mykiss*. In particular, a large region of one chromosome, Omy5, is strongly associated with life-history differentiation in multiple above-barrier populations of rainbow trout and their anadromous steelhead ancestors. The associated loci are in strong linkage disequilibrium, suggesting the presence of a chromosomal inversion or other rearrangement limiting recombination. Analysis of variation in individual migratory tendency also shows sex-specific associations between Omy5 genotype and expression of anadromy. These results provide evidence of a common genomic basis for life-history variation in *O. mykiss* in a geographically diverse set of populations, and extend our knowledge of the heritable basis of rapid adaptation of complex traits in novel habitats.

Pop-X: Detecting unrepresented populations in fishery mixtures

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Presenter: Serena Rogers Olive, 907-267-2162, serena.olive@alaska.gov

Non-convergence among MCMC chains while performing mixed stock analysis in *BAYES* often indicates a problem with the analysis. Problems can include either missing baseline populations or errors in the genotypic data of the mixture. Our lab employs a strict quality control process that greatly reduces the chance of analyzing data with errors, leading us to investigate whether there are missing baseline populations when non-convergence arises. We explored this issue with programs such as *HWLER*, which identifies individuals from extra-baseline populations (Pop-X) within a mixture. In addition to *BAYES* and *HWLER*, we also used methods in *R* to assist in determining the approximate geographic location of Pop-X to narrow the search area for new collections to fill baseline gaps. We present two case studies of Alaska sockeye salmon fisheries where this issue arose and how we ultimately determined these baselines were incomplete.

Evaluating a spring Chinook salmon reintroduction above a high-head dam in Oregon: Inference from genetic monitoring

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Although large runs of spring Chinook salmon (*Oncorhynchus tshawytscha*) were previously supported by the McKenzie River and other tributaries within the upper Willamette River basin, marked declines in abundance has resulted in the listing of this population as threatened under the U.S. Endangered Species Act. Cougar Dam, on the South Fork McKenzie River, impedes Chinook access to 40 kilometers of historical spawning habitat. Recently, managers have begun to reintroduce hatchery origin Chinook above Cougar Dam to aid in their recovery. We sampled nearly all Chinook (99.8%) reintroduced above the dam since 2007 for genetic analysis, and recorded the date and location they were released. Beginning in 2010, we sampled natural origin (NOR) Chinook that returned to a trap and haul facility built at the base of the dam, hereafter Cougar Trap. These fish were subsequently reintroduced along with hatchery fish above the dam. We used molecular parentage methods to identify NOR progeny of reintroduced Chinook. We found that the majority of Chinook collected at the Cougar Trap in 2012 (64%) and 2013 (68%) were produced above Cougar Dam. Interestingly, most of the Chinook that returned before September 1st were produced above the dam in 2012 (85%) and 2013 (87%), but those returning after that date were not (21% and 20%, respectively). Parent-offspring assignments were used to estimate total lifetime fitness (TLF) of adults reintroduced in 2007 and 2008. We found that mean TLF decreased as Chinook were released later in the spawning season ($p=0.015$), however release location did not affect TLF ($p=0.674$). Overall, Chinook reintroduced in 2007 and 2008 did not meet replacement (Cohort replacement rate: 0.41 and 0.31, respectively). Our research findings are integrated into management decisions related to the Chinook reintroduction above Cougar Dam, and broadly benefit others planning salmon reintroductions intended to support their long-term viability.

Examining power of parentage analysis for detecting effects on reproductive success of hatchery straying into natural pink salmon populations

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Parentage studies and pedigree reconstruction via genetic analysis have become widely available for addressing a broad range of evolutionary and ecological questions. In Alaska, these applications will be used to evaluate the potential fitness effects of hatchery straying on wild salmon populations by measuring the relative reproductive success (RRS) of hatchery-origin to natural-origin fish. However, due to limitations of working in these systems, not all parents or offspring can be sampled. We performed a power analysis on simulated genetic data to assess our ability to detect differences in RRS based on two different hatchery stray rates, six sampling levels of spawners, six sampling levels of recruits, and four effect sizes (true RRS of hatchery-origin to natural origin fish). For simplicity, the analysis was performed using pink salmon life history; one of the species under study. RRS was modeled as survival of adult offspring, and was calculated both by cross type (parent pairs) and sex (single parents). Parentage analysis was performed with SOLOMON, an exclusion-Bayesian parentage analysis package in R, on a simulated dataset of 96 SNPs with an average MAF of ~0.34. Our findings demonstrate a clear need to sample a high proportion (1/2 or greater) of both spawners and recruits to reliably detect fitness differences between hatchery-origin and natural-origin fish, especially for systems with a low stray rates and when fitness differences are less than 50%.

Stillaguamish River Chinook salmon abundance estimated using trans-generational genetic mark-recapture

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Presenter: Maureen P. Small, 360-902-2682, Maureen.Small@dfw.wa.gov

The Stillaguamish River Chinook salmon are listed for protection under the US Endangered Species Act and are a stock of concern under the Pacific Salmon Treaty due to declines from historic levels, current low abundance and limitations this imposes on fisheries management. Using visual surveys (redd counts) to estimate spawner abundance is difficult due to limited visibility and access because of freshets during the spawning period. We used a genetic application of traditional mark recapture (Genetic Mark-Recapture, GMR) to estimate spawner abundance for five brood years. The first sampling event (marks) included carcasses collected in the fall, and the second sampling event (captures) included juveniles collected in the spring from a juvenile outmigrant trap. Recaptures were parental genotypes recaptured in juveniles assigning back to carcasses. We compared GMR estimates from the Lincoln-Peterson model to redd-based estimates. In all years, precision of the GMR estimate was high (CV $\leq$ 15%) and the GMR abundance estimate was higher than the redd-based estimates. The GMR is a useful tool for fisheries management where environmental conditions prevent accurate counts and when it is important to assess the uncertainty in spawner abundance estimates.

SNP-based genetic analysis of hatchery steelhead from the Central Valley of California

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Iteroparous salmonids are more difficult to study than semelparous ones because carcasses are rarely encountered and they are released alive from hatcheries after spawning. Single Nucleotide Polymorphism markers have been shown to be useful in pedigree reconstruction, investigations of stock structure and individual identification and provide biological information that is not available with traditional physical tags. We collected data for 95 SNP markers from more than 9,000 steelhead (the anadromous form of *Oncorhynchus mykiss*) used as broodstock between 2011 and 2014 in the four California Central Valley steelhead hatchery programs: Coleman, Feather River, Mokelumne River and Nimbus hatcheries. Assignment tests allowed us to estimate migration rates between hatcheries and to confirm the clear distinction of the Nimbus Hatchery population, which was founded with coastal steelhead stocks from the other Central Valley hatcheries. Similarly, we confirmed that Mokelumne River Hatchery steelhead are genetically similar to Feather River Hatchery stock, from which they were derived. The identification of parents-offspring trios allowed us to evaluate age structure and variance in family size in all hatcheries. Interestingly, we found a high proportion of 2 year old spawners in three of these programs, and none in Nimbus. Finally, we looked for matching genotypes to count how many fish spawned more than once in the same season. In contrast with program goals, we identified a significant number of fish that reproduced multiple times in the same season. We also used this approach to investigate iteroparity rates for each hatchery separately. The comparison of the first spawning date with spawning dates in subsequent spawning events for iteroparous individuals identified a strong correlation, consistent with the heritability of spawning date. This study shows the power of SNP-based genetic analysis to elucidate key life history variables and, as a consequence, its utility in formulating effective conservation and management strategies.

Managed gene flow reduces adaptation to captivity in supportive breeding programs: A multi-generational analysis of a Chinook salmon hatchery

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Conservation and management programs are increasingly reliant on captive rearing to support declining wild populations. However, adaptation to captivity can decrease the fitness of captive individuals when released in the wild and may reduce the overall fitness and genetic diversity of wild populations. Managed gene flow, or incorporating wild individuals as broodstock in breeding programs, can theoretically reduce genetic differentiation caused by adaptation to captivity, but the effectiveness of this strategy is uncertain. We examined the potential of this practice to reduce differentiation using two hatchery lines of Chinook salmon, *Oncorhynchus tshawytscha.* The "integrated" line uses natural origin individuals as broodstock, while the "segregated" line has no gene flow from the wild. The founding wild population and three generations (sampled in 2002, 2006, 2010) of both hatchery lines were compared at 4,405 polymorphic, mapped loci identified through restriction-site associated (RAD) sequencing. Measures of population differentiation (F_{ST}) compared to the wild founders were small for all populations, though differentiation for the 2010 segregated line (F_{ST}=0.0096, $p<0.001$) was nearly an order of magnitude higher than the 2010 integrated line (F_{ST}=0.001, $p>0.05$). Genome scans across the chromosomes identified regions of elevated divergence from the wild founders in both hatchery lines. However, "outlier" regions in the segregated line were higher in frequency, magnitude, and consistency across generations, suggesting domestication selection. These results were also supported by the identification of outlier loci using two other methods. Temporal estimates of effective population size were 553 in the integrated line and 90 in the segregated line, indicating that genetic drift is more likely to cause divergence in the segregated line. This study shows that managed gene flow has been effective at reducing genetic differentiation in captivity caused by domestication selection and genetic drift and can be used to maximize the success of conservation-focused aquaculture programs.

ABSTRACTS: POSTER PRESENTATIONS (alphabetical order by presenter)

Jumping the Falls? Interactions Between Resident and Anadromous O. mykiss Populations at a Putative Natural Barrier, Big Bear Falls, Potlatch River, Idaho

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Presenter: Michael W. Ackerman, 208-939-6713, mike.ackerman@idfg.idaho.gov

Big Bear Creek in Potlatch River, ID contains a strong wild *O. mykiss* population despite significant habitat degradation within the drainage. The population is comprised of both anadromous and resident *O. mykiss* life histories. Anadromous populations spawn and rear in lower Big Bear Creek, whereas resident populations occur approximately 20 kilometers upstream in the headwaters. Located between the populations is Big Bear Falls; a putative upstream migration barrier. This experiment was conducted to determine the effect of the falls on steelhead upstream migration to guide potential habitat restoration approaches in Big Bear Creek. We collected tissue samples from 424 anadromous and resident *O. mykiss* throughout Big Bear Creek; all individuals were genotyped at 191 SNPs. Using multi-locus SNP data we evaluated directional gene flow in the creek, specifically at the waterfall. Our objectives were two-fold: 1) identify whether Big Bear Falls is a complete barrier to upstream migration for adult steelhead, and 2) gauge evidence for downstream migration from resident fish into the anadromous population. Principal correspondence analyses of allele frequency data shows that anadromous and resident populations are highly differentiated and that exchange of genetic material between populations is limited. However, we determined that juvenile *O. mykiss* captured directly above the waterfall were offspring of anadromous steelhead that successfully migrated and reproduced above the waterfall. Further, we identified evidence of downstream gene flow, suggesting that resident fish may contribute genetic material to anadromous populations. The Big Bear Creek drainage is a candidate for habitat restoration efforts that would likely benefit both native resident and anadromous *O. mykiss* life history forms in the drainage.

Historical samples: temporal population genetic structure and SNP design optimization for steelhead

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Historical samples can provide important insights on how genetic diversity and relationships among populations have changed over time due to anthropogenic impacts. Specimens from archival sampling efforts and museum collections can be used as a reference baseline for comparisons with contemporary populations and to inform management decisions and aid conservation efforts. One of the major historical recreational fisheries along the California coast – anadromous steelhead (*Oncorhynchus mykiss)* – has declined over the past century due to destruction of in-river spawning and rearing habitat. Many Distinct Population Segments (DPSs) are now listed as threatened or endangered. Two rivers within the Northern California DPS, Eel River and Mad River, have experienced roughly hundredfold declines in steelhead run numbers, and both rivers have been impacted by dams, fish stocking, hatcheries and commercial operations since the mid-1800s. In order to assess how population genetic structure has changed over the past century we will compare historic samples from the Eel River and Mad River with contemporary samples using a panel of 95 single nucleotide polymorphisms (SNPs). In order to determine how to optimize SNP design for historical or degraded samples, we will also evaluate successful genotyping rate and SNP design parameters for at least 500 historic samples. This will enable us to incorporate lower quality samples of historical significance into other future comparative studies.

Stock composition estimates of Chinook salmon incidentally taken as bycatch in the 2012 Bering Sea and Gulf of Alaska Trawl Fisheries

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Presenter: Charles M. Guthrie III, 907-789-6093, chuck.guthrie@noaa.gov

The Bering Sea and the Gulf of Alaska (GOA) are known feeding habitats for multiple brood years of Chinook salmon (*Oncorhynchus tshawytscha*) originating from North America and Asia. Determining the geographic origin and stock composition of salmon caught in federally managed fisheries is essential to understanding whether fisheries management could address conservation concerns. Changes implemented through Amendment 91 to the Fishery Management Plan for Groundfish of the Bering Sea and Aleutian Island Management Area (BSAI) made possible the systematic random sampling of the BSAI salmon bycatch starting in 2011. Samples from the 2012 BSAI walleye pollock (*Gadus chalcogrammus*) trawl fishery were genotyped for 43 single nucleotide polymorphism DNA markers. Coastal Western Alaska stocks dominated (63%) in the analysis of 1,111 Chinook bycatch samples collected throughout the 2012 BSAI walleye pollock trawl fishery, Genetic samples were also collected from Chinook salmon taken in the bycatch of the 2012 GOA pollock trawl fisheries. Genetic samples were collected opportunistically in the GOA during 2012; consequently, the resulting stock composition estimates should be considered as stock compositions of the sample set. Based on the analysis of 948 Chinook salmon bycatch samples, British Columbia (49%), West Coast U.S. Coast (28%), and Coastal Southeast Alaska (20%) stocks comprised the largest stock groups. Stock composition estimates of Chinook salmon from tests of salmon excluder devices performed in February 2012 in an area north of Unimak Pass in the Bering Sea showed that the majority of the 249 Chinook salmon collected originated from Coastal Western Alaska (69%).

Environmental adaptation in Chinook salmon (*Oncorhynhcus tshawytscha*) throughout their geographic range

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Presenter: Benjamin C. Hecht, 208-837-9096 x1127; hecb@critfc.org

Throughout their native range, Chinook salmon (*Oncorhynhcus tshawytscha*) occupy a variety of habitats with varying environmental features which influence the overall genetic diversity of this species. However, understanding the effects of landscape and environmental features on genomic variation throughout the geographic range of this species remains relatively unexplored. Here we use a high throughput genotyping by sequencing (GBS) approach to interrogate 21,504 SNPs in 1,957 individuals from 46 populations to evaluate associations between environmental features and genetic variation. Samples were collected throughout the native range of Chinook salmon from Western Alaska to Northern California. Using a mixed linear model approach that accounts for population structure and relatedness, we identified candidate loci associated with adaptation to variance in latitude, longitude, elevation, precipitation, temperature, migration distance and stream order. Sequences will be aligned to those from a published Chinook salmon linkage map in order to identify regions of the genome associated with environmental adaptation.

Evaluating the accuracy of sibling reconstruction programs using steelhead SNPs

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The ability to determine genealogical relationships among individuals within a sample of fish without parental information has many important conservation and management applications. Although several methods are currently available to estimate these relationships, they are computationally intensive and require highly informative genetic markers that are free of genotyping errors and mutations in order to provide accurate reconstruction. In this study, we used a powerful new set of 188 single nucleotide polymorphic markers (SNPs) developed for steelhead to compare the effectiveness of existing sibling reconstruction computer programs in correctly reconstructing family relationships using SNP genotypes from hatchery offspring with known parentage. The verification of the accuracy and performance of these methods could provide opportunities for assessing patterns of dispersal and estimating effective population size in future research programs where field collections often only target one or two cohorts and may not include parents.

Project CROOS: Collaborative Research Identifies the Distributions of Chinook Salmon Stocks off the Oregon Coast

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In 2005, anticipating fishery restrictions on the harvest of Klamath River Chinook salmon, a collaboration of commercial fishermen, scientists, and seafood marketers initiated Project CROOS (Collaborative Research on Oregon Ocean Salmon) to better understand the distributions of Chinook salmon stocks in the ocean and apply this information to improve fisheries management. In this unique industry collaborative fisherman are the front-line researchers, gathering biological samples, and data, recording the GPS location of each Chinook caught. For fin-clips, GSI was used to assign fish to most likely stock of orgin using the GAPS baseline. Our work has provided fisheries managers with more robust and timely information about stock distributions as a tool to mitigate impacts on weak stocks. CROOS, California, and Washington joined to form the West Coast Salmon Genetic Stock Identification collaboration. In Oregon, Project CROOS has gathered 20,000 individual stock assignments distributed over 6 years of sampling. Utilizing the R package RGL to display spatial and temporal stock distributions has provided new insights into specific stock movements that have been difficult to detect in the past. In addition, to better understanding stock distributions our highly polymorphic microsatellites have been used to infer migration patterns among sibling in the open ocean. Collectively our work demonstrates how industry, academia, and regulators can work together to protect weak stocks while maintaining a healthy fishery.

The genetic basis of age at maturity in hatchery and natural origin chinook salmon (*Oncorhynchus tshawytscha*)

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Chinook salmon exhibit tremendous variation in age and size at sexual maturity. Hatchery and natural origin fish often have very different maturation schedules, with a shift toward early maturation and "jacking" in hatchery males relative to natural origin males. Although environmental factors contribute to variation in age at maturity, substantial heritable genetic variation for age at sexual maturity also exists, though the number and distribution of associated genetic loci underlying this trait are unknown. We perform a genome-wide association analysis of thousands of RAD-tag SNP markers in two populations of Chinook salmon to examine the genome regions associated with age at sexual maturity and jacking in natural and hatchery origin males. Analyses include 15,329 SNP loci in 428 individuals from the Wenatchee River and 12,882 loci in 391 individuals from Johnson Creek, both tributaries of the Columbia River (11,251 shared loci). Relative genomic position and distribution of loci were determined by aligning loci against a published Chinook salmon linkage map, and loci were further annotated for linkage to functional genes by alignment to related salmonid genome and transcriptome databases. Our results contribute to an understanding of the genetic basis to age at maturity and will assist conservation and management goals for Pacific salmon.

Differential Reproductive Success in a Skagit River Spring Chinook (*Onchorhynchus tshawystcha*) Hatchery Broodstock

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The ability of hatchery programs to promote the conservation and sustainable harvest of natural populations is dependent on their production of reproductively fit individuals. Our study compares the relative reproductive success (RRS) of the 2008 Marblemount Hatchery (Skagit River, WA) spring Chinook (*Onchorhynchus tshawystcha*) spawners (N = 312; 156 males and females each). We evaluated RRS using the number of 3 – 5- year old adult offspring returning to the hatchery in 2011 – 2013, and the proportion of offspring sired by primary and secondary (backup) males. In addition, we compared the number of returning adult offspring for each female to the female's fecundity. Individuals were genotyped using 191 single-nucleotide polymorphisms (SNPs), and parent-offspring relationships were determined by the likelihood method implemented in the program FRANz v. 2.0.0. Our preliminary results indicated that the number of returning offspring varied widely for both male and female spawners. Secondary males sired 110 of the 1552 returning offspring. These 110 offspring were distributed among 41 female spawners, including 2 females that produced offspring sired exclusively by secondary males. Our preliminary analysis signified that there was no relationship between female RRS and fecundity. These data will be included in a RAD sequencing-based genome-wide association study designed to better understand the correlates of fitness in hatchery-reared Chinook salmon.

Conflicting production and conservation goals degrade genetic integrity of hatchery steelhead

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We examined whether a steelhead, Oncorhynchus mykiss, supplementation program in southwestern Washington, USA could produce hatchery fish that contained genetic characteristics of the endemic population from which it was derived and simultaneously meet a production goal of 20,000 smolts annually. Hatchery fish were produced for three consecutive years by using broodstock comprised of endemic juveniles that were caught in the wild and raised to maturity and then the program transitioned to an integrated broodstock comprised of wild and hatchery adults that returned to spawn. Importantly, some auxiliary conservation-based husbandry protocols were attempted (i.e., pairwise mating between males and females) but not always completed due to insufficient broodstock and conflict between production and conservation goals. The hatchery met production goals in 6 of 9 years, but wild-type genetic integrity of hatchery fish was degraded every year. Specifically, we analyzed ten microsatellites and observed a 60% reduction in the effective number of breeders in the hatchery (harmonic mean Nb = 45) compared to the wild (Nb = 111). Hatchery fish consequently displayed reduced genetic diversity and large temporal genetic divergence compared to wild fish. To ensure the benefit of conservation-based husbandry, spawning protocols should be based on scientific theory and be practical within the physical and biological constraints of the system. Finally, if 28 conservation issues are considered to be the most important issue for hatchery propagation, then production goals may need to be forfeited.

Use of sibship to infer number of parents gives higher estimate of spawning escapement than redd/carcass surveys in Chinook salmon

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Juvenile Chinook salmon in the South Fork of the Nooksack River (draining into Bellingham Bay, WA) were genotyped at 14 microsatellite loci over 4 years (Brood years 2007-2010, total N = 15,677), with individuals classified using individual assignment to one of three populations known to occur in the Nooksack River: North Fork spring, South Fork spring, and fall. For each Brood year, the full and half-sib relationships were inferred for juveniles from each population using the program COLONY. Rarefaction analysis applied to the inferred parentage of those sibships was then used to estimate the successful number of spawners, across all populations. Estimates of successful spawners ranged from 150% to 340% of the total estimated adult escapement (i.e., census size, abundance) for each of the four years based on visual monitoring methods using redd surveys and carcass counts. For visual surveys, population-specific escapement estimates were generated by genetically assigning Chinook salmon carcasses to population-of-origin and then partitioning the overall escapement estimate by the proportion each population represented in the recovered carcasses. In contrast, parental reconstruction from juvenile genetic data inferred more parents in most cases than redd counts and carcass surveys suggested were present, but the largest increase was for the juveniles assigned to the South Fork spring population. For the years 2007-2010 the redd count/carcass survey estimates were based on a total of 188 recovered carcasses across four years, with total escapement estimated to be 1804. Of those 188 carcasses, only 27 were assigned to the South Fork spring population (range = 2-16 per year), which equated to a South Fork spring total escapement estimate of 181. In comparison, genetic rarefaction estimated the successful number of breeders present in the SF over that same period to be 604. Difficulties with observing redds, finding carcasses, and assigning those carcasses to population-of-origin may have contributed to the observed discrepancy between visual and genetic-based population measures.

Realizing the promise of Parentage Based Tagging for addressing conservation and management of steelhead in the Columbia River basin

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Since 2008, cooperating state, tribal, and federal agencies have genetically sampled and genotyped steelhead broodstock at all hatcheries in the Snake River Basin in Idaho, Oregon, and Washington. This regional implementation of Parentage Based Tagging has resulted in the genetic tagging of >95% of the hatchery smolts produced in the Snake River (~12 million smolts per year). This accounts for ~61% of the hatchery steelhead that are released in the entire Columbia River basin each year. The IDFG and CRITFC are committed to using PBT technology to complement existing mechanical tagging evaluations, or in some cases replace mechanical tags for assessments where their use may have limited precision or uncertain accuracy. This poster provides examples of current sampling programs that are in place throughout the Columbia River basin that utilize the Snake River PBT baseline to address conservation and management questions throughout the region. Collaborative efforts are currently underway to extend this technology throughout the Columbia River Basin.

Stock-specific distributions of yearling Chinook salmon along the Oregon and Washington coasts

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We used a regional GAPS microsatellite DNA baseline and genetic stock identification methods to estimate the origins of yearling Chinook salmon sampled in May (2006-2012) and June (1998-2012) at a series of fixed trawling sites along the Oregon and Washington coasts. Yearlings were largely from 6 Columbia River Basin genetic stocks (>95%) and were nearly all (>93%) hatchery fish. Spatial distributions were characterized by calculating the mean latitude and distance from shore of each stock. In late May, yearlings from interior basin populations, including those from the Snake River, were distributed farther offshore and not as far north as fish from the lower basin (Willamette River and West Cascade spring stocks). The relatively late release of yearlings from interior basin hatcheries (e.g., in March and April), their long-distance downstream migrations, and later ocean entry timing likely shape these differences in initial distributions. However, intrinsic differences in ocean migration behavior become apparent from analyses of samples collected one month later. By late June, the more rapidly migrating interior basin spring run fish are significantly farther north than yearlings from the lower basin and from summer/fall run populations. Moreover, the summer/fall and lower basin yearlings are more spread out in latitude, an attribute evident for these stocks in previous coast-wide studies. We found that the stocks also differ in mean distance from shore with interior basin spring yearlings farthest offshore, lower river springs closest to shore, and summer/fall run fish intermediate in location. The contrasting distributions outlined above occur consistently each outmigration year. Our results suggest that stock-specific differences in ocean distributions are influenced initially by factors prior to and during emigration from freshwater and subsequently by life-history or behavioral differences that are expressed after ocean entry.