



Session 7: Genetic & Genomic Applications Towards Improved Management Practices in Recreational Fisheries

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Genome-Wide Management and Conservation of Introgressed Local Mediterranean Brown Trout Populations

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The brown trout *Salmo trutta L.* is a widely distributed Eurasian species strongly impacted by human activities such as introductions of individuals from distinct origins into natural recipient populations. The Atlantic hatchery lineage has been domesticated for decades and largely used for restocking and enhancement of small local Mediterranean populations. Understanding the adaptive and detrimental outcomes of stocking practices on wild populations are of great concern for evolutionary ecology and conservation. Here, we used a genome-wide dataset of mapped SNPs to detect introgressed haplotypes and to provide a detailed picture of introgression patterns across the genome. The length distribution of admixture tracts was used to determine the timing of introgression taking variation in local recombination rate into account. We then asked whether the frequency of introgression within genomic regions is linked with their recombination rate. Finally, we tested whether stocking practices induce adaptive introgression and/or associative overdominance of domestic alleles, or on the contrary prevents the introgression of maladaptive alleles and/or reproductive isolation loci. Our study provides information about the fitness consequences of recent admixture, thus enabling future assessment of the long-term effects of introgression in a conservation perspective.



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Neutral and Functional Genetic Structure and the Management of the Babine Lake Rainbow Trout Fishery: Tributary Genetic Drift and Local Adaptation Contribute to Lake Population Variation

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Resident rainbow trout in Babine Lake, British Columbia are the focus of regionally important recreational and First Nations food fisheries. While the lake population derives from multiple tributary spawning areas, the relative contribution from these tributaries is not known. This study investigates the roles of dispersal, local adaptation and genetic drift on lake-wide population genetic structure and the distribution of the highly desirable large-bodied adult morphotype. Using microsatellite data we found strong neutral genetic divergence among tributary juveniles: genetic drift due to low effective population size was initially identified as the likely cause. However, an analysis of gene transcription at metabolic and immune function candidate loci showed that the juvenile rainbow trout had diverged in their gene transcription responses to environmental challenges as well. The transcription response profiles correlated with stream temperature and microbial community structure, indicative of locally adaptive differences. The combination of neutral and functional genetic divergence among the tributaries drive highly skewed contributions to the large-bodied morph in the lake. Our study highlights the importance of exploring both neutral (drift) and selective (local adaptation) divergence among source populations contributing to valuable recreational and First Nations fisheries. Our data highlight the need for Evolutionary processes to be included for effective management and conservation action.



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Collaborative Population Monitoring of Walleye (*Sander vitreus*) in Mistassini Lake, Quebec, Through Complementary Science and Traditional Harvest Practices of First Nations People

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Collaborative population monitoring that integrates scientific and traditional harvest practices is integral to community-based population management. The Cree Nation of Mistissini, QC, have been collaborating to manage walleye (*Sander vitreus*) populations in Mistassini Lake. Walleye populations in Mistassini Lake were sampled for life history characters' total length and mass in 2002/2003 and 2015, in four different rivers (southern: 1-3; northern: 1). Linear models revealed that between these time points reductions in both length (between 11 and 21%), and mass (between 24 and 39%) have occurred in the three southern rivers, those closest to the only human settlement on the lake, but not in the northern river. The greatest size reductions occurred in female fish. Over this time period there has also been a considerable increase in local human population size and in fishing-based tourism. Genomics screening (genome-wide SNPs generated using genotyping-by-sequencing) of both historical and contemporary walleye samples is currently underway to determine whether body length and mass reductions are associated with reductions in effective population size, genome-wide diversity, or loci under selection. Based on results to date, management and monitoring plans for these populations have been undertaken that are complementary to traditional customs and fishing techniques, showing leadership towards maintaining aquatic biodiversity.



I5

Genetic Variation and Physiological Plasticity of High pH Tolerance in Rainbow Trout (*Oncorhynchus mykiss*)

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Currently, a quarter of the lakes stocked in British Columbia by Freshwater Fisheries Society of British Columbia (FFSBC) have pH > 8.5, which is negatively impacting sport fisheries. To determine whether rearing trout at high pH improves pH tolerance, trout from three strains were reared in well water (~pH 7.4), and at elevated pH (pH 8.5 or pH 8.8). Fish reared in well water were also acclimated to pH 8.8. One strain had consistently poorer tolerance of acute exposure to high pH challenge (pH 9.5), but either rearing at pH 8.8 or acclimation to this pH resulted in substantially improved tolerance in all strains. To test the relevance of these laboratory results to real-world conditions, control fish and fish from the pH 8.8 rearing and acclimated treatments were stocked into lakes of differing pH, and short-term survival was assessed. Fish acclimated to or reared at pH 8.8 had higher survival than did control fish in the high pH lakes, and survival did not differ in lower pH lakes. High-throughput genotyping and transcriptome analysis was used to assess the mechanisms associated with these differences. These results will allow the FFSBC to optimize their stocking practices for high pH lakes.



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DNA Methylation as an Epigenetic Mechanism for Local Adaptation in Chinook Salmon

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Chinook salmon are a prized sport fish in the Pacific Ocean, with millions of dollars spent on stock replenishment each year. Understanding local adaptation is critical for the management of the Chinook sport fishery to successfully replenish stocks and preserve natural variation, including the coveted “Tyee” type. Salmon have been shown to exhibit local adaptation through variation in migration timing, developmental timing, phenotypic traits, and transcription. Local adaptation is often driven by transcriptional differences among populations rather than differences in DNA coding regions, though the molecular mechanisms underlying such differences are not well known. DNA methylation, the addition of a methyl group to CpG cytosines, results in the suppression of transcription and can thus change the expression levels of particular genes. Moreover, methylation is sensitive to the environment, often heritable, and hypothesized to be involved in environmental adaptation. Here we collected 48 Chinook salmon eyed eggs from eight federal government run hatcheries (Fisheries and Oceans Canada) across British Columbia, to investigate the role of DNA methylation in Chinook local adaptation. We quantified methylation using a PCR-based Next-Generation sequencing assay for loci involved in development, metabolism, stress, and immune response. We show population level differences in locus-specific methylation. These results increase our understanding of how Chinook adapt to their environment through heritable epigenetic mechanisms and have direct implications to salmonid conservation and supplementation efforts. This study supports DNA methylation as a potential adaptive mechanism in Chinook salmon and provides insight into the molecular basis of local adaptation.



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Population and Individual Identification of Coho Salmon in British Columbia Through Parentage-Based Tagging and Genetic Stock Identification as an Alternative to Coded-Wire Tags

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Parentage-based tagging (PBT) and genetic stock identification (GSI) were used to identify individual Coho Salmon (*Oncorhynchus kisutch*) to specific populations and broodyears in British Columbia. Coho Salmon from 15 populations were assigned via parentage analysis that required the genotypes of both parents, with 304 SNPs available from genotyping, and with 117 populations in a baseline that included over 20,000 individuals genotyped. The overall accuracy of assignment for 1,939 Coho Salmon to the correct population was 100%, and to correct broodyear within population was also 100%. Inclusion of individuals requiring only a single parental genotype for identification resulted in assignments of 2,101 individuals, with an accuracy of 99.95% (2,000/2,001) to population and 100.0% to age. A PBT/GSI or PBT system of identification will provide an alternate method of identification in the assessment and management of Canadian-origin Coho Salmon relative to the existing coded-wire tag program, and will be applied to samples obtained from 2017 recreational fisheries for Coho Salmon in British Columbia in order to determine stock of origin of individuals caught in the fishery.



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Major Histocompatibility Complex Variation Among Alternative Reproductive Tactics of Chinook Salmon

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To investigate genetic diversity in Lake Ontario Chinook salmon, we genotyped males representing two alternative reproductive tactics, jacks (small sneaker males) and hooknoses (large guarding males). We genotyped fish from the population at neutral (microsatellites) and functional (MHC II β 1) markers. Estimates of genetic diversity, including number of alleles, allelic richness and heterozygosity, were greatest for jacks compared to both hooknoses and females at the MHC. Females showed the lowest levels of genetic diversity, where only 50% of the females were heterozygous. Pairwise genetic divergence was calculated between the groups. Jacks and females were significantly genetically divergent, whereas all other pairwise comparisons were not genetically divergent. Genetic diversity estimates from neutral markers were similar among groups, with the exception of number of alleles, likely due to differences in number of individuals genotyped. There was no significant genetic divergence between jacks, hooknoses and females. These results suggest that there are genetic differences between alternative reproductive tactics that ought to be taken into account when examining the genetic make-up of the Lake Ontario population of Chinook salmon.



I10

Individual Behavioural Variation and Diel Patterns Among Rainbow Trout in a Small, Remote Lake

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A hydroacoustic telemetry system was deployed in Gnawed Lake, a small lake located in the interior of British Columbia, Canada. Thirty-two triploid rainbow trout angled from the lake were surgically implanted with acoustic tags and monitored for movement beginning in May 2016. Six consecutive days of 2D positioning data from September 2016 were analyzed to assess lake usage and behavior on an individual level. This preliminary study revealed differences in swim speed, home range and habitat use among individuals, as well as potential differences between strains of rainbow trout. A significant diel cycle was displayed by a subset of the tracked fish, consisting of reduced swim speed at night and faster speeds during the day, with peaks in exploration area at crepuscular periods. Many fish also showed individual preference in nightly site fidelity, returning to the same region of the lake each night of the study. Additional research is needed to determine if these trends persist in the long term and in different seasons; however, this novel observation emphasizes the importance of examining individual behavioural variation within fish populations.



I11

Genomic Changes Associated with Sockeye Salmon Ecotype Divergence Provide Tools for Recreational Fisheries Management

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Mechanisms underlying adaptive evolution can best be explored using paired populations displaying similar phenotypic divergence, illuminating the genomic changes associated with specific life history traits. Here we used paired migratory [anadromous vs. resident (kokanee)] and reproductive (shore- vs. stream-spawning kokanee) ecotypes of sockeye salmon (*Oncorhynchus nerka*) sampled from seven lakes and two rivers spanning three catchments (Columbia, Fraser, Skeena drainages) in British Columbia, Canada to investigate the patterns and processes underlying their divergence. Restriction-site associated DNA sequencing was used to genotype this sampling at 7,347 single nucleotide polymorphisms (SNPs), 219 of which were identified as outlier loci and candidates for divergent selection between resident and anadromous forms. Of the 126 outlier SNPs identified between shore- and stream-spawning kokanee population pairs, one was shared across multiple comparisons and was uniformly the most highly differentiated SNP. We further genotyped 1519 anadromous sockeye and resident kokanee from 47 shore- and streamspawning populations across their pan-Pacific distribution using a newly-developed TaqMan assay targeting this SNP, revealing directional divergence associated with spawning habitat. Subsequent sequencing of ~23,000 base pairs surrounding the SNP revealed evidence for an ancient selective sweep underlying divergence of the 'shore-spawning' and 'stream-spawning' alleles, likely pre-dating the Pleistocene. Overall, the identified SNPs and genomic regions offer a range of mechanistic hypotheses associated with the genetic basis of *O. nerka* life history variation and provide new tools for informing management applications that require identifying individuals to ecotype. Applications of resulting SNP panels to stock assessment, restocking programs and broodstock selection will be presented.



I12

The Temporal Change of Japanese Eel Distribution and the Habitat Monitoring Using Environmental DNA in Japan

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Japanese eel (*Anguilla japonica*) is not only traditional fishery resource but also significant indicator species of watershed ecosystem in Japan. Then the whole life history of eel is directly affected by both watershed and marine ecosystem. We are regarding this specific life cycle as “The linkages between forests, rivers, SATOYAMA and sea” symbolically.

Now unfortunately, critical decreasing of eel resource is not only a Japanese domestic issue but serious international concerns. In this study, we estimated the temporal changes of eel distribution in whole Japan.

Then we tried to find out the cause of the decreasing of eel resource based on statistical data analysis and GIS procedure. Additionally, we tested a new ecosystem monitoring method using Environmental DNA (eDNA) analysis to detect the habitat of eel.

The objectives of our research are as follows. 1) The construction of nationwide scale GIS databases on long term eel habitat distribution, statistics of fisheries and artificial river structures. 2) The analysis of the spatio-temporal changes of eel habitat and its relation to watershed structure. 3) GIS mapping to understand the present status of Japanese eel distribution and to detect candidate catchment for eel habitat restoration in the target region “Seto Inland Sea of Japan”. 4) Testing a new ecosystem monitoring approach using eDNA analysis.

Through these four steps, we grasp the change of eel habitat, further we detect some remarkable area including habitat loss and degradation. Finally, we discuss about candidate restoration sites for Japanese eel in an effective and efficient manner.



I13

Aquatic Biodiversity in a Coastal British Columbia Stream: Relationship Between Prey Availability and Fish Diet

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Next generation sequencing (NGS) was used to compare the presence of aquatic invertebrate taxa in environmental DNA (eDNA) samples from water and ethanol preservative from Surber samples collected in a central British Columbia coastal stream. Stomach contents were also examined from three fish species; rainbow trout, Dolly Varden, and coastrange sculpin sampled from the stream. The greatest diversity of taxa was found in the water samples that also detected terrestrial species. Fish preyed on a subset of relatively few taxa identified in Chist Creek across most Orders, except Ephemeroptera where over 50% of potential taxa identified in the eDNA were also found to be prey. Although the trout and char typically occupy different depths in the water column from sculpins, juvenile salmonids from Chist Creek appear to exploit benthic dwelling invertebrates and eat a similar diet to sculpin. NGS of eDNA can provide a more comprehensive and inclusive description of the available prey community for fish, while analysis of the stomach contents leads to high prey diversity detection and taxonomic resolution