Abstracts
Coastwide Salmonid Genetics Meeting 2018

Oral Presentations
(in alphabetical order by first author’s last name)

1. A geographic and genomic survey of variation at the GREB1L region in *Oncorhynchus mykiss*
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Two recent studies (Hess et al. 2016 and Prince et al. 2017) have identified an association between variation in the GREB1L region on Chromosome 28 and the premature migration life history in steelhead Trout (*Oncorhynchus mykiss*). We report on two surveys of genetic variation in this region across a broad geographic range. First, we successfully designed assays for 7 of the SNPs within a 70 Kb region found to be associated with premature migration in Prince et al. Then we genotyped these SNPs in 1,218 fish across 31 anadromous and resident populations from California, Oregon and Washington. Our results confirm the occurrence of premature-migration-associated (PMA) alleles in populations of summer steelhead. They also indicate strong linkage disequilibrium in the GREB1L region, abundant heterozygotes at the PMA SNPs, and the occurrence of haplotypes carrying many PMA alleles in widely dispersed regions, including Southern California. Subsequently we used the whole genome sequence data of 123 fish from throughout the range to investigate the haplotypic structure in the GREB1L region. There are at least three substantially different haplotypes amongst those in premature-migrating populations, and nearly identical haplotypes are found broadly dispersed, for example, from Alaska to the Middle Fork Eel River. The PMA haplotypes are markedly diverged from all other haplotypes, but are closer in genetic distance to a Chinook Salmon outgroup than the other haplotype lineages. This all suggests a long and complex history for the GREB1L region in *O. mykiss*.

2. Retention of a chromosomal inversion from an ocean-going ancestor provides the genetic basis for alternative freshwater ecotypes
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Migratory and resident behavior patterns in animals are controlled by a complex genetic architecture. Rainbow Trout (*Oncorhynchus mykiss*) is a salmonid fish that spawns in streams but exhibits three primary life history alternatives: stream-resident (fluvial), lake-migrant (adfluvial), and ocean-migrant (anadromous). Previous studies established the adaptive genetic divergence of fluvial and anadromous *O. mykiss*, including the presence of an inversion within chromosome 5 (Omy05) that maintains a suite of linked genes controlling migratory behavior. However, adfluvial trout are migratory without being
anadromous, and this dichotomy has not been investigated from evolutionary perspectives. We assessed adaptive genetic divergence of wild, native nonanadromous Rainbow Trout occupying connected stream and lake habitats in a southwest Alaskan watershed to determine if divergence of a suite of traits associated with migration between fluvial and adfluvial fish were present and analogous to that documented in fluvial and anadromous *O. mykiss*. Restriction site-associated DNA (RAD) sequencing revealed both the Omy05 inversion and other putative adaptive single nucleotide polymorphisms (SNPs) associated with migratory behavior, confirming the genetic divergence of adfluvial and fluvial individuals in sympatry. The presence of a genetic basis for migration into lakes, parallel to that documented for anadromy, indicates that the adfluvial ecotype must be recognized separately from the fluvial form of *O. mykiss* even though both are nonanadromous. These results augment our knowledge of the genetic architecture underlying migration and the importance of chromosomal inversions in promoting and sustaining intraspecific diversity.

3. **Comparison of CWT with parentage-based tagging and genetic stock identification in a large-scale Coho Salmon fisheries application in British Columbia**

Terry D. Beacham, Colin Wallace, Kim Jonsen, Brenda McIntosh, John R. Candy, David Willis, Cheryl Lynch, Jean-Sébastien Moore, Louis Bernatchez, and Ruth E. Withler

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Parentage-based tagging (PBT) and genetic stock identification (GSI) were used to identify individual Coho Salmon (*Oncorhynchus kisutch*) sampled in fisheries and escapements in British Columbia to specific conservation units (CU), populations, and broodyears. Individuals were genotyped at 304 single nucleotide polymorphisms (SNPs) via direct sequencing of amplicons. Accuracy of assignment via PBT for 543 jack (age 2) and 191 coded-wire tag (CWT, age 3) Coho Salmon to the correct population was 100%, with a 236-population baseline available for analysis. For eight populations present in the sample of 573 jacks, the average error utilizing GSI only was 0.5% per population, declining to 0.2% utilizing both PBT and GSI. Application of a PBT+GSI system of identification to over 7,000 individuals in 2017 fishery samples and 8,000 individuals in escapements provided high-resolution estimates of stock composition, catch, and exploitation rate by CU or population, and thus provided an alternate and more effective method relative to CWTs in the assessment and management of Canadian-origin Coho Salmon.

4. **Development of a genetic linkage map for Cisco (Coregonus artedi) to facilitate integrated studies of adaptive diversity**

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Throughout their circumpolar range, species within the coregonine complex are ecologically and socioeconomically important and are heavily impacted by human activities. In the Laurentian Great Lakes, abundance and diversity of ciscoes is well below historic levels. The species complex has generally been preserved in Lake Superior, Lakes Huron and Michigan still contain at least one deepwater cisco form and one pelagic form, Lake Ontario only contains pelagic form, and ciscoes have been extirpated from Lake Erie. Accurate identification of forms is critical for the development of effective restoration and management plans. Currently, form classifications are based on morphometric variation. However, the relative influence of phenotypic plasticity and heritable genetic differences in
determining these forms is not well understood. The overall goal of this research is to construct sex-specific linkage maps using data from thousands of genetic markers genotyped in haploid and diploid families produced from *C. ardedi* collected in northern Lake Huron. The linkage map will be used as a genetic resource that will facilitate research with the aim of determining the degree of heritable genetic differences among cisco forms.

5. **Evaluating the impact of reference genome choice on analysis of a Coho Salmon RADseq dataset**  
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The advent of high-throughput sequencing (HTS) and its rapidly declining cost has made genomic-level analyses feasible for non-model organisms. A critical step of many HTS pipelines involves aligning reads to a reference genome and calling variants based on discrepancies between observed base calls and the reference sequences. Only a small percentage of species have publically-available reference genomes. Therefore, a common practice is to align reads to the reference genome of an organism related to the target species; however, it is unknown whether this will impact read alignment and bias genotyping. There are also no guidelines as to how phylogenetically similar the target species and reference genome should be. In this study I conducted an experiment using RADseq data generated for Coho Salmon to address these questions. A Coho reference genome is available, as are genomes for salmonids of varying phylogenetic distance from this species (Chinook Salmon, Rainbow Trout, Atlantic Salmon, Arctic char, and European Grayling). I aligned the Coho RADseq reads to all six of these salmonid genomes using different alignment programs and identified variants using different genotype callers. The results provide a comparison of how phylogenetic distance between the target species and reference genome impacts read mapping, variant calling, and biological inference. I also assessed whether certain genotyping approaches, such as those based on estimating genotype probabilities, are more robust to the reference genome choice. These findings highlight the importance of critically evaluating the selection of variables for bioinformatics pipelines in HTS studies. It also emphasizes the need to identify best practices and guidelines for the burgeoning field of conservation genomics.

6. **Population Genetic Analysis of Chehalis River Basin Chinook Salmon (Oncorhynchus tshawytscha)**  
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Understanding the population structure of wild salmonids in the Chehalis River is an important part of the Chehalis Flood and Aquatic Species Project and contributes to the Chehalis Basin Flood Hazard Project and Aquatic Species Enhancement Plan. Here we examined the population structure of wild Chinook Salmon (*Oncorhynchus tshawytscha*) in the Chehalis river basin. Our objectives were to 1) identify population structure within the Chehalis River and its tributaries, 2) investigate if run timing (spring and fall runs) influenced the population structure within the Chehalis basin, and 3) determine the
population structure of the Chehalis basin in relation to baseline populations from Washington state and British Columbia. Genetic data indicate, that within the Chehalis basin, the population structure consists of two general clusters, 1) a downstream group (Wynoochee River, Wishkah River, Satsop River, Black River and the Chehalis mainstem) and 2) an upstream group (South Fork and Upper Chehalis River, Newaukum River and Skookumchuck River). This pattern of slight differentiation between downstream and upstream collections, appears to be largely driven by isolation by distance, which is a common driver of population structure in salmonid populations. Clustering and tests of genetic differentiation revealed that fall and spring runs were not genetically distinct. Analysis of the population structure of the Chehalis basin and Washington state Chinook Salmon baseline populations revealed three major branches 1: Puget Sound and British Columbia, 2) Lower Columbia, and 3) Washington Coast. Within the Washington Coast group, the Chehalis basin clustered most closely with Willapa Bay Rivers (North River, Fall River, Naselle River, Nemah River and Forks Creek).

7.
Development and evaluation of a SNP marker panel for PBT of Yellowstone Cutthroat Trout in Henrys Lake, Idaho
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Henrys Lake is a stronghold for Yellowstone Cutthroat Trout (YCT) and a popular trophy fishing lake in Idaho. Over the last 30 years, IDFG has assisted with habitat restoration in tributaries to the lake in an effort to increase natural recruitment of adfluvial YCT. In the past decade, these efforts have increased substantially. Confounding the ability to estimate natural recruitment and judge the success of habitat restoration efforts, is the large population of hatchery YCT stocked annually (~1,000,000 per year), of which only a small fraction (~10%) are marked with an adipose clip. Managers are currently interested in whether the Parentage Based Tagging (PBT) of the hatchery broodstock could be a cost effective method of providing more precise estimates of natural recruitment in the lake, as well as improve harvest and survival monitoring of hatchery and wild YCT. This presentation summarizes the first year of work which included the development and optimization of a SNP genetic marker panel, the sampling and genotyping of all hatchery broodstock (N = 1,806), and the testing of dual and single parentage assignments on juveniles of known parentage.

8.
Monitoring genetic diversity from marine fisheries: using GSI assigned individuals to estimate effective population size
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Vast amount of genotypic data are available from fisheries management applications along the coast of British Columbia for a number of salmon species. Using stock assignments obtained from genetic stock identification, may provide a supplemental use of these data in monitoring genetic diversity of harvested stocks. As an example of this application, we analyzed 42,135 genotypes from north coast British Columbia Chinook Salmon fisheries near Haida Gwaii collected since 2000. These fisheries cast a broad
net, intercepting returning Chinook Salmon along the entire coast from Nass-Skeena rivers to Southern Oregon coastal rivers. Recently the dominant catch in these fisheries are the interior sub-yearling stocks from the South Thompson River (Shuswap Summers age 0.3 and South Thompson Summers age 0.3) and Columbia River (Interior Columbia Summer/Falls). Estimates of effective population size ($Ne^e$) are of great interest because they inform the genetic health of a population. $Ne^e$ has been applied mostly to small populations of conservation concern, seeing limited application for larger harvested populations. Using the Linkage Disequilibrium (LDNe) method we focus on the two South Thompson River Conservation Units. A number of challenges arise when determining $Ne^e$ including, GSI accuracy, metapopulational effects, multiple age structure, minimum allele frequencies, and accuracy of drift measures with larger populations. Simulations may inform us about the uncertainties around the LDNe estimation.

9. **The Chum Technical Committee: serving the Pacific Salmon Commission since 1985**  
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Since the implementation of the Pacific Salmon Treaty in 1985, a technical work group consisting of Canadian and US biologists and geneticists has been active in coordinating and conducting genetic stock identification (GSI) surveys of relevant mixed stock fisheries of Chum Salmon in southern BC and WA state. Since 2008 the PSC Chum Technical Committee has analyzed ~4,000 individuals annually from major fisheries in Canadian waters, Johnstone Strait (Areas 12 and 13), east coast of Vancouver Island (Areas 14 to 18) and in US waters near the San Juan Islands/Point Roberts (Areas 7/7a). The current Chum Salmon mixed stock analysis uses a 14 locus microsatellite baseline consisting of 130 reference collections, including stocks from the northern tip of Vancouver Island to Puget Sound and Coastal Washington. WDFW and CDFO labs are now shifting technologies from microsatellites to single nucleotide polymorphisms (SNPs). An initial Chum SNP baseline includes 31 Chum Salmon populations from the US and CAN Southern Boundary region genotyped with 186 SNPs. Simulations show that mixed stock components are better resolved with SNPs. We present a short video describing a bilateral genetics study conducted in the Strait of Juan de Fuca exploring run timing and abundance of Chum stocks moving through the US and CA portions of the strait.

10. **Fitness tradeoffs and frequency-dependent selection explain persistent life history variation in Steelhead (Oncorhynchus mykiss)**  
Mark Christie$^{1,2}$, Gordon McNickle$^1$, Rod French$^3$ and Michael Blouin$^2$  
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Steelhead exhibit a wide variety of life history strategies, yet how this variation is maintained is unclear. We used a 16-year pedigree of winter-run steelhead from the Hood River to examine the maintenance of variation in two life history traits: the number of lifetime spawning events (semelparity versus iteroparity) and number of years spent at sea before first spawning. Repeat-spawning fish had double the lifetime fitness of single-spawning fish, but fewer offspring than single-spawners the first time they
spawned. Thus, repeat-spawners appear to trade early fitness for an increased probability of the big payoff if they can return a second time. As for age of return, males showed the expected increase in fitness with increasing age at return. For females, on the other hand, 3-year olds had the highest average fitness, even though 4 and 5-year olds are larger and more fecund. However, there was a strong negative relationship between proportion of the run that was 4 or 5 year olds and their average fitness. Thus, there appears to be negative frequency dependent selection on age of return, a form of balancing selection that could easily maintain genetic variation for this trait. Using a combination of mathematical and individual-based models parameterized with our empirical estimates, we demonstrate that both fitness trade-offs and negative frequency-dependent selection could maintain the diverse life history strategies found in this population.

11. Physiological and genomic signatures of evolutionary thermal adaptation in Redband Trout from extreme climates
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Salmonids have strict thermal requirements in the progression of life-history events such as development, migration and reproduction. Understanding the underlying physiological and genetic components of thermal requirements can address broad questions in areas of adaptive capacity and biogeographical limitations under scenarios of climate change. Here, we used a comparative approach in a well-characterized model system for thermal adaptation, which is the Redband Trout (*Oncorhynchus mykiss gairdneri*) in the interior Columbia River of the United States that occupy diverse environmental conditions from hot desert, through cool montane to cold montane streams. We present evidence for adaptive divergence among populations in cardiac function and genomic regions. Cardiac phenotypes of individual fish were measured in the field with a custom-built electrocardiogram apparatus. Maximum heart rate and its rate-limiting temperature during acute warming were significantly higher in fish that have evolved in desert climates compared to montane climates. Association mapping with 526,301 SNPs revealed signatures of thermal selection both within and among ecotypes. Among desert and montane populations, 413 SNPs were identified as outliers for adaptive selection and ~5% of these loci showed significant association with average summer water temperatures. Within ecotypes, 207 genomic regions were strongly associated with either maximum heart rate or rate limiting temperatures among individuals. Annotation of candidate markers provided candidate genes that underlie thermal adaptation, including pathways associated with cardiac function, neuroendocrine system and stress response. Results here advance our knowledge on evolutionary processes of thermal adaptation in aquatic ectotherms.
12. **Assembling the Arctic Charr, Chinook, Sockeye, Pink, and Chum Salmon genomes and identifying orthologs between species**
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An outline of the progress and results of the project to sequence and assemble several of the Pacific salmon and Arctic Charr genomes will be presented. In addition, the preliminary results of attempts to identify orthologs between all salmonid species will be discussed. The presented methodology for identifying orthologs utilizes synteny and protein similarity to identify orthologs. This methodology was developed to mitigate the difficulties in identifying orthologous genes between salmonid species, which can be complicated by multiple gene copies and differing nomenclatures between species. Instead of individual researchers independently identifying orthologous genes repeatedly, our hope is that they would be able to look up all orthologs from a table that used well documented methodologies. With the identified orthologs between species, we also hope to identify genes that have unique gene expression profiles within a species and may have influenced species specific traits.

13. **Genetic stock identification in California: the recent past and near future**
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From 2012-2016, California implemented intensive sampling of the commercial Chinook Salmon fishery, coupled with GPS monitoring of fishing effort and catch locations. By assigning these fishery samples to the SNP baseline of Clemento et al. 2014, we were able to determine population structure of the catch through both space and time. In addition to the GSI analyses, we were able to recover offspring from hatchery and wild stocks that have been more intensively sampled and monitored via parentage-based tagging (PBT), revealing Cohort and family information. This talk will explore the spatial and temporal patterns of population-specific ocean recoveries and the important inference available from the PBT analyses. We will also discuss the potential of microhaplotypes for building upon and expanding this work in the future.

14. **Investigating the effects of early-rearing environment on sperm DNA methylation programming in hatchery reared Steelhead (Oncorhynchus mykiss)**
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Relative reproductive success studies have documented substantial fitness loss for wild steelhead after a single generation of rearing in the hatchery, but the relative contribution of genetic selection and/or environmentally-induced heritable epigenetic changes passed through the germline are relatively unknown. The aim of this work is to examine the effects of early-rearing environment on epigenetic programming in steelhead. In an initial study, we described epigenetic variation in hatchery and natural-
origin (wild) steelhead from the Methow River. We identified significant differences in DNA methylation between hatchery and natural-origin fish, but also observed a high degree of epigenetic variation among individuals necessitating studies on how epigenetic and genetic variation interplay to promote such differences, and how much epigenetic variation is inherited. To limit the potential confounding effects of genetic variation, a second study using controlled genetic backgrounds and simulated ‘hatchery’ and ‘natural’ environments was performed. Steelhead embryos from 20 families were split across hatchery and natural treatments. After 8 months in the treatment environments fish were tagged and raised to maturity in a common environment. Sperm samples were analyzed using RRBS. Hierarchical clustering of genome-wide methylation patterns shows strong clustering within family regardless of rearing environment. These results highlight a major challenge in DNA methylation studies in natural populations, where population structure and kinship among samples is typically not known, let alone controlled for. Our findings emphasize the importance of understanding the effects of kinship among studied individuals in order to properly analyze and interpret DNA methylation data.

15. Recovery strategies for listed fish: the release of mature Coho Salmon (Oncorhynchus kisutch) into spawning habitat in central California
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Populations of Coho Salmon in the Central California Coast (CCC) Coho Salmon ESU are ESA-listed as Endangered. The challenges of being a Coho Salmon in California are numerous: small effective population size, inbreeding, low genetic diversity, habitat loss, drought, wildfire and/or disease have adversely impacted these populations. In many basins, extinction risk is high and ever-present. In spite of this overall decline, some CCC streams, e.g., Lagunitas Creek, continue to sustain populations with relatively high genetic diversity. Warm Springs Hatchery (WSH), a mitigation facility on the Russian River, operates a captive breeding program for Coho, and is a hub for conservation efforts in Marin and Sonoma counties. Supplementing traditional genetic broodstock management techniques (e.g., inbreeding avoidance and managed outbreeding) employed in the hatchery setting, a relatively new strategy sees excess broodstock individuals released as maturing adults directly into spawning habitat. This strategy has been employed in Salmon and Walker creeks, from which Coho Salmon previously were extirpated. Parentage analysis of wild juveniles revealed evidence of successful natural spawning by the adults released there. The presence of juveniles in Walker Creek in subsequent years, when no adults were released, suggests continued natural spawning by descendants of released adults. We find further evidence of successful reproduction by released adults in Redwood Creek (Muir Woods), where wild Coho juveniles were rescued from drying habitat during the 2012-2016 drought, reared to maturity at WSH, and released as adults back into their natal stream, where they produced offspring. Here we highlight key results from the first fourteen years of the adult release program.
16. **Salmon genetics research within the Alaska Fisheries Science Center**  
Jeffrey R. Guyon, Christine M. Kondzela, Charles M. Guthrie III, Sharon Wildes, Hanhvan T. Nguyen, Jacqueline A. Whittle, Maxwell Marsh, Genevieve Johnson, and Dione Quadra  
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The Alaska Fisheries Science Center at Auke Bay Laboratories has a long history of salmon genetics in Alaska, working collaboratively with Federal, state, academic, and international partners in the management of our fisheries. Outlined in this presentation are some of the projects from the past and how they've framed our current salmon projects, guiding our understanding of bycatch impacts in Alaskan communities and, through partnerships with the Alaska Department of Fish and Game, catch in Treaty delimited fisheries.

17. **The road to diploid and the fate of ohnologs: Partial tetrasomy enables conservation of duplicate genes in Rainbow Trout**  
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A whole-genome duplication event occurred in the common ancestor of the salmonid fishes approximately 88 million years ago. Since that event, salmonid genomes have reverted partially to diploidy, with ~10-15% still exhibiting tetrasomic inheritance. It is well known that tetrasomic inheritance is maintained in homologs of these regions throughout the salmonid family. However, why the inheritance patterns of these regions are maintained as tetrasomic remain largely unknown. To that end, we utilized the most recent Rainbow Trout genome assembly and transcriptome data to examine the fate of ohnologs following the salmonid whole-genome duplication. Sequence identity between ohnologs located within tetrasomic regions is higher than between ohnologs found in disomic regions, suggesting tetrasomic inheritance suppresses mutation and recombination. In addition, gene expression patterns are more similar between tetrasomically inherited ohnologs than disomically inherited ohnologs, suggesting reduced neofunctionalization in tetrasomic regions. Enrichment testing for Gene Ontology terms identified 16 over-represented terms in tetrasomically inherited ohnologs including terms associated with oxygen binding and utilization of iron. However, why these genes remain in tetrasomic regions is difficult to answer. It could be that we have identified "dangerous duplicates", i.e., genes that cannot take on new roles following whole-genome duplications. Alternatively, there may be an adaptive advantage for retaining genes as functional duplicates in tetrasomic regions. Presumably, there is considerable selection pressure maintaining these genes in tetrasomic regions as movement of these genes into disomic regions could affect both their sequence identity and their gene expression patterns.
18. Adaptation of the genotyping-in-thousands by sequencing (GTseq) protocol in a high throughput lab  
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The Gene Conservation Laboratory (GCL) at the Alaska Department of Fish and Game is responsible for protecting the genetic integrity of wild populations of fish, wildlife, and aquatic plants, and for using genetic information to help manage these resources in a sustainable manner. The GCL currently processes more than 85,000 genetic samples per year and houses an archive of more than 4 million samples from Alaska and around the world. Genotyping-in-thousands by sequencing (GTseq) protocol is currently used by other fish genetics labs; adaptation of that protocol was necessary to reach the high-throughput goals of the GCL. The GCL implemented a workflow that included multiple complex liquid handling instruments to increase production and reduce errors. A case study processing 10,144 fish for 665 markers in a 6-week timeframe will be discussed. Although genotyping was successful in this study, we observed a general decrease in the proportion of mapped reads and increase in non-target product and look forward to discussing ideas for optimizing the protocol.

19. Application of parentage-based tagging for monitoring steelhead returning to Mad River Hatchery, California  
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Integrated hatchery programs require application of marking methods that allow separate tracking of hatchery and natural populations so that the genetic effects of domestication and divergence between hatchery and natural populations can be monitored and avoided. Parentage-based tagging (PBT) is a powerful approach for monitoring hatchery populations of salmonids. Here we applied parentage-based tagging methods to monitor steelhead returning to the Mad River Hatchery (MRH), an integrated program that has received relatively little monitoring, but supports one of the most popular steelhead fishing locations in California. We generated SNP genotypes at 96 loci for all adult steelhead broodstock spawned at MRH over a nine year period (N=1572; 2009-2017) and using parentage analysis identified 965 trios (both parents and offspring). Our analysis resolved a large difference in the proportion of hatchery-origin individuals used as broodstock as indicated by pedigrees (0.87) and traditional adipose fin tagging (0.58). The difference between approaches likely resulted from a failure to clip 100% of hatchery releases, which in turn caused hatchery-origin individuals to be falsely assigned as natural-origin when the fish returned to the hatchery to spawn. Our results indicate that the MRH is not meeting its 50:50 natural to hatchery integration target, a goal put in place to minimize domestication through artificial selection. The pedigree reconstruction also allowed for estimation of narrow sense heritability for spawn day at 0.242 to 0.470, indicating this trait is expected to exhibit a strong response to any artificial selection imposed by hatchery spawning.
20. Phenotypic factors affecting fitness in a supplemented population of Chinook Salmon
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Supportive breeding has become a common practice for species of conservation concern, yet the fitness effects of captive breeding programs render them controversial. In order to evaluate the effects of supplementation and determine the phenotypic factors influencing the fitness of a threatened population of Chinook Salmon (Oncorhynchus tshawytscha), we used Genotyping-in-Thousands by Sequencing (GT-seq) to genotype samples and generate pedigrees from fish returning to Johnson Creek, Idaho over 19 years. We estimated reproductive success and used generalized linear models to determine if origin (hatchery or natural) or phenotypic traits (timing of arrival to spawning grounds and body length) significantly predicted reproductive success. We show that this supplementation program with 100% natural-origin broodstock provided a long-term demographic boost to the population, but hatchery-origin fish were less successful at reproducing in the wild and produced fewer offspring compared to natural-origin fish (p<0.05). However, when hatchery-origin fish did reproduce successfully, they had similar fitness as natural-origin fish (mean hatchery by hatchery cross relative reproductive success=1.04 females, 1.20 males) and did not reduce the fitness of natural-origin fish when mating together (mean hatchery by natural cross relative reproductive success=1.11 females, 1.13 males). While arrival year and body length were significant predictors of fitness for both males and females (p<0.01), arrival day was significant for males (p<0.01) but not females (p>0.05). These results indicate that supplementation programs can be effective at meeting conservation goals of increasing abundance while limiting fitness effects on wild populations.

21. Understanding the genetic basis of ecotypic variation in Sockeye Salmon from across Alaska
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The genetic mechanisms that facilitate adaptive radiation remain poorly understood, especially in non-model organisms. Here, we genotyped neutral SNPs, SNPs in islands of divergence identified in a previous study, and a region of the major histocompatibility complex in 32 populations of sockeye Salmon to investigate signatures of selection across Alaska. Populations from multiple ecotypes were sampled from seven drainages spanning a range of 2,000 km, facilitating investigation of adaptive radiation in systems with differing habitats and colonization histories. We found strong signatures of parallel selection across drainages, suggesting that the same loci undergo divergent selection during adaptive radiation. However, patterns of differentiation at loci that were putatively under selection were not associated with ecotypes and were not correlated among drainages, suggesting that these loci are responding differently to a mosaic of selective pressures. Our study provides some of the first evidence that conserved genomic islands may be involved in adaptive divergence of salmon populations. Additionally, our data provide further support for the hypothesis that sockeye Salmon inhabiting rivers that are not connected to lakes are the ancestral form and that these populations have repeatedly recolonized lake systems as they have become available after glacial recession. Finally, our results
highlight the value and importance of validating outlier loci by screening additional populations and regions, a practice that will hopefully become more common in the future.

22. **What can we learn from small annual samples of Fraser River Sockeye caught in Alaska?**


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Infrequent bycatch of Fraser sockeye in Alaskan Pink Salmon fisheries (mean <1%) can constitute a non-negligible fraction of the Fraser sockeye abundance in some years. As stated in the Pacific Salmon Treaty, however, “the extent of these incidental catches is unpredictable from year to year.” A cross-agency, two-stage GSI process was initiated in 2011 to identify specific Fraser sockeye stocks in Alaskan catches, with the goal of accumulating a long-term data set for studying the migrations of these fish and, eventually, for making successful predictions regarding their various marine distributions and vulnerabilities to harvest. Individuals identified as probable southern migrants using SNPs were subsequently analyzed against a Fraser-specific microsatellite baseline, and we studied inter- and intra-annual variation within Fraser stock compositions in Alaskan catches. We compared these samples to collections taken over the same time periods near the Fraser River. On an annual basis, compositions of Fraser sockeye in Alaska differed consistently from the compositions observed in fish returning to the Fraser, e.g. stocks that return to the Fraser earlier and take a more southern route around Vancouver Island were under-represented in Alaskan samples. In contrast, when analyzed on a weekly basis, Alaskan samples were similar to samples collected near the Fraser River, as revealed by subjecting timing indices (defined by the progression of stock mixtures over time) to ANCOVA. This concordance challenges assumptions about the behavior of Fraser sockeye and has implications for the interpretation of estimated interceptions in Alaska. Combined with CPUE estimates, this analytical framework may improve our ability to track marine distributions as climate changes.

23. **Genetic monitoring of a Sockeye Salmon reintroduction: a case study**

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Sockeye Salmon (*Oncorhynchus nerka*) often utilize lake shore habitat for spawning, and typically depend on nursery lakes for juvenile rearing. These habitat-specific life history aspects are unique among Pacific salmon species, but limit the distribution of Sockeye Salmon in the southern portion of the species range. During the last century, Sockeye Salmon were extirpated from several lake systems in the Columbia River Basin as migratory paths became obstructed by dams. Recently there has been concerted interest in reestablishing natural spawning populations where Sockeye Salmon were historically present. In 2009 a reintroduction program was initiated in Cle Elum Reservoir using two outplant donor stocks from Osoyoos Lake (OSO) and Lake Wenatchee (WEN) in the upper Columbia River. We used genetic stock identification methods to differentiate between outplant stocks and to evaluate reproductive success in the reservoir environment where anadromous fish had been absent for over 100 years. We observed stock distinctions in both spatial and temporal use of habitat. Carcass
survey data indicated an earlier spawn time and greater spawner abundance farther upstream for WEN fish, while OSO fish tended to spawn later in the season and in greater abundance downstream or near the lake shore. Hybrid individuals (WEN-x-OSO) accounted for only 5% of sampled juveniles and 4% of natural origin adult returns. Unequal abundances of pure stock (75% WEN and 25% OSO) and temporally variable age structure among emigrating smolts suggests stock-specific differential growth rates and survival during the juvenile rearing period. However, the mean fork length size of smolts emigrating from Cle Elum Reservoir was significantly larger (size-at-age) compared to those in either donor population.

24. **Detection of a novel chromosome inversion in Western Alaska Chum Salmon**
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Chromosomal inversions result in regions of suppressed recombination between chromosomal forms. Ultimately, this can lead to fixation of alternate alleles and the efficient selection of co-adapted gene complexes. Inversions have been detected in multiple species of salmon, most notably the Omy5 inversion in Rainbow Trout that is associated with migratory life-history variation. Here we report the detection of a novel chromosomal inversion in Western Alaska Chum Salmon based on patterns of extended linkage disequilibrium (LD). We identified two independent and overlapping patterns of LD that spanned 20 Mb on the Chum Salmon ortholog of Omy28. Examination of genotype patterns in these LD blocks revealed that one pattern of LD was consistent with a genomic inversion while the other was consistent with a sex-determining region. Genotype patterns are consistent with the inversion originating on the X-chromosome. The co-location of an inversion and sex-determining region has important implications for evolutionary potential and may facilitate the evolution of sexually antagonistic traits.

25. **Three generation pedigree reconstruction in wild Sockeye Salmon (O. nerka) using a GTseq amplicon panel**
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Pedigree analysis can provide insight into a broad range of questions related to the evolutionary biology, ecology, and behavior of species. Here we reconstruct a pedigree from 12 years of sockeye Salmon runs from the upper Wood River System, Bristol Bay, Alaska. This system is composed of two small adjacent creeks, making it ideal for examining the role of gene flow in influencing the adaptation of fitness related traits. Recent developments in multiplex amplicon sequencing, such as GTseq, have made it cost effective to develop and use panels of hundreds of single nucleotide polymorphisms (SNPs) for parentage assignment in thousands of individuals. SNP panels have the benefit of being modular and efficient; different groups of SNPs can be combined in a panel to address a variety of questions in downstream analyses. Here we describe the development and application of a GTseq SNP panel of 200 loci, designed to address the following tasks: (1) pedigree reconstruction, (2) population assignment, and
(3) study of evolutionary processes based on loci recently identified in the literature. We intend to use this panel to address ecological and evolutionary questions related to population processes, such as the effects of return timing, straying, and inbreeding on reproductive success, adaptive potential, and population productivity.

26. **Genetic mixture analysis supports re-calibration of the Fishery Regulation Assessment Model**

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Management of the commercially important Washington coastal Chinook Salmon troll fishery depends on the Chinook Fishery Regulation Assessment Model (FRAM). The Chinook FRAM uses historical and contemporary coded-wire tag (CWT) recoveries to estimate abundance and exploitation rates for particular indicator stocks. Those estimates are used to set limits on overall harvest and protect sensitive stocks. Current efforts are underway to implement a newer “base period” (time period on which exploitation rates are based). Our collaboration of science, management, and industry used genetic mixture modeling to provide independent stock composition estimates supporting FRAM recalibration. Genetic modeling suggests total catch includes a much smaller proportion of a limiting Columbia River stock and a larger fraction of Canadian stocks, as well as an abundant Oregon coastal stock not previously included in the FRAM. Our results focus attention on particular stocks that will benefit from refinements in the Chinook FRAM.

27. **Applied genomics for conservation of distinct stocks and phenotypic diversity in Chinook Salmon**

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Genomic tools that allow for conservation of diverse phenotypes are still early in development but a novel reference genome was recently assembled for a Chinook Salmon (2.36 GB) from the interior Columbia River to enable association mapping of life history variation and phenotypic traits. Whole genome resequencing of populations with distinct life history traits provided evidence that divergent selection was extensive throughout the genome within and among phylogenetic lineages, suggesting a broad portfolio of phenotypic diversity exists in this species that is related to local adaptation and life history variation. Incorporating genetic markers associated with specific traits such as thermal tolerance, premature migration, adult run-timing, and age-at-maturity into high-throughput genotyping panels is expected to allow for expanded monitoring to maintain phenotypic diversity in natural populations and avoid unintentional artificial selection in conservation aquaculture programs.
28. Genetic analysis of a multi-generational salmon pedigree
Kathleen G. Neely, Jeff J. Hard, James Myers, and Mike Ford
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We are examining a multi-generation pedigree of natural- and hatchery-origin Wenatchee River Chinook Salmon (O. tshawytscha) with Bayesian generalized linear mixed models to estimate the genetic and environmental influences on variation in several life history traits in this population. We are also examining these data for evidence of natural selection on these traits, which include size, run timing, age, and lifetime reproductive success. This talk will go over the history of the population, the collection and organization of data for analysis, descriptions of the parameters we are looking at, what we have learned so far, and what we hope to learn when the analyses are complete.

29. Ancestry and adaptation of Rainbow Trout in Yosemite National Park
Devon Pearse
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The California Central Valley contains an abundance of rivers with historical and potential productivity for anadromous salmonids that are currently limited by impacts such as dams, water diversions, and high temperatures. We evaluated genetic variation in Rainbow Trout Oncorhynchus mykiss within the upper Tuolumne and Merced Rivers in and around Yosemite National Park in the context of both population origins (ancestry) and the evolutionary response to natural and artificial barriers to migration (adaptation). This analysis revealed that despite extensive stocking with hatchery Rainbow Trout strains throughout the study area, most populations retain largely indigenous ancestry. Adaptive genomic variation associated with anadromy was distributed throughout the study area, particularly in populations connected to reservoirs and known to support adfluvial life history variants. The fish in these rivers experience temperatures near the upper thermal limit for salmonids and represent an important reservoir of genomic diversity for adaptation to climate change. These results highlight the importance of local adaptation and the potential for resident trout populations above barrier dams to contribute to the recovery of anadromous O. mykiss through re-establishment of migratory connectivity between upstream spawning and rearing habitats and the ocean.

30. Rapture PBT facilitates inexpensive and high-throughput genetic assignment in salmonids
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Accurate tagging methods are crucial and widely implemented for management of migratory salmonids. Wild salmon populations are important for healthy fisheries economies, environments, and indigenous cultures. Physical tagging methods currently used can have difficulty with marker retention and give limited information on tagged individuals. Genetic tagging alternatives are not as cost efficient, have not been proven to work across species, and do not have flexible markers or easily identified regions for sequencing. Here we show the feasibility of using a new genomic method as a form of parent-based
tagging (PBT) where individuals are recorded through the inherent genetic relationships with their parents. We found that Rapture sequencing sufficiently provides data for parentage assignment and the same bait set can be used for both *O. mykiss* and *O. tshawytscha*. Our results also revealed that sperm contamination during hatchery spawning occurred in 13.5% of offspring, further confirming the need for genetic markers in accurate individual tagging. We found that Rapture PBT successfully assigned the progeny to parents with 98.3% accuracy and a cost of $3.10 per sample. We conclude that Rapture PBT provides a cost-effective and accurate alternative to coded wire tags, and other genetic-based methods.

31. Premature migration in Chinook Salmon from California’s Central Valley depends on the same genotype as premature migration in coastal populations
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Previous work determined that the GREB1L locus is highly associated with adult migration category in coastal locations containing both spring and fall runs of Chinook Salmon (*Onchorynchus tshawytscha*). Patterns of variation at the GREB1L locus in these populations suggested that alleles necessary for spring run Chinook Salmon resulted from a single evolutionary event. The Central Valley watershed of California (CV) is unique in that it contains four distinct runs of Chinook Salmon: spring, fall, late-fall, and winter. Similar to the spring run, the winter run enters freshwater sexually immature and spends months in freshwater prior to spawning. Thus, both the spring and winter runs display an uncoupling of freshwater entry and spawn time which has been referred to as premature migration. Here, we use sequence-capture methods and conduct phylogenetic analyses of the GREB1L locus to investigate the evolutionary history of premature migration in both coastal and CV Chinook Salmon populations. The increased sequence resolution in the GREB1L region revealed near-complete association between variation in the GREB1L region and migration category while patterns of variation at this locus demonstrated reciprocal monophyly with respect to migration category across all populations (coastal and CV). These findings suggest that premature migrating populations in the CV depend on the same premature migration alleles thought to be necessary in coastal populations. Results from this study further support premature migration alleles as the product of a single evolutionary event, increase the range of populations shown to depend on specific variation in the GREB1L region, and provide diagnostic SNP markers for this significant life-history variation across a broad range.

32. Progress on the Coho Salmon genome assembly project and whole genome re-sequencing in Canadian Rainbow Trout
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With this presentation, I will be discussing two related projects. First, to assist in wild stock management and to further develop hatchery and aquaculture stocks, genomic tools for Coho Salmon (*Oncorhynchus kisutch*) are being developed. Such efforts are complicated by the salmonid whole-
genome duplication event approximately 80-100 MYA. The status of the Coho Salmon genome, including the current chromosome-anchored assembly and ongoing work on improving assembly contiguity, will be presented. Additional work in genome annotation through 15-tissue RNA-seq, and SNP identification by way of 135 re-sequenced individuals, representing most of the geographic range of Coho Salmon in North America, will also be discussed. Second, while Rainbow Trout (*Oncorhynchus mykiss*) have been successfully introduced worldwide and are a staple in aquaculture, shifting conditions in warmth and acidity in their home range lead to concerns of susceptibility of small, unique populations. Cataloguing genetic variation will allow the development of genomic tools to support management of current populations and to select resilient trout in stocking programs. In this work, we use 66 re-sequenced trout to characterize whole-genome diversity within western Canada, with highly structured, low diversity interior populations standing in contrast with the highly diverse coastal populations that include anadromous steelhead. Incorporating an additional individuals from American populations allows us to look at phylogenetics range-wide and enabled the construction of a new 200K high-density SNP array. The development of genomic resources in these salmonid species will aid in management and conservation of wild populations, the analysis of hatchery efficacy and improvements in aquaculture production.

33. **Population genetic analysis of Chehalis River watershed winter steelhead (*Oncorhynchus mykiss*)**

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Understanding the population structure wild salmon and steelhead (*Oncorhynchus* spp.) in the Chehalis River is an important part of the Chehalis Flood and Aquatic Species Project and contributes to the Chehalis Basin Flood Hazard Project and Aquatic Species Enhancement Plan. Here, we examined the genetic population structure of wild winter-run steelhead (*O. mykiss*) in the Chehalis River basin. Specifically, our objectives were to determine the genetic relationship of Chehalis River steelhead with other *O. mykiss* in Washington State and to examine the genetic structure of *O. mykiss* within the Chehalis River basin. Chehalis River *O. mykiss* were more closely related to *O. mykiss* in nearby watersheds (Willapa River, Quinault River) than to more geographically distant populations. Within the Chehalis Basin, Chehalis steelhead were structured hierarchically. At the least inclusive hierarchical level, *O. mykiss* populations in the Chehalis were structured by spawning tributary, and this structure was temporally stable. At the most inclusive hierarchical level, spawning tributaries were clustered by headwater geography. Skookumchuck River collections had the reduced diversity typically seen in WDFWs hatchery Rainbow Trout and steelhead populations, which may be due to a population bottleneck, likely due to hatchery propagation. The Newaukum collection appeared to be composed of members of several different populations. Additional sampling and analysis of Black River *O. mykiss* may be interesting given its location in the transition zone from Olympic Mountains to Cascade Mountains headwaters, and of samples of Rainbow Trout from upstream of Skookumchuck Dam, which may provide additional insights into the genetic diversity issues of the Skookumchuck River collections.
34. **Integrating genetic data across programs and agencies to better understand harvest of Southeast Alaska Chinook Salmon throughout the Gulf of Alaska**
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Southeast Alaska (SEAK) has experienced a decline in Chinook Salmon productivity over the past decade, with abundance currently at an all-time low. While the decline in productivity is largely due to poor marine survival, heavy restrictions to commercial and sport fisheries have been imposed in SEAK to increase escapements. Recently there has been increased sampling and reporting of stock-composition using genetic mixed stock analysis and coded wire tags in a number of fisheries occurring across the Gulf of Alaska. Knowledge of the harvests of these declining stocks can improve fishery management. Here we attempt to synthesize data across these various programs to understand the magnitude and distribution of harvest in the Gulf of Alaska fisheries of Chinook Salmon originating from SEAK.

35. **Abundance estimates for Stillaguamish River Chinook Salmon using trans-generational genetic mark recapture and adjustment to historical redd count abundance**
Maureen P. Small, Charlotte Scofield, Jason Griffith, Adrian Spidle, Jennifer Whitney, Pete Verhey, Todd Seamons, Kris Ryding, and Dan Rawding
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The Stillaguamish River Chinook Salmon are one of seven escapement indicator stocks in Puget Sound whose abundance reflect effectiveness of management regimes. Their abundance has declined 10-fold from historic levels (~10,000 to ~1,000), which imposes limits on fisheries that might encounter the stock. Estimating their abundance with precision is difficult because they enter the river in fall when storms often raise water level and increase turbidity. We used a transgenerational genetic mark-recapture (tGMR) protocol to estimate spawning escapements for brood years 2008-2016. The tGMR employs genotypes from carcasses collected in the fall and outmigrants captured via smolt trapping the following winter and spring. We genotyped fish at the 13 GAPS microsatellite loci and assigned parents to smolts. Using Chapman’s (1951) approximation to the hypergeometric estimator, we calculated spawner abundances, and compared tGMR estimates to estimates derived from redd count expansions. Because historical redd counts were estimated either from aerial surveys or from ground counts and both methods were used in parallel two years, we used the ratio of the aerial to ground surveys in the years with both methods to standardize aerial redd count estimates to ground counts. Using the regression of the tGMR estimates on the redd count estimates from 2008-2016, we developed a correction factor to standardize historical redd count estimates.
36. Captive brood program to rescue spring Chinook Salmon in the South Fork Nooksack River
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Two populations, South Fork and North Fork, of spring Chinook Salmon are found in the Nooksack River basin, both of which must be recovered in order for the Puget Sound Evolutionarily Significant Unit (ESU) of Chinook Salmon to be delisted from threatened status under the United States Endangered Species Act (ESA). In addition to the ESA-listed spring Chinook, there is also a population of fall Chinook that is not included in the ESU and does not contribute to recovery. Tissue samples for baselines of genotypes of the three populations in the Nooksack River were collected in the 1980s and 1990s. Over the years 2008-2012, ~20,000 juveniles of natural origin were collected out of the South Fork Nooksack and individually assigned to the baselines of the three populations in the system. 4,401 juveniles were identified as South Fork Nooksack in origin and retained for rearing in captivity to maturation. 1,641 captive-reared fish were spawned from 2010-2017, with mate-choice informed by relatedness estimates based on genotypes. Roughly 1.6 million smolts, progeny of captive-reared fish, were released from 2012-2017.

37. The value of chromosomal information for studies in salmonid evolution, population genomics and transcriptomics
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We are now in a post-genomic era. Reference genomes of target species or close relatives are often available, even for non-model organisms. This information can be leveraged to greatly improve genetic analyses. In this presentation, I will discuss background on salmonid genome evolution from a variety of sources to highlight unique aspects of salmonid genomics, such as the impacts of residual tetraploidy and heterochiasmy, as well as more general phenomena also valuable to consider in the salmonids such as the influence of centromeres, telomeres, repetitive element content, and chromosome enrichment of specific co-expressed gene clusters. I will then put these elements into an applied context that is relevant to species conservation or to the characterization of biological processes and pathways within the salmonids. Further, although sex chromosomes in salmonids are often not described as heteromorphic, the salmonid sex chromosomes are nonetheless unique environments in which genes are contained, and thus the knowledge of the genes within these chromosomes and the evolutionary history of the genomic position of the master sex determining gene are important for both evolutionary and population genetic studies. Finally, the co-expression of genes, in addition to being relevant to evolution, can be a useful tool in characterizing various physiological states of salmonids; co-expression clusters put into context of genomic location furthers the knowledge of the underlying mechanisms of gene regulation of critical response pathways. I will conclude the synthesis with suggestions to unify comparative genomics studies among the salmonids with examples of how cross-species comparisons have strengthened studies
and how these are enabled in a genomic context. Anadromous returns from the captive brood program began to be incorporated in 2014. By 2017, 392 pairs of salmon were spawned in the South Fork Nooksack program, ~75% involving crosses of anadromous returns to the hatchery program, and ~12% each using the remaining captive fish and natural-origin volunteers to the hatchery facility. 2016 and 2017 saw the two largest years of returns to the South Fork Nooksack in decades. I will describe use of genetic information in operation of this recovery program, and detail the retention of genetic diversity in the current anadromous returns relative to the juveniles collected and the original baseline."

38. SNP data describe contemporary population structure and diversity in the lineages of Pink Salmon
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We used RADseq to explore differences in the population genetic structure of the lineages of Pink Salmon. We expanded upon our previous work in the system that found that the strongest signal of differentiation was between the lineages and identified parallel population structure within each lineage. To better understand the relationship between the lineages, we increased the total number of populations from 14 to 18 and were able to genotype 23,759 SNPs in 465 Pink Salmon from those 9 paired populations spread across the Pink Salmon range from Japan to Washington State. In addition to population and lineage genetic characterization, our aim is to use the haplotype data associated with these 23,759 SNPs to build two GT-seq panels, one for each of the lineages, which can be used to assign Pink Salmon of a particular lineage back to their region of origin.

39. What makes a successful hatchery fish? Using microhaplotypes to understand correlates of broodstock reproductive success in winter-run Chinook Salmon
Neil Thompson, Anthony Clemento, Jennifer Von Bargen, Christian Smith, Joshua Israel, and Carlos Garza
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Supplementation hatchery programs are designed to conserve and recover the receiving population, yet adaptation to captivity is pervasive in Pacific salmon and can reduce reproductive success of hatchery-reared fish spawning in the wild. Understanding the correlates of reproductive success in hatchery-origin fish is important to inform conservation practices and to further understand adaptation to captivity. Using a novel panel of microhaplotype markers in a GTseq framework, we evaluate 5 brood years of winter-run Chinook Salmon from the Livingston Stone National Fish Hatchery and identify broodstock traits that correlate with reproductive success. Determining the traits linked to adaptation to captivity will give hatchery managers, biologists and conservationists a more thorough understanding of population dynamics in hatchery Cohorts and potentially inform the best use of hatchery-reared fish for the conservation and recovery of winter-run Chinook Salmon in the Sacramento River.
40. **Anthropogenic habitat alteration leads to rapid loss of adaptive variation and restoration potential in wild salmon populations**

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Anthropogenic habitat alterations can drive phenotypic changes in wild populations. However, the underlying mechanism (i.e., phenotypic plasticity or genetic evolution) and potential to recover historic phenotypic characteristics are unclear. Here we investigate the underlying mechanism and long-term consequences of the decline of the spring-run phenotype in wild Chinook Salmon populations. Strikingly, we find that dramatic allele frequency change from strong selection at a single locus (GREB1L) explains the rapid phenotypic shift observed after recent dam construction on the Rogue River, OR. Furthermore, ancient DNA analysis confirms the presence of spring-run alleles in historic habitat that will soon become accessible through a large restoration project (Klamath dam removal). However, analysis of contemporary samples suggests the restoration of spring Chinook will be challenged by loss of spring-run alleles from potential source populations. These results highlight the need to conserve and restore critical adaptive genetic variation before the potential for recovery is lost.

41. **Genetics as a tool for conservation hatcheries**

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Anthropogenic activities and natural environmental events have impacted many species throughout the world. The winter run Chinook Salmon (*Oncorhynchus tshawytscha*) found in the Sacramento River, California is one of these impacted species. Two of the dams built on the Sacramento River effectively eliminated a large portion of the spawning habitat for the winter run Chinook Salmon, Shasta Dam (1945) and Keswick Dam (1950). The winter run Chinook Salmon were listed as threatened under the U.S. Endangered Species Act in 1989 and upgraded to endangered in 1994. The United States Fish and Wildlife Service in 1997 built Livingston Stone National Fish Hatchery at the base of Shasta Dam to help propagate winter run Chinook Salmon with conservation as its main goal. Conservation of genetic resources and the use of genetic tools to monitor this species played important roles in shaping the program. Genetic analysis using pairwise estimates of relatedness has helped hatchery staff reduce the chance of spawning related individuals. Over time the hatchery managers have continued to make adjustments in their culture practices to compensate for changes in the environment outside the hatchery. Genetic data continues to inform hatchery managers and play a key role in recovery actions for this endangered species.
Genetic analyses provide insights into stock specific early ocean migration behavior of juvenile Columbia River Steelhead

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For anadromous Pacific Salmon (Oncorhynchus sp.), ocean conditions during their initial entry into the marine environment can greatly affect their survival. Different life history types or stocks may experience different conditions during this time, as early marine migration routes among types or stocks can differ. Steelhead (O. mykiss) from the Columbia River are believed to migrate offshore quickly once they enter the ocean, but little is known if life history or stock specific differences in early marine migration exist. We assembled a baseline of steelhead genetic data that allowed us to make stock specific estimates of juvenile steelhead that had been caught off the coasts of Washington and Oregon. We found that the location of the plume of freshwater emanating from the Columbia River influenced the initial migration direction of steelhead from the river. We also found that among winter-run steelhead from the lower Columbia River, natural origin fish moved northward and offshore at a faster rate than did hatchery origin fish. Furthermore, an increase in the number of steelhead smolts transported downriver via barges one year appears to have increased the number of fish we caught in our trawls.

Rapid search and development of sex-linked markers for non-model organisms using RAD method for conservation of native fish and suppression of non-native fish

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The identification of sex-specific DNA markers are valuable for ascertaining mechanisms of sex determination and the evolution of sex chromosomes, for managing conservation and commercial broodstocks, development of Trojan YY technology, and in understanding the demographic history and phylogenetic relationships among populations. Traditional methods of developing sex-specific markers historically have been costly, time consuming, labor intensive and limited in scope from a genome scale perspective. With the advent of NGS technology and in particular RAD sequencing, we have the ability to search across genome for sex-linked markers at affordable cost and on a variety of non-model organisms and relatively quickly. We demonstrated the utility of RAD method for four fish species of commercial and conservation significance: Burbot, Westslope Cutthroat Trout, Common Carp and Brook Trout. Of significantly, we were able to identify SNP markers for each species that could discriminate between X and Y chromosomes. For Brook Trout and common Carp these sex-linked markers are being used in the development and maintenance of YY broodstocks and assessing performance of Trojan YY technology.
Genetic and phenotypic effects of inbreeding across two different hatchery management regimes in Chinook salmon
Charles D. Waters, Jeffrey J. Hard, David E. Fast, Kenneth I. Warheit, Curtis M. Knudsen, William J. Bosch, and Kerry A. Naish
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The consequences of inbreeding in captive breeding programs have received insufficient attention compared to domestication selection, partly because detection of inbred individuals traditionally relied on pedigrees. However, genomic approaches now enable inbreeding coefficients to be accurately estimated from molecular markers. Here, we quantified levels of pairwise relatedness and inbreeding, as well as the effects of inbreeding on eight fitness-related traits, in two hatchery populations of adult Chinook salmon across four generations using 6805 restriction-site associated (RAD) loci. The hatchery populations were derived from the same source but are now managed as two lines that are integrated with and segregated from the founding wild stock. Relatedness and inbreeding were then compared between the two management strategies to evaluate the effectiveness of integrated management, or managed gene flow, to reduce risks of inbreeding in captive populations. Levels of inbreeding were similar between the two hatchery lines in the first, third, and fourth generations, despite 3- to 27-fold differences in estimates of effective numbers of breeders. However, inbreeding in the segregated line was significantly higher in the second generation. The segregated line also had slight but significantly lower levels of relatedness than the integrated line in the first generation but significantly higher levels in the third and fourth generations. Inbreeding coefficient did not affect fecundity, reproductive effort, return timing, and fork length. In contrast, inbreeding significantly affected spawn timing, weight, condition factor, and daily growth coefficient, although the effects varied by sex, hatchery line, and generation. While our results indicate that integrated management may reduce the genetic risks of inbreeding, they also suggest that short-term risks may not be severe in small, segregated hatchery populations. The effects of inbreeding on fitness varied and thus require further exploration, particularly at earlier life stages.
Should I stay or should I go? Analyzing the genetic basis of migration-related traits in Rainbow Trout (*Oncorhynchus mykiss*)
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Fishes of the Salmonidae family display many life history tactics, including obligate anadromy, partial anadromy, and residency. Across species, anadromy is controlled by both genetic and environmental factors. While the environmental influences on migration are well-known, the genetic basis of migration remains in question. Rainbow Trout (*Oncorhynchus mykiss*), which exhibit partial anadromy, are well-suited for studying the genetic basis of migration due to the phenotypic differences between residents and migrants. Here, we used data from a common garden experiment to identify SNPs associated with anadromy in the F1 generation of a resident-by-resident (RxR) and a migrant-by-migrant (AxA) cross. We genotyped 192 F1 individuals on an Affymetrix SNP chip at 57,501 known polymorphic positions across the genome, and performed sliding window analyses for various population genetic metrics to identify regions of the genome potentially under selection. We identified 4,994 and 436 significant SNPs in the AxA and RxR families, respectively. Within the AxA family, we located significant markers associated with 28 genes with functions connected to smoltification-related pathways. Across both families, one region on chromosome 5, displaying negative Tajima’s D, low observed and expected heterozygosities, and low FST, stood out across sliding window analyses. A QTL for development rate, which is in turn associated with life history, has been previously identified on chromosome 5 and is believed to overlap with the region identified here. These data suggest that life history is controlled via a complex, polygenic pattern of inheritance, and that some regions of the genome are under selection, possibly indicating parallel evolution occurring across *O. mykiss* populations.
Exploring the performance of COLONY in estimating parameters for trans-generational genetic mark recapture
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Despite the increasing popularity of trans-generational genetic mark recapture (tGMR) for estimating abundance of Pacific Salmon (Oncorhynchus spp.), little research has explored the performance of the software used for parameter estimation (COLONY). Two modified versions of the Lincoln Peterson estimator (N=MC/R) have been adapted to yield population estimates, generally described as “with replacement” and “without replacement”. Here the number of recaptures (R) are estimated for both equations, while the number of captures (C) is only estimated for the “without replacement” equation. We explored the performance of the program COLONY at estimating these parameters by simulating a population of Coho Salmon (Oncorhynchus kisutch) with known allele frequencies. In total, 32 scenarios (100 iterations each) were evaluated that differed in the proportion of adults and offspring sampled as well as the number SNP loci examined. Results indicate that COLONY can accurately estimate the number of recaptures (R) for both the “with replacement” and “without replacement” equations. However, we uncovered bias in COLONY’s ability to estimate the number of captures (C) for the “without replacement” estimator. For the “without replacement” estimator, C is the number of unique parents responsible for the juvenile sub-sample. Estimation of this parameter was substantially biased (-0.40 to 0.23), with reductions in bias occurring when more parents, offspring, and loci were examined. As a result of bias in estimates of C using COLONY, the “without replacement” estimator may result in unreliable population estimates.
POSTERS
(in alphabetical order by first author’s last name)

47. What’s going on inside? Gene expression in hatchery Steelhead fed diets with differing lipid levels
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The Abernathy Fish Technology Center developed an integrated steelhead (Oncorhynchus mykiss) broodstock in 1999 starting with pre-smolt natural-origin (NOR) juveniles collected from throughout Abernathy Creek, WA and then rearing the broodstock to maturity in the hatchery. With the return of the first adults produced from the original 1999 broodstock, AFTC has had a policy of maintaining ~25% NOR integration in the broodstock, with the remaining returning NOR steelhead being released back into the stream to reproduce naturally. Beginning in 2015, hatchery-origin (HOR) juvenile rearing was modified to determine if nutritional condition could be altered to match equivalent NOR smolts. One group of juveniles was fed a diet typical of that fed hatchery steelhead in our region, and the other group was fed a diet with lipid levels typical of those thought to be present in diets of typical NOR steelhead. We then compared patterns of gene expression in tissues sampled from the two groups. Tissue samples were collected from juvenile fish over an eight month period before release into the stream. Total RNA was extracted from collected tissue and initial subsets of samples were sequenced via next-generation RNA-sequencing (RNA-seq). The resulting dataset will allow us to determine gene pathway differences with altered lipid levels in HOR juvenile steelhead rearing.

48. Genome wide markers of reproductive success and mate choice in Coho Salmon
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Because individuals are limited in their ability to produce offspring, it is important not to mate randomly, but select high quality and/or genetically compatible partners. In nature, with the exception of coercive or sneaky mating, individuals can choose reproductive partners by strategically allocating mating effort towards and/or accepting copulation from specific individuals. The ability to choose mates and the natural variation in mate choice has important evolutionary significance, including maintenance of genetic diversity within populations, and speciation. Mate choice can be important for conservation or population recovery efforts since individuals who choose mates often have greater mating success than those who do not. However, even when given the opportunity to choose mates, reduced reproductive success has been observed in hatchery fish relative to their wild counterparts, suggesting a reduced ability of hatchery fish to select appropriate mates which could be the result of the parental generation of hatchery fish not being able to select their own mates and thus producing less sexually competitive offspring or another selection pressure in the hatchery environment. Using genotyping-by-sequencing, we identify single nucleotide polymorphisms (SNPs) associated with variation in both individual reproductive success and mate pairings in hatchery and wild Coho Salmon (Oncorhynchus kisutch). Preliminary results suggest variation in reproductive success may in part be attributable to certain specific SNPs or interactions between them. Our results additionally indicate that reproductive success differences previously observed between fish of either hatchery or wild origin may correlate with differences in mate choice patterns we infer from their pedigree.
49. 
Relative reproductive success of hatchery-reared spring Chinook Salmon in Catherine Creek (Grande Ronde Basin, OR)
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Spring Chinook salmon populations in many streams in the Columbia River and Snake River Basins have experienced severe declines in abundance over the past several decades (Nehlsen et al. 1991). Historically, the Grande Ronde River and tributaries in northeast Oregon produced annual returns of approximately 12,200 spring Chinook salmon (U.S. Army Corps of Engineers 1975). Mitigation attempts beginning in the late 1970s, utilizing both native and non-native stocks, failed to halt this decline, and in the mid 1990s a Spring Chinook salmon captive broodstock program was initiated in the Grande Ronde sub-basin. In the early 2000s this program began transitioning to a more conventional broodstock design. A genetic monitoring program was established for this system in 2002, and measures of relative reproductive success (RRS) are now available for natural- and hatchery-origin spawners for over a decade (2002-2013). This dataset combines both earlier microsatellite data as well as current SNP data, and examines the potential effects of a number of key factors: hatchery vs. wild origin, age-at-return, size-at-return, captive vs. conventional program, and mate characteristics. Unlike the substantial decline in RRS seen in *O. mykiss*, the RRS of Catherine Creek hatchery-origin Chinook when measured with juvenile offspring was not significantly different from that of natural-origin. When measured with adult offspring, the geometric mean was slightly lower at 0.96. There was considerable annual variation in RRS, however, with values ranging from 0.49 to 3.47. We are performing Generalized Linear Modeling to determine any attributes that may be associated with higher or lower RRS.

50. 
Evaluating the fitness of reintroduced spring Chinook Salmon in Fall Creek, Oregon
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On Fall Creek, a tributary of the Middle Fork Willamette River, access to historical spawning habitat for spring Chinook Salmon (*Oncorhynchus tshawytscha*) is impeded by Fall Creek Dam. Beginning in 1998, primarily hatchery-origin (HOR) spring Chinook Salmon were released above Fall Creek Dam with the aim of re-establishing natural production on these historical spawning grounds. Since 2010, only unmarked, natural-origin (NOR), spring Chinook Salmon have been reintroduced above the dam. We evaluated the efficacy of the reintroduction program by reconstructing a genetic pedigree and assigning the 2014 and 2015 adult recruits to salmon previously reintroduced in 2011 and 2012. We assigned 10% of the 2014 and 87% of the 2015 adult returns to salmon previously released in 2011 and 2012. Preliminary fitness for the 2011 Cohort averaged less than one progeny and preliminary replacement rates were 0.32 for males and 0.46 for females; however, our estimates did not include age-5 progeny. Notably, the proportion of age-3 males returning to Fall Creek Dam tripled from 2014 to 2015. We also genotyped the same individuals at 298 SNPs using GT-seq (Campbell et al. 2015). We compared results from both methods to determine if GT-seq is a more effective tool to evaluate conservation efforts of threatened spring Chinook Salmon.
51. Microhaplotype marker development for Coho Salmon
Ellen M. Campbell, Cassondra D. Columbus, Elena C. A. Correa, Elizabeth A. Gilbert-Horvath, Anthony J. Clemento, and John Carlos Garza.
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Coho Salmon (*Oncorhynchus kisutch*) is a North American anadromous fish whose range extends from central California to the Aleutian Islands in Alaska. Reduced numbers of Coho Salmon, due to anthropomorphic impacts such as overfishing and freshwater habitat alteration, have led to many Evolutionary Significant Units (ESUs) being listed as threatened or endangered under the Endangered Species Act. The two Coho Salmon ESUs in California – the southern end of the species range – are of particular concern and are therefore important to protect as part of the effort to conserve the species. Currently, we use a 96 single nucleotide polymorphism (SNP) panel for parentage, genetic stock identification (GSI), and other population genetic analyses. With the increased availability and cost-effectiveness of next-generation sequencing technology, short-read sequencing as a means of genotyping is becoming more popular. Directly translating a standard SNP panel to a next-generation amplicon panel potentially ignores additional nucleotide variation within the sequenced regions. Microhaplotypes are short targeted regions of the genome that contain multiple SNPs, giving these markers more power for parentage analysis than a standard SNP panel. Our project involves the development of a microhaplotype panel for Coho Salmon in California. Using double-digest restriction site-associated DNA sequencing (ddRADseq), we screened 64 samples from 19 populations across the southern end of the species range to identify potential microhaplotype target sites. We will test the panel and determine its effectiveness for parentage and GSI analyses compared to our current panel of SNPs.

52. Microhaplotypes Vs. SNPs: comparing power for relationship inference and population genetic analyses in *Oncorhynchus mykiss*
Cassondra D. Columbus, Ellen M. Campbell, Elena C. A. Correa, Noé Barthelemy, Anthony J. Clemento, John Carlos Garza, and Devon Pearse
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The use of next-generation sequencing (NGS) for genotyping has been increasing as this data-rich technology has become more widely available and cost-effective. However, translating panels of single nucleotide polymorphisms (SNPs) directly into amplicon sequencing panels ignores informative variation surrounding the target SNP. Microhaplotypes are short regions of the genome which contain multiple SNPs. These markers make a more optimized use of NGS tools for populations genetics and have been demonstrated to greatly increase power for relationship inference, particularly for parentage analysis with incomplete sampling. We developed a panel of 130 microhaplotype loci in steelhead (*Oncorhynchus mykiss*) for use in parentage and population genetic analysis, identify sex, and survey known adaptive genomic variation. We used a simulation power analysis and genotype data from known parent-offspring-parent trios from Coleman Hatchery in the Central Valley of California to compare the power of the microhaplotype panel to a standard 96 SNP panel to determine if we can achieve an objective not yet feasible with the 96 SNPs panel: accurately identify single parent-offspring pairs. We will also evaluate the capability of the microhaplotype panel to do population genetic analyses (eg.
population structure) and detect stronger signals of introgression by hatchery Rainbow Trout strains into natural populations.

53. Genetic stock composition analysis of the Chinook Salmon bycatch samples from the 2016 Gulf of Alaska trawl fisheries
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A genetic analysis of samples from the Chinook Salmon (Oncorhynchus tshawytscha) Prohibited Species Catch (bycatch) of the 2016 Gulf of Alaska (GOA) trawl fisheries for walleye pollock (Gadus chalcogrammus) and rockfish (Sebastes spp.), was undertaken to determine the stock composition of the sample sets. Samples were genotyped for 43 single nucleotide polymorphism (SNP) DNA markers and results were estimated using the Alaska Department of Fish and Game SNP baseline. In 2016, genetic samples were collected from Chinook Salmon taken in the bycatch of the GOA pollock trawl fisheries using a simple random sample protocol with trip being the primary unit. This was the third year for this sampling protocol and which resulted in the largest available genetic sample set to date with 24% of the estimated salmon bycatch from the pollock fishery successfully genotyped. Based on analysis of 4,962 Chinook Salmon bycatch samples, British Columbia (42%), West Coast US (40%), and Coastal Southeast Alaska (15%) comprised the largest stock groups, at an estimated 8,602, 8,301, and 3,080 Chinook Salmon, respectively, out of 20,589 fish total. In 2016, genetic samples from the bycatch of the GOA rockfish CV fishery were collected by the fishing industry using a census sampling protocol. Based on the genotyping of 493 Chinook Salmon bycatch samples collected from this fishery in NMFS Statistical Areas 620 and 630, West Coast US stocks represented the largest stock group (62%) with smaller contributions from British Columbia (27%), Coastal Southeast Alaska (7%), and Northwest GOA (4%) stock groups.

54. Expansion of Parentage-based Tagging (PBT) baselines for salmonid hatchery stocks throughout the Columbia River Basin
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Parentage-based tagging (PBT) is a large-scale tagging technology for monitoring and evaluating salmonid hatchery stocks. Implementation of PBT involves annual non-lethal sampling of hatchery broodstock to create a temporally structured parental genotype baseline. Offspring produced by these parents can be sampled either as juveniles or adults, and then genotyped to be assigned back to their true parent pair – thus identifying their age and hatchery of origin. A large-scale demonstration of PBT is currently being applied to Chinook Salmon and steelhead hatcheries in the Snake River basin, Idaho (2008-present), and efforts to expand annual tissue collection to Chinook Salmon, steelhead, and Coho Salmon hatcheries above Bonneville Dam began in 2012. PBT continues to be valuable for: characterization of stock composition in fisheries, estimation of stock-specific abundance and run-timing at dams, identification of physically unmarked hatchery fish, estimation of proportion of hatchery fish on spawning grounds, identification of stocks using thermal refugia during migration, and monitoring
trends in hatchery production. Adopting PBT more broadly in the Columbia River basin facilitates our ability to track millions of hatchery fish and the opportunity to address a variety of parentage-based research and management questions.

55. Quantifying impacts of floodplain availability on Chinook Salmon (*Oncorhynchus tshawytscha*)
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Water quality and quantity can be highly variable in California’s Central Valley Region due to environmental and anthropogenic changes. This presents unique challenges for the federally listed Central Valley Chinook Salmon (*Oncorhynchus tshawytscha*), which use the limited floodplain in the Central Valley as rearing habitat. Flood plains, such as the Yolo Bypass, can be disproportionately affected by drought and stream flow changes, affecting the fitness of Chinook Salmon. We are interested in understanding how different water years (drought versus flood) influence the run composition and abundance of juvenile Chinook Salmon in the floodplain (Yolo Bypass) versus the mainstem of the Sacramento River. Chinook from the Yolo Bypass and areas along the Sacramento River were sampled and genotyped with an innovative genetic panel and identified at the run level (Fall, Late Fall, Winter, and Spring) from 1998-2017. These genetic data can help answer important questions about the impact of drought and flood years, and if specific runs are adversely affected by different water conditions. This study will also provide important information on the loss of genetic diversity due to environmental or anthropogenic changes in the Sacramento River. Chinook are of enormous economic, cultural, and ecological value in California, making a better understanding of how these changes are affecting this species of special importance.

56. Genetic characterization of juvenile Chum Salmon (*Oncorhynchus keta*) migrating out of the Yukon River delta
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To identify critical life history stages for salmon survival, it may be informative to compare adult returns with abundances at various life-history stages. Past genetic studies demonstrated that relative abundances of Yukon summer-run and fall-run juvenile Chum Salmon (*Oncorhynchus keta*) caught on the Eastern Bering Sea shelf during late summer/early fall are correlated with adult returns for their respective year-classes. We are interested in testing whether earlier life history stages are also correlated with adult returns. Our project aims to estimate the relative proportions of Yukon summer-run and fall-run juvenile Chum Salmon outmigration from the Yukon River during 2016. We genotyped 1,784 individuals from 9 field sites on the Yukon River delta at 14 microsatellite loci. These estimates of juvenile proportions will be compared to the proportions of returning adults to the Yukon in the summer and fall.
57. A single gene is associated with spawning-timing in anadromous steelhead (*Oncorhynchus mykiss*)
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The timing of reproduction in natural populations dictates the abiotic and biotic conditions that both parents and their offspring encounter. Therefore, different selective pressures can act on organisms at various life stages from the same location due to reproductive differences. Spawn-timing variation within populations has been observed in Pacific Northwestern Steelhead Trout (*Oncorhynchus mykiss*) and has become a focus of hatchery production and maintenance of diverse phenology traits in nature. However, the genetic basis for this trait remains unknown. To elucidate the genetic basis of this trait, we classified early and late spawning phenotypes with spawning dates from breeding programs at various steelhead hatcheries. Using whole-genome resequencing and the PoolParty analysis pipeline, we detected 2 million SNPs across 12 libraries of early and late spawners. Results show that a single genomic region encompassing a single gene is responsible for early vs. late spawn timing that differs from other known phenology traits. Results from this study can be used to screen genetic markers of interest which can determine if migrating steelhead are early or late spawners and further clarifies the genetic basis of complex life history traits seen in salmonids.

58. Fine-scale homing and density dependence: Implications for fitness in wild Sockeye Salmon (*O. nerka*) populations
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The specialized homing ability in Salmonids plays an important role in population fitness, affecting processes such as recruitment. It is therefore important to characterize the factors that influence fine scale homing and identify whether such factors affect mate choice and reproductive success. Here, we investigated fine scale homing in two sockeye salmon (*Oncorhynchus nerka*) populations in small adjacent creeks in the Wood River System, Bristol Bay, Alaska. We hypothesized that homing may occur on a fine-scale of tens of meters and may be highly density-dependent, due to finite spawning habitat availability. Spatial autocorrelation based on 11 microsatellite loci was used to investigate the spatial distribution of relatedness between individuals in these small populations. We used these analyses to determine the relationship between relatedness and dispersal distance. At low densities, we expect relatedness to be inversely correlated with distance given that salmonids home precisely to their natal site. At high densities, on the other hand, space availability reaches its limit and may lead to dispersal, thus reducing spatial autocorrelation and, correspondingly, inbreeding. In the near future, we intend to expand this work to a three-generation pedigree, thus allowing us to investigate the influence of different densities and environmental conditions on fine scale homing. The impacts of homing and density on inbreeding and relatedness could have important implications for the management of salmonid fisheries, as fitness may influence recruitment and a population’s ability to sustain harvest activities.
59. DNA barcoding as a tool for generic and species level identification of salmonid redds
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Generic and species identification at early life-history stages can provide timely information to managers developing plans for invasive species control and native species conservation and recovery efforts. We successfully extracted DNA from fish eggs (n=19) and from larval fish specimens (n=20) collected from Redds. We amplified samples to target Cytochrome c oxidase subunit 1 (CO1) and the targeted region was visualized using Sanger-Sequencing. After visually confirming and aligning sequences, we performed a Blast search against the GenBank DNA sequence repository of the National Institute of Health (NIH) and compared our sequences side-by-side against sequences of fishes known to inhabit the geographical range in question. The results provided compelling evidence for generic level identification of each individual and species level identification of the eggs. For the larval specimens, CO1 did not provide adequate resolution alone to confidently distinguish amongst a closely related clade of Arctic char species. However, since only one species of this clade is known to inhabit the geographic region in question, we were confident in species identifying these samples, also. This study highlights the advantages and limitations of this technique as a tool for conservation.

60. Contemporary genetic structure of wild Steelhead in the Snake River Basin
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Genetic divergence and geographic distance are expected to be positively correlated when the dispersal of individuals is restricted by the landscape. This correlation, known as isolation-by-distance, has been observed among steelhead (Oncorhynchus mykiss) populations throughout their range. Here we examine patterns of isolation-by-distance and genetic structure in wild adult steelhead populations across the Snake River Basin. We genotyped 8,725 wild returns to PIT-tag arrays within the Snake River Basin between 2010 and 2017 at 176 single nucleotide polymorphisms. Individuals were grouped into 20 collections based on the return to locations within the defined geographic ranges of Interior Columbia River Basin Technical Recovery Team populations. We detected a signature of isolation-by-distance across all collections in the Snake River Basin. However, a phylogenetic analysis clustered the collections from the upper Salmon River with collections from the middle Snake River below Hells Canyon Dam. This clustering was consistent with the observed low levels of genetic differentiation between collections from the lower basin and collections from the upper Salmon River, despite their geographic separation. These results mirror the founding history of hatchery populations in the upper Salmon River using broodstock trapped at Hells Canyon Dam. When we equated the geographic location of the upper Salmon River collections to Hells Canyon Dam we observed a pattern of isolation-by-distance indistinguishable from that observed when these collections were removed from analysis. Therefore, the genetic structure we observe in the Snake River Basin may be altered from historic conditions due to contemporary gene flow.
Life history trait characterization of a wild Steelhead population on the Eel River, California
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Understanding life history trait variation in species of conservation concern is essential for effective management. Steelhead (O. mykiss) are extensively supplemented through hatcheries to ensure their continued persistence, but this has been shown to lead to divergence in life history traits from wild populations. We monitored a wild steelhead population at the top of the mainstem Eel River from 2009 - 2017. The Van Arsdale Fisheries Station and fishway (1922) allows steelhead to reach the spawning grounds above Van Arsdale Reservoir, which constitute about 8% of all steelhead habitat in the basin. We conducted a large-scale pedigree reconstruction with 86 SNPs. In addition, we sequenced five 150 bp regions of the genome in a region of Omy28 associated with ecotypic differentiation. We were able to reconstruct ~570 parent-offspring trios with high confidence and found that most offspring returned as three and four year olds. Iteroparity rates were higher than hatchery populations (8.7 % of fish returned in subsequent years) and were mostly females. Comparisons of relatedness ($r_{xy}$) between simulated random mating and actual mating showed no deviation from random mating in this system. The Omy28 SNPs identified likely summer run steelhead entering the fishway in August 2011, as well as a number of heterozygous adults (4%). Some of these heterozygous individuals produced offspring that returned in subsequent years.

Population structure analysis of Oncorhynchus mykiss in two Deschutes River tributaries demonstrates introgression from out-of-basin hatchery strays
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Hatchery steelhead (Oncorhynchus mykiss) spawning naturally with wild fish may impact the ability of the wild stock to maintain their genetic integrity, potentially reducing the fitness of the wild population. Previous analyses using coded-wire tags and parentage-based tagging suggest that large proportions of the hatchery strays found in the Deschutes River originate from out-of-basin hatcheries located in the Snake River basin. The impact that these hatchery strays have on the genetic structure of the wild population is not well known, but it is of concern because wild steelhead are an important component of the sport and tribal fisheries in the Deschutes River basin and remain listed as a threatened species. We describe the genetic structure of the wild and hatchery O. mykiss populations in two Deschutes River tributaries. Our results demonstrate the wild steelhead populations are genetically more similar to Snake River hatchery steelhead than they are to the resident O. mykiss populations. This is a novel discovery which strongly suggests that the native steelhead populations in these two Deschutes River tributaries are experiencing introgression from out-of-basin populations with distinct evolutionary histories. This information is relevant to those interested in maintaining the genetic integrity and long term adaptive evolutionary potential of native steelhead stocks.
Reproductive success of reconditioned kelt Steelhead in the Yakima River Basin
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Reconditioning of kelt (post-spawned) steelhead may be an effective strategy to mitigate for high mortality inflicted on this ESA listed species by the hydrosystem. We evaluated the effectiveness of this strategy by testing whether reconditioned kelts provide a demographic boost to the natural population in the Yakima River Basin. Specifically, we compared four spawn years of relative reproductive success of reconditioned kelts to that of anadromous adult steelhead captured as either upstream migrants at Prosser Dam or downstream post spawn fish captured at the Chandler Juvenile Monitoring Facility. Successful reproduction by the reconditioned kelts has been confirmed and appears sufficient to provide a demographic boost for this species and to retain genetic diversity and its iteroparous (i.e. repeat spawning) life history.