47th Annual Meeting of the Atlantic International Chapter of the American Fisheries Society

In collaboration with

The Northeastern Division of the American Fisheries Society

47th Congres annuel du Chapitre international de l'Atlantique
En collaboration avec
Division Nord-Est de l'American Fisheries Society

14-17 October 2023
Saint John, New Brunswick

MEETING SCHEDULE

Saturday, October 14th — *Hilton Saint John: Kennebecasis rooms 1 & 2*

16:00	17:00	Check-in	
17:00	19:00	Registration	
19:00	19:15	Informal Welcome	
		Dr. Russell Easy	AIC President
SESSION 1		"Tech Talk" Hors d'oeuvres + cash bar	
19:15	19:40	**Hugo Marques**	OregonRFID
		Advantages of HDX PIT Technology	
19:40	20:05	**Silvana Germana**	Innovasea
		What's New in Acoustic Telemetry?	

Sunday, October 15th

Hilton Saint John, Montagu rooms 1, 2, 3 & Foyer

8:00	9:00	Registration + Breakfast (Provided)	
9:00	9:15	Welcome Address **Dr. Russell Easy & Dr. Heather Stewart,** AIC & NED Presidents **Todd Ross,** University of New Brunswick: Indigenous Advisor	

SESSION 2: "Freshwater Ecology: From Tropic to Lentic"

9:15	9:30	**Emma-Jean Freeman** Diving into Diversity: Phylogenetic Insights into Costa Rica's Freshwater Mussels	Acadia University
9:30	9:45	**Abby Culberson** Using stable isotopes to compare the trophic niche of largemouth bass (*Micropterus salmoides*) with local sportfish species in the Wolastoq (Saint John) River, New Brunswick, Canada	Canadian Rivers Institute
9:45	10:00	**Matthew G. Warner** Lake Trout (*Salvelinus namaycush*) in Sherbrooke Lake, Nova Scotia: Critical Habitat and Origin	Acadia University
10:00	10:15	Coffee break	

SESSION 3: "Lobster-Fest"

10:15	10:30	**L. Grace Walls** Investigating the effect of the fishermen – How does bait preparation affect lobster foraging responses?	St. Francis Xavier University
10:30	10:45	**Mary Whipple** Can hatch time of the American lobster (*Homarus americanus*) be accurately predicted using embryos raised detached from a female's brood?	University of New Brunswick
10:45	11:00	**Emily Blacklock** Contribution of seasonal migrations to embryo development and connectivity of adult American lobster (*Homarus americanus*) in the Bay of Fundy	University of New Brunswick

KEYNOTE SPEAKER

11:00	12:00	**Dr. Anaïs Lacoursière-Roussel** Innovating aquatic management strategies using environmental DNA	Université Laval
12:00	13:00	Lunch (Provided)	

SESSION 4

13:00	13:15	**Jake Reicker** Monitoring Inter-dam Distribution of Aquatic Species with Environmental DNA	Canadian Rivers Institute
13:15	13:30	**Leah ML Creaser** Tewapskik (Annapolis River), Nova Scotia, species assemblage monitoring: a comparative analysis following cessation of a tidal power station	Acadia University
13:30	13:45	**Roman Javorek** Sea Star Wasting as a Generalized Stress Response	Acadia University
13:45	14:00	**Deborah F. Alademehin** Can Freshwater Fisheries Provide Sustenance in an Age of Scarcity, Simplification, and Strife? A Biophysical Economic Analysis of Ice-Angling for Panfish in Central Maine	University of Maine
14:00	14:15	**Hannah Green** Assessment and Mapping Of The Drivers Of Thermal Refuge Temperatures On The Restigouche River Watershed	University of New Brunswick
14:15	14:30	**Gabriela Ulmo Diaz** Geography-linked epigenomic methylation signatures in the panmictic American Eel	Université Laval
14:30	14:45	**Chandler Stairs** How to catch a sea monster: an acoustic telemetry case study of Atlantic wolffish	University of New Brunswick
14:45	15:00	**Nicole J. Daigle** Validation of a microwave energy meter to non-lethally estimate energetic reserves in adult sturgeon	University of New Brunswick
15:00	15:15	Coffee break	

SESSION 5

15:15	15:30	**Jeffrey K. Fryer** 30 years of trans-boundary collaboration in restoring Okanagan Basin Sockeye		Columbia River Inter-Tribal Fish Commission
15:30	15:45	**Mary Finch** Watershed Management in Prince Edward Island		PEI Dept. of Environment, Energy and Climate Action
15:45	16:00	**Amanda Xuereb** Genomic Applications for Eastern oyster (*Crassostrea virginica*) production and management in Atlantic Canada		Université Laval
16:00	16:15	**Lael Will** Utilizing eDNA technology to gain current information on the distribution of Sea Lamprey (*Petromyzon marinus*) and American Eel (*Anguilla rostrata*) in the Connecticut River watershed		Vermont Fish & Wildlife Dept.
16:15	16:30	**Alexa J. Cacacie** Estimating estuarine habitat use of Rainbow Smelt using otolith geochemistry		University of New England
16:30	16:45	**Michael D. Nguyen** Innovation for a Bycatch-Free Longline Fishery: Demonstrating the Efficacy of a Novel Microprocessor-Based Bycatch Reduction Device		University of New England
16:45	17:00	**Nate Hermann** Patterns in existing bioenergetics model parameters and their utility for the development of future species models		University of New Hampshire
17:30	18:30	POSTER SESSION	Hors d'oeuvres + cash bar	
18:30	19:30	SOCIAL MIXER	Hors d'oeuvres + cash bar	

Monday, October 16th

Hilton Saint John, Montagu rooms 1, 2, 3 & Foyer

8:00	9:00	Breakfast (Provided)	
9:00	9:15	Welcome Address	

SESSION 6: "Striped Bass Ecology & Management"

9:15	9:30	**Keeler Colton** Seasonal Residency and Overwintering Behaviour of Striped Bass *Morone saxitilis* in The Annapolis River, Nova Scotia	Acadia University
9:30	9:45	**Nathalie LeBlanc** Development of a high-thoroughput SNP panel for individual identification and mixed stock analysis of Striped Bass	University of New Brunswick
10:00	10:15	Coffee break	

SESSION 7

10:15	10:30	**Kate Gingles** The Role of Atlantic Salmon (*Salmo salar*) in Ecological Restoration: Insights from Five Atlantic Canadian National Parks	University of New Brunswick
10:30	10:45	**Mike Dadswell** The Decline and Impending Collapse of the Atlantic Salmon Population in the North Atlantic Ocean	Acadia University
10:45	11:00	**Jack Nason** An Assessment of Inner Bay of Fundy Atlantic Salmon (*Salmo salar*) Spawning Success in Fundy National Park	University of New Brunswick
11:00	11:15	**Katherine L. Dalby** "All Hands in the Tank": Analyzing the social networks of captive rearing and stocking programs for Atlantic salmon conservation in Nova Scotia, Canada	Dalhousie University
11:15	11:30	**Erin McCavour** Stable isotope and lipid assessment of Atlantic salmon (*Salmo salar*) smolts across regional populations in Eastern Canada	University of New Brunswick

11:30	11:45	**Lauren Cyr** Impact of Restoration on Smolt Age Class Distribution and Growth Rates in a recovering Atlantic Salmon (*Salmo salar*) Population	University of New Brunswick
11:45	12:00	**Jagger Watters-Gray** Linking the environment with environmental DNA: modelling environmental dynamics alongside quantitative eDNA data for the enumeration of Atlantic salmon (*Salmo salar*)	University of New Brunswick
12:00	13:00	Lunch (NOT provided)	

SESSION 8: "Fisheries Management"

13:00	13:15	**Kathryn Collet** Keeping it Real	DNRED/MRNDE
13:15	13:30	**Merry Gallagher** Maine's wild Brook Trout: Building a conservation strategy and fostering resiliency for an iconic native coldwater fish species	Maine Inland Fisheries & Wildlife Dept.
13:30	13:45	**Levi Brown** Uncertainties Related to Minnow Trap Bycatch in Vermont	Vermont Fish & Wildlife Dept.
13:45	14:00	**John Magee** Fisheries Management in New Hampshire	New Hampshire Fish & Game Dept.
14:00	14:15	**Rosanne MacFarlane** Fishing for Likes: Why social media is a double-edged sword for fisheries managers	PEI Forests, Fish and Wildlife
14:15	14:45	**Roundtable Q/A with Session 8 presenters**	

15:00	15:30	Coffee break
15:30	17:30	NED Business Meeting
		A remote meeting link has been distributed via email
18:30	21:00	Banquet Diner (Provided + cash bar)
		Dress casual attire suggested, not required

Tuesday, October 17th

*NOTE Location change! *Delta Saint John, Ballroom A*

8:00	9:00	Breakfast (NOT provided)
9:00	11:00	AIC Business Meeting
11:00	11:45	Lunch (Provided)
11:45	12:45	Awards, silent auction winners, raffles
12:45		Departure

PRESENTERS

(Bold indicates speaker)

Advantages of HDX PIT Technology

Hugo Marques, OregonRFID

What's New in Acoustic Telemetry?

Silvana Germana, Innovasea

Diving into Diversity: Phylogenetic Insights into Costa Rica's Freshwater Mussels

Emma-Jean Freeman*, Dr. Don Stewart, Dr. Russell Easy
Acadia University, Wolfville, Nova Scotia, Canada

Freshwater mussels (Family: Unionidae) are integral invertebrates within freshwater ecosystems and play a crucial role in nutrient cycling and maintaining water quality. However, bivalves are also one of the most vulnerable animal groups due to climate change and anthropogenic factors such as habitat destruction and pollution. Therefore, monitoring of bivalve population numbers and distribution is imperative as their environments continue to change. However, research on the phylogeny and distribution of freshwater mussels is described as geographically biased as monitoring activities in some parts of the world, including Mesoamerica, are limited. Also, a lack of available molecular sequence data for many Mesoamerican species of freshwater bivalves has limited evolutionary analyses in this group. In 2019, mussels were collected in Guanacaste, Costa Rica and were identified using cox1 DNA barcoding and assessment of morphological characters. These analyses confirmed the identities of *Nephronaias tempisquensis* and invasive *Sinanodonta woodiana*. These specimens were further examined for doubly uniparental inheritance, an uncommon form of

mitochondrial DNA inheritance only observed in some bivalves. Finally, phylogenetic analyses of *N. tempisquensis* revealed a close association with the *Popenaiadini* tribe of freshwater mussels. The project presented here not only expands our knowledge of aquatic diversity in Costa Rica but also aims to provide crucial molecular sequence data currently lacking for Mesoamerican bivalves. This information can be used in future identification efforts and analyses of the molecular evolution of bivalves found in Mesoamerica. Ultimately, these efforts will become increasingly significant as conservation and monitoring strategies are developed to accommodate our changing climate and species evolution in hopes of maintaining the health and diversity of freshwater ecosystems.

Using stable isotopes to compare the trophic niche of largemouth bass (*Micropterus salmoides*) with local sportfish species in the Wolastoq (Saint John) River, New Brunswick, Canada

Abigale E. Culberson[1,2], Tommi Linnansaari[1,2,3], Kelly Munkittrick[1,4], R. Allen Curry[1,2,3] and Phillip M. Harrison[1,2,3]

[1]Canadian Rivers Institute, University of New Brunswick, Fredericton, NB, Canada
[2]Faculty of Forestry and Environmental Management, University of New Brunswick, Fredericton, NB, Canada
[3]Department of Biology, University of New Brunswick, Fredericton, NB, Canada
[4]Department of Biological Services, University of Calgary, Calgary, AB, Canada

Invasive species are organisms which have been introduced to a new environment and have the potential to cause harm to native biodiversity and endemic species in recipient ecosystems. The popularity of largemouth bass (*Micropterus salmoides*) among anglers in North America has resulted in frequent introductions outside their native range. However, largemouth bass can cause significant negative impacts in ecosystems to which they are not native. In 2014, largemouth bass were discovered in the Wolastoq (Saint John) River, New Brunswick. This study aims to investigate the trophic niche of invasive largemouth bass in the Wolastoq River compared to other local sportfish in the same area. Using carbon ($\delta^{13}C$) and nitrogen ($\delta^{15}N$) stable isotope analysis, this study compares trophic overlap between largemouth bass, smallmouth bass (*Micropterus dolomieu),* chain pickerel (*Esox niger*), and yellow perch (*Perca flavescens*). Samples were obtained by taking a fin clip from each fish's dorsal fin and comparing each species' values to stable isotope baseline samples to identify food sources. Results are expected to provide a significant contribution to our understanding of the interspecific competition between this recently introduced predatory fish and other valuable sportfish in the area.

Lake Trout (*Salvelinus namaycush*) in Sherbrooke Lake, Nova Scotia: Critical Habitat and Origin

Matthew G. Warner[1*], Sam Andrews[1], Andrew Lowles[2], John MacMillan[2], Benjamin Marcy-Quay[3], Cam Solda[1], Mike J.W. Stokesbury[1]

[1]Biology Department, Acadia University, Wolfville, Nova Scotia
[2]Nova Scotia Department of Fisheries and Aquaculture: Inland Fisheries Division
[3]Rubenstein Ecosystem Science Laboratory, University of Vermont, Burlington, Vermont, USA

The first research program focused on Lake Trout (*Salvelinus namaycush)* in Nova Scotia (NS) was performed to examine critical habitat, and to determine if the species is native to the province. A recent synthesis of Lake Trout in the Maritime Provinces of Canada indicated that, despite extensive historical stocking, Lake Trout are likely native to NS. The species may now be under threat of extirpation, leaving those in Sherbrooke Lake, Lunenburg County, as the province's only confirmed breeding population. In Sherbrooke Lake, Lake Trout habitat requirements were measured through a combination of water temperature monitoring, bathymetric mapping, and acoustic telemetry. Lake Trout origin in Sherbrooke Lake was determined though genetic analysis. In 2022, 11 Lake Trout were acoustically tracked, and inhabited a purely hypolimnetic depth residency, with temperatures ranging from 8.5 to 10 °C between 12 and 24 m. Due to the effects of Hurricane Fiona, this suitable depth and temperature range was compressed to a 2 m depth range for the month of October, having a disproportionate affect on mature Lake Trout. Genetic analysis determined

that the Lake Trout population in Sherbrooke Lake was highly distinct from other potential stocking source populations from across North America, providing evidence that Lake Trout are native to NS. Highly restricted critical thermal habitat for Lake Trout in Sherbrooke Lake may be under threat from the effects of climate change. As this population has been identified as native, continued decline in the quantity and quality of their habitat could lead to the extirpation of a genetically distinct and important component of Lake Trout genetic diversity.

Investigating the effect of the fishermen – How does bait preparation affect lobster foraging responses?

L. Grace Walls[1,2*], Iain J. McGaw[2], Russell C Wyeth[1],

[1] Department of Biology, St. Francis Xavier University, Antigonish, NS, Canada
[2] Department of Ocean Sciences, 0 Marine Lab Road, Memorial University, St. John's, Newfoundland

The American lobster, *Homarus americanus*, is a species of both ecological and economic importance. As mid-trophic level opportunistic omnivores in the western North Atlantic, lobsters feed on a variety of vertebrate, invertebrate, and macroalgal species, and can constitute a considerable proportion of the collective consumer biomass. As the target of an extensive fishery, substantial quantities of bait are deployed into the nearshore benthic ecosystem by harvesters to attract lobsters to traps. However, across the lobster fishing industry there is a historically wide variety of both bait choice and of bait preparation tactics. These differences in preparation are expected (by the harvesters) to affect effectiveness of the bait (presumably by changing the nature and extent of the odor plume created), but no consensus among harvesters nor scientific evidence to support one strategy over the others has been found. During May and June of 2022, Baited Underwater Video Tripods (BUVT) were deployed in the Northumberland Strait to investigate lobster responses to different preparations of bait. BUVT incorporated downward facing cameras to record numbers of foraging lobsters surrounding a bait bag filled with different types of bait (always with the same wet weight). In experiment 1, Alewife (*Alosa pseudoharengus*) was frozen and divided into four different pieces before being deployed beneath the cameras. Baits included two by-product options of heads and racks (spine and tail with head and fillets removed), and two commercially valuable options of uncut whole fish and fillets. The effect of specific body part was also tested in experiment 2 with Acadian redfish (*Sebastes fasciatus*), with 3 different pieces. These included the commercially valuable options of whole uncut fish and whole fish cut into cubes, and the by-product option of racks. In both experiments there was a non-significant trend of fewer lobsters surrounding uncut baits. The fact that lobsters showed no preference for a specific piece of the body is noteworthy as it suggests that by-products (heads/racks) from other fisheries could be used as bait, thus saving the commercially valuable portions (cubed fish/fillets/whole) for direct human consumption. A separate pair of experiments using *S. faciatus* explored the effect of treatment of bait by deploying the same pieces of both by-product (racks) and commercial bait (whole fish cut into cubes) following different treatments. In experiment 3, *S. fasciatus* racks were deployed either fresh (never frozen) or frozen, and in experiment 4, cubed *S. faciatus* was deployed fresh, frozen, and aged (previously frozen fish, thawed, and left for two weeks at room temperature). Both experiments found different bait treatments to have a highly significant effect on the number of lobster present. Fresh *S. fasciatus*, (both cubed and racks) attracted significantly fewer lobsters than frozen or aged baits. This again illustrates the value in marine by-products, many of which are currently destined for landfills, as a possible alternative to commercially harvested bait fish. Looking forward, we hope to expand the use of BUVT to test alternative sustainable bait options with the goal of improving the efficiency and sustainability of the lobster fishery.

Can hatch time of the American lobster (*Homarus americanus*) be accurately predicted using embryos raised detached from a female's brood?

Mary Whipple, Remy Rochette
University of New Brunswick

The success of American lobster (*Homarus americanus*) larvae is dependent on food availability, temperature, and predation, which are highly affected by when hatch occurs. In Canada, hatch mostly occurs outside of

fishing seasons, preventing its direct observation in collaboration with fishermen, and hence making monitoring of hatch over large areas prohibitively expensive. An alternative to direct observation is using temperature-based functions to predict development and hatch of embryo. In hopes of facilitating the simultaneous development of such functions for many lobsters and locations, this study aims to determine if we can accurately predict hatch of American lobster using embryos raised separately from a female's brood. To address this objective, we compared the (i) development rate, (ii) development status at hatch, (iii) mean hatch date and (iv) progression of hatch of embryos raised in the laboratory attached and detached from the brood of 28 female lobsters from the Bay of Fundy. Comparison of hatch in attached and detached embryos determined that embryos raised detached from a female's brood can be used to accurately predict mean hatch date of a group of females and can also be used to study hatching behaviour of embryos of individual females but with a limited scope.

Contribution of seasonal migrations to embryo development and connectivity of adult American lobster (*Homarus americanus*) in the Bay of Fundy

Emily Blacklock
University of New Brunswick

American lobster, Homarus americanus, support a significant commercial fishery in both Canada and the US. In Canada, lobster landings were valued at over $2 billion in 2021, and the fishery is divided into 45 distinct lobster fishing areas (LFAs). Five of these LFAs are located within the Bay of Fundy and have accounted for 40% of the total lobster landings in Canada for the last two decades. Despite its considerable socio-economic importance, important knowledge gaps still exist concerning this resource, including the seasonal migration paths of the species. From previous studies, lobster within the Bay of Fundy have shown movement to deeper waters in the fall and to shallower waters in the spring. This study will utilize pop-up satellite archival tags (PSATs) to examine the migration patterns of adult American lobster in the Bay of Fundy. PSATs collect information of depth and temperature experienced by the lobster at regular intervals. These data will then be combined with depth and temperature data to reconstruct the most-likely movement tracks. This study aims to understand the impact of movements on the connectivity between the inshore and offshore populations of lobster, as well as between the currently defined LFAs. It also aims to increase our understanding of where egg-bearing females hatch their embryos and where adult male and female lobsters go to overwinter. This presentation will highlight the methods used, the results so far and the next steps of this study. The utilization of PSATs in the examination of lobster migration will allow this study to provide the most detailed empirical data to date concerning the movement of adult American lobster within the Bay of Fundy.

KEYNOTE SPEAKER

Innovating aquatic management strategies using environmental DNA

Dr. Anaïs Lacoursière-Roussel
Université Laval

Analysis of DNA from environmental samples (i.e., environmental DNA or eDNA) is increasingly being used as a non-intrusive, sensitive, and often cost-effective aquatic monitoring approach. eDNA is a revolutionary approach for increasing our ability to quantify, characterize and describe aquatic species, and to better understanding how biological and physical factors are altering populations. The talk will present the recent progress of aquatic eDNA, including new technologies, population predictive models and how DFO is handling the integration of this new information within management decisions. I will explain why understanding how temporal eDNA trends are altered by biological and physical factors, such as species behaviour (e.g., seasonal migration) and life cycle (e.g., spawning period and larvae stages of benthic organisms) will refine the power of eDNA to study aquatic species ecology and community dynamics. Our work highlighted the importance of how eDNA can inform sensitive stages of species at risk, such as Atlantic salmon smolt and their migration patterns. Moreover, a massive amount of eDNA data have been obtained in the last decade and the global network of eDNA collaborators is expected to continue expanding

exponentially, becoming a catalyst for research on biodiversity, ecosystem services, and sustainability. I will present the new DFO initiative to build an evidence-based ocean observation system with cross-latitudinal time-series eDNA data. GOTeDNA is a centralized interactive online tool currently in development aiming to report and visualize trends in spatiotemporal eDNA distributions and provide guidance on optimal sampling strategy. GOTeDNA is a machine learning application for ocean ecology and sustainable natural resource management with the potential to radically improve the motivation of organizations to organize, share and utilize their data. Currently, the tool is developed using consistent and comprehensive available databases from south of Maine to the eastern Arctic; however, by updating the tool as data are accrued, the degree of confidence in predicted optimal eDNA sampling periods will increase and be spatially-refined. This evidence-based guidance will provide capacity to conduct efficient and scientifically tenable eDNA-based surveillance and monitoring programs while optimizing human/financial resources. Furthermore, this comprehensive approach will improve confidence by streamlining operational requests, addressing inconsistencies in reporting among eDNA studies, and facilitating integration of results in management decisions. The development of this project was motivated by the challenges we have experienced in making eDNA results easily accessible for non-scientist groups who have shown a strong desire to access aquatic biodiversity data. Continued communication among eDNA end-users, science, and national and international policy-makers is crucial to transfer knowledge and empower nations to adopt eDNA-based monitoring methods and inform decision-making.

Monitoring Inter-dam Distribution of Aquatic Species with Environmental DNA

Jacob Reicker*, Philip Harrison†, Larissa Roehl* Allen R. Curry†, Scott A. Pavey*

*Canadian Rivers Institute (CRI), University of New Brunswick, Saint John, Canada. †Canadian Rivers Institute, University of New Brunswick, Fredericton, Canada.

The Wolastoq (Saint John) River in New Brunswick supports freshwater, anadromous, and catadromous fishes. It is difficult to monitor fish movement through traditional capture methods alone, due in part to the immensity of the river system, spanning more than the entire length of the province. Moreover, it is not yet understood how the transport of various species over the Mactaquac Dam, which traverses the river 15 kilometres west of Fredericton, New Brunswick, influences their movements and spawning habitat choices. Environmental DNA, trace genetic material left behind in the water column, has become a widely accepted tool in ecological studies due to its scale and affordability. We have made use of environmental DNA to monitor the distribution of several important species – Atlantic salmon (*Salmo salar*), American shad (*Alosa sapidissima*), Alewife and Blueback herring (*Alosa pseudoharengus* and *Alosa aestivalis*, respectively; collectively known as River herring), Largemouth bass (*Micropterus salmoides*), and American eel (*Anguilla rostrata*) – along the Saint John River, and key tributaries, between Fredericton and Perth-Andover. We collected triplicate one-litre water samples from 12 sites on a weekly/biweekly basis from April to October, 2022; in total, 680 litres were collected. Samples were filtered, extracted, and prepared for qPCR in separate, environmental DNA-only facilities to avoid contamination. Quantification using species-specific primer-probe assays revealed changes in concentrations of target DNA at each site over the sampling period. This research will contribute to the Mactaquac Aquatic Ecosystem Study's growing knowledge of fish movement within the inter-dam system and help inform future fish-passage options.

Tewapskik (Annapolis River), Nova Scotia, species assemblage monitoring: a comparative analysis following cessation of a tidal power station

Leah Creaser, Dr. Trevor Avery
Acadia University

The barrage style Annapolis Tidal Generating Station (ATiGS) in Annapolis Royal, Nova Scotia was Canada's only power generating station using the tides of the Bay of Fundy. In 2019, ATiGS's power generating operations ceased, although structurally it remains. Since ATiGS's operations started in 1984, significant

habitat changes occurred. Annapolis River contains two at-risk fish species: Striped Bass (*Morone saxatilis)* presumed to be an extirpated population, and Atlantic Sturgeon (*Acipenser oxyrhynchus).* Maritimes population currently COSEWIC assessed as endangered. Beach seining was completed by DFO in 2000 and 2001, and over five years from 2010 to 2015 (except 2012) to quantify species assemblages during ATiGS operations and to determine if Striped Bass were present. After cessation, contemporary monitoring began in 2021, continued from July to December 2022 and from April to November 2023. Historical sampling sites were sampled to provide continuity; new sites were added to provide spatial extent. Post cessation survey data are compared with historical survey data to characterize changes in species presence, abundance, diversity, and potential recolonization of Striped Bass.

Sea Star Wasting as a Generalized Stress Response

Roman Javorek
Acadia University

Sea Star Wasting Syndrome (SSWS) is a broadly defined suite of conditions, including loss of turgor, body wall lesions and limb detachment. The wasting phenotype has been recorded in at least twenty sea star species native to the North American Pacific coast (Alaska Peninsula to Baja California), with some regions reporting 80% mortality since the 2014 onset. The causative agent of the syndrome is yet to be determined, as the initial attribution to the sea star-associated densovirus (SSaDV) has been dismissed due to the ubiquity of the virus among unaffected stars. Given that sea star wasting syndrome is the largest ever recorded marine epidemic and that sea stars are keystone predator species, it is of utmost importance to determine what is causing the 'melting' phenotype. My study explores the hypothesis that the phenotype is a manifestation of a self-induced condition brought on by environmental stress, with the differential mortality rates among populations being caused by genetic tolerance rather than the distribution of pathogens. This study focuses on manipulating conditions in a controlled environment to induce sea star wasting. Molecular analyses will target genes coding for matrix metalloproteinases (MMP) and tissue inhibitors of matrix metalloproteinases-like (TIMP-like). MMPs and TIMPs are highly conserved proteases implicated in numerous degenerative diseases in other species, including humans. It is suggested that by exploring endogenous causes of SSWD, the intrinsic nature of the disease can be confirmed.

Can Freshwater Fisheries Provide Sustenance in an Age of Scarcity, Simplification, and Strife? A Biophysical Economic Analysis of Ice-Angling for Panfish in Central Maine

Deborah Alademehin[1] and Stephen Coghlan[1,2]

[1]Department of Wildlife, Fisheries, and Conservation Biology, University of Maine, Orono
[2]Center for the Advancement of the Steady-State Economy (CASSE).

Resource depletion, pollution, climate heating, inflation, and sociopolitical unraveling are all indicators to the present and impending economic downturn that awaits humanity as ecological footprint downsizes to fit local, regional, and planetary carrying capacity. In response to this, some Mainers will turn directly to their local environment for sustenance through fishing, hunting, foraging, and other back-to-land activities. Hence, this research will investigate the capacity of ice-angling for Black Crappie and other Sunfishes to provide sustenance for Mainers during a future of scarcity, simplification, and strife. We will combine traditional fisheries science and biophysical economic analysis to assess the capacity of ice-angling to provide sustenance for Mainers. Specifically, we will 1) Use otoliths from harvested Panfish spanning 10+ years to infer vital characteristics of individuals and populations: survival, growth, longevity, age and size structure, and biomass production; 2) Incorporate results from otolith analysis with food web models to investigate capacity of local Panfish populations to feed Maine anglers; 3) Use biophysical economic models to explore various harvesting scenarios and estimate return on investment for individual anglers; and 4) explore how climate heating and economic shocks conspire to change angler behavior and harvest pressure. Analysis has just begun, and preliminary results are forthcoming. So far, ~2,000 otoliths showed diversity in ages (1-23 years), sizes (37-290mm) and productivity differences across ponds. Under increasing harvest, we would expect to find earlier maturation, significant decline in mean age of harvested fish, evolutionary shifts of fish stocks.

Eventually our study will compare protein demand of Maine anglers with productive potential of reference ponds and explore impacts of regulations/management prescriptions. Whether Maine panfisheries, especially via ice angling, can be sustained through the emerging polycrisis is impossible to predict, but our research approach should be informative.

Assessment and Mapping Of The Drivers Of Thermal Refuge Temperatures On The Restigouche River Watershed

Hannah Green, Jae Ogilvie, Carole-Anne Gillis, Charles Sacobie
University of New Brunswick

With the effects of climate change continuing to have major effects on riverine ecosystems, the need for holistic knowledge of thermal refuge conservation is increasing. Thermal refuges are cold-water patches found in rivers that can be utilized by aquatic species to protect against passing physiological thresholds. For Atlantic salmon (*Salmo salar*), high water temperatures cause thermal stress, and in extreme cases, mortality. Tributary confluence plumes are one of the seven classifications of thermal refuges found on the Restigouche River watershed. While driven by groundwater, other landscape and hydrological attributes drive the cooling of tributary confluence plumes. Three drivers were identified to have influence on water temperature, including canopy cover, soil drainage and slope percentage. The drivers were input into global and reach-specific temperature prediction models, where predicted temperatures were compared against previously measured temperature data from the watershed using multiple linear regression analysis. The results indicated that the global fit model did not provide effective results, while the reach-specific model provided stronger predictions between measured and predicted temperatures. The Little Main Restigouche (n=15) and the Upsalquitch SW (n=12) tributaries showed significant results (high R^2) while the Restigouche (n=75) and Upsalquitch (n=31) showed less significant results (low R^2). Variation may be due to differing sample sizes, discrepancies between timing of measured temperatures and associated geospatial data, as well as the absence of provincial data from the southern Quebec portion of the watershed. While the reach-specific model performed higher than the global model, additional model parameters are required to increase the accuracy of predictions at tributary confluence plumes. With the addition of further parameters for higher prediction accuracy, the model can be used to identify areas of high conservation need on the watershed.

Geography-linked epigenomic methylation signatures in the panmictic American Eel

Gabriela Ulmo-Diaz, Eric Normandeau, Louis Bernatchez
Université Laval

Epigenetic modifications contribute to phenotypic plasticity, driving life history and phenotypic differences in what could be considered epigenetic-based adaptation. For panmictic and clonal species, epigenetic modifications such as methylation can mediate locally adapted phenotypes, creating epigenetic population structure. We found that this is the case for the American Eel, a panmictic fish central to commercial and traditional subsistence fisheries in Eastern North America and classified as Endangered by the International Union for Conservation of Nature (IUCN). Using whole genome bisulfate sequencing (11X), we obtained whole genome methylation profiles for 72 sexually immature adults from 6 localities (12 per locality) in Canada and observed a stable epigenetic population structure pattern across different cohorts, with methylation profiles differentiating eels from three different regions (St. Lawrence R., Gulf of St. Lawrence, Atlantic coast) after analyzing 88290 differentially methylated loci. We explore how methylation patterns differ between localities and evaluate its implications for eels' conservation.

How to catch a sea monster: an acoustic telemetry case study of Atlantic wolffish

Chandler Stairs, University of New Brunswick

Atlantic wolffish (*Anarhichas lupus*) was the first fully marine species listed as an at-risk species by Canada's Species at Risk Act (SARA), following an estimated 87% population decline between the late 1970s to the mid-1990s, with an estimated 60% decline in the mature population. Populations from the Scotian Shelf have declined 65% since 1980 and continue to decline. The current management plan excludes the identification of critical habitat due to the limited knowledge of wolffish biology. To address this, we employed acoustic telemetry to track continuous movements and used scuba surveys to observe the in-situ behaviours of Atlantic wolffish from Deer Island Point, New Brunswick. Results revealed seasonal migrations associated with spawning and foraging, the courtship and formation of bonded pairs, den usage patterns, and egg-guarding. This study identified Deer Island Point as critical habitat for Atlantic wolffish and contributed insights into the ecological role of Atlantic wolffish in the Bay of Fundy.

Validation of a microwave energy meter to non-lethally estimate energetic reserves in adult sturgeon

Nicole J. Daigle*, Matea A. Djokic, Kevin M. Kappenman, T. Gibson Gaylord, Sierra Quinn, Christine E. Verhille
University of New Brunswick

Whole-body (WB) energetic reserves influence fish survival, growth, and reproduction but are typically quantified using lethal methods (i.e., proximate analyses) or interpreted through body condition indices. Energetic reserves can impact population dynamics through influences on growth rates, age-at-first-reproductive-maturity, and spawning periodicity at the individual-fish level, especially in long-lived sturgeon species. Therefore, a nonlethal tool to track the energetic reserves of endangered sturgeon populations could inform adaptive management and further our understanding of the sturgeon's biology. The Distell Fatmeter is a microwave energy meter that has been validated to nonlethally estimate energetic reserves in some fish species, but never successfully for sturgeon. Here, step-wise linear regressions were applied to test commonly monitored body metrics and Fatmeter measurements at nine different anatomical sites on captive adult pallid sturgeon (*Scaphirhynchus albus*; total length of 790-1015mm; WB lipid of 13.9-33.3%) compared to WB lipid and energy content determined by proximate analyses. Fatmeter measurements alone explained approximately 70% of the variation in WB energetic reserves, which improved upon models considering body metrics alone by approximately 20%. The AICc top-ranked models included a combination of body metrics and Fatmeter measurements and accounted for up to 76% of the variation in WB lipid and energy. We recommend the incorporation of Fatmeter measurements at a single site located dorsally to the lateral scutes at the posterior end of the fish above the pelvic fins (U-P) into conservation monitoring programs for adult pallid sturgeon (TL≥790mm; FL≥715mm) and the cautious application of Fatmeter measurements for sturgeon between 435-790mm TL (375-715mm FL). Measurements at this U-P site combined with body mass explained approximately 75% of the variation in WB lipid and energy.

30 years of trans-boundary collaboration in restoring Okanagan Basin Sockeye

Jeffrey K. Fryer
Columbia River Inter-Tribal Fish Commission

The Okanagan Basin was historically one of the two major producers of Sockeye Salmon in the Columbia Basin. Sockeye once returned in the millions to the Columbia Basin, with a large percentage bound for the Okanagan, however, dams, habitat destruction, overfishing, and neglect had driven this the Okanagan stock down to fewer than 1700 fish by in 1994 and the run seemed destined for extinction. However less than 30 years later in 2022, this stock was the major contributor to a record run of over 660,000 Sockeye counted entering the Columbia River. This was the largest number of Sockeye salmon returning to the Columbia Basin since dam counts became available in the 1930s. The role of the Okanagan Nation Alliance and Canada Department of Fisheries and Oceans, using funds primarily from U.S. dam operators was one key to this turning around this Sockeye Salmon run. This presentation will narrate this rare, and incredible, success story which I have had the privilege of being a small part of.

Watershed Management in Prince Edward Island

Mary Finch, Watershed Ecologist
Forests, Fish and Wildlife Division, Department of Environment, Energy and Climate Action, Government of Prince Edward Island

There are 25 community-based watershed groups in Prince Edward Island working towards local solutions for environmental issues. While PEI is a small province geographically, there are 260 watersheds and residents have a deep connection to their local waterways. Core funding for groups is provided through the provincial Watershed Management Fund and watershed groups have created a local and provincial network to complete stewardship, education, rehabilitation, beneficial management practices, monitoring and research projects. This presentation will talk about the history of watershed management on PEI, the types of work completed by groups, partnerships created, and challenges faced.

Genomic Applications for Eastern oyster (Crassostrea virginica) production and management in Atlantic Canada

Amanda Xuereb*, Rodrigo Marín Nahuelpi, Eric Normandeau, Charles Babin, Martin Laporte, André Mallet, José M. Yàñez, Martin Mallet, Louis Bernatchez
Université Laval

The Eastern oyster (**Crassostrea virginica**) is one of the most economically valued shellfish species in Canada and the American Atlantic coast. Genomic tools have the power to enhance management and aquaculture practices but have been lacking for oyster populations in Eastern Canada. With a collaboration between two academic institutions (Université Laval and Universidad de Chile) and L'Étang Ruisseau Bar Ltée., a leading shellfish hatchery in Atlantic Canada, our goals were to (a) design and validate a high-density (200K) SNP chip and (b) characterize the extent of population genetic structure in wild C. virginica populations. The SNP chip represents a critical step toward the development of the first selectively bred eastern oyster strain in Canada and will be a valuable tool for aquaculture applications including genomic selection for accelerated production. We assessed population genetic structure in wild populations using low-coverage whole-genome sequencing of 950 oysters sampled from 19 locations spanning the Atlantic coast. We found strong genetic differentiation between most sampling locations, corroborating earlier findings based on reduced-representation sequencing, and more pronounced genetic structure compared to many marine species in Eastern Canada. These results have important implications for the management of this valuable resource by improving our understanding of the extent to which local populations are genetically distinct and provides a baseline for monitoring and regulating interactions between wild and farmed populations. This academic-industry partnership, funded by the Genomic Applications Partnership Program (GAPP) of Genome Canada, will have direct benefits on the success and sustainability of the Canadian Atlantic oyster industry.

Utilizing eDNA technology to gain current information on the distribution of Sea Lamprey (*Petromyzon marinus*) and American Eel (*Anguilla rostrata*) in the Connecticut River watershed

Lael Will
Vermont Fish and Wildlife Department

Vermont is one of the four partnering states that manages diadromous species within the Connecticut River under the Connecticut River Atlantic Salmon Commission (CRASC). Recreationally and ecologically important species include American Eel and Sea Lamprey. Targeted surveys to identify current distribution of Sea Lamprey and American Eel in Vermont tributaries are lacking. Field surveys for spawning Sea Lamprey were initiated in 2015 to locate nests and carcasses at know Sea Lamprey spawning tributaries. Additionally, we are utilizing eDNA technology to identify species presence and assess temporal changes in detection for potential future use to evaluate distribution. Water samples were collected using a Smith Root eDNA filter pack using self-preserving filters at known and unknown Sea Lamprey spawning locations, and American Eel rearing locations. Since adult Sea Lamprey occur in freshwater during the spawning period and juveniles (ammocoetes) rear in the substrate year-round sites were sampled in replicate during the summer (June/July) and autumn (October) during low flow to collect eDNA from adults and juveniles (summer), and juveniles only

(autumn). During the 2022 field season, a total of three streams, and eight stream reaches were surveyed to identify and geo-reference Sea Lamprey nests. A total of 142 Sea Lamprey nests were observed and geo-referenced. Nine streams were sampled in replicate to collect eDNA samples. A total of 26 eDNA samples were collected during the 2022 field season. Results indicate that collecting eDNA samples during the summer period more accurately detects Sea Lamprey DNA. We will discuss our results in more detail and provide information on ways to improve the sampling methods in the future. Understanding the status and trends of these diadromous populations, will improve our ability to protect and manage these species and their habitats including improved fish passage at barriers, improved flows at regulated rivers as well as other habitat conservation measures.

Estimating estuarine habitat use of Rainbow Smelt using otolith geochemistry

Alexa Cacacie[1], Chloe Pearson[4], Nathan Miller[2], Benjamin Walther[3], Nathan B. Furey[4], John A Mohan[1]

[1]The University of New England; [2]The University of Texas at Austin; [3]Texas A&M University -Corpus Christi, [4]The University of New Hampshire

Successful management of diadromous fish species relies on knowledge of seasonal migration patterns. Diadromous Rainbow Smelt (*Osmerus mordax*) contribute to popular recreational ice fisheries throughout New England and support the base of food webs as forage fish. However, due to human activity, migratory populations of Rainbow Smelt have declined considerably in recent decades and are now listed at state and federal levels as species of concern. Given the importance of Rainbow Smelt, the goal of this study was to determine estuarine residency throughout Great Bay, New Hampshire and four of its tributaries. Elemental analysis of chronological growth layers in otoliths provides continuous life history records of estuarine habitat use. Specifically, the concentrations of strontium (Sr) and barium (Ba) can record movement throughout estuarine salinity gradients. We quantified Sr and Ba concentrations from otolith cores (birth) to edges (capture) in adult Rainbow Smelt (n = 79; TL=149 mm-232 mm) to determine estuarine residency and movement across salinity gradients. Partition coefficients (D) for each element (D_{Sr} = 1.08 ± 0.27; D_{Ba} = 0.01 ± 0.01) established a salinity threshold ($Sr_{otolith}$ = 4.80 mmol/mol Ca; $Ba_{otolith}$ = 1.08 µmol/mol Ca) that was used to quantify lifetime salinity experiences. Further analyses of otolith microchemistry confirmed diadromous migratory patterns of rainbow smelt. This study increases our understanding of estuarine use by Rainbow Smelt by identifying important habitats and characterizing connectivity among freshwater, estuarine, and marine systems to optimize current management efforts.

Innovation for a Bycatch-Free Longline Fishery: Demonstrating the Efficacy of a Novel Microprocessor-Based Bycatch Reduction Device

Michael D. Nguyen[1], Sara, Mirabilio[2], Richard Brill[3], Peter Bushnell[4], Walter Golet[5], Ilan Levine[4], Brian Davis[4] John A. Mohan[1]

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Shark bycatch reduces catch rates of targeted species in longline fisheries and threatens shark populations vulnerable to overfishing. We have developed a microprocessor-based bycatch reduction device (MB-BRD) that emits electrical signals to deter sharks from biting hooks by overstimulating their electrosensory system. To test the efficacy of MB-BRDs, we conducted laboratory experiments with Spiny Dogfish (*Squalus acanthias*) and a MB-BRD producing a fixed 5V 6Hz AC signal at 100% and 50% duty cycles. We were specifically testing the hypothesis that electrical fields emitted by MB-BRDs significantly decrease final bite responses. Bait consumption by groups of adult Spiny Dogfish declined to zero in all 100% duty cycle trials (N=144; 80 active, 64 control) and declined by 27% in all 50% duty cycle trials (N=144; 72 active, 72 control). MB-BRDs were then deployed in twenty experimental pelagic longline sets in North Carolina using a 5V 6Hz AC pseudorandom pattern and produced a notable reduction in shark bycatch, but no significant reduction of

catch rates of targeted tunas (Bigeye, Yellowfin, and Blackfin tunas, *Thunnus obesus, Thunnus albacares, Thunnus atlanticus* respectively).

Patterns in existing bioenergetics model parameters and their utility for the development of future species models

Nathan T. Hermann and Nathan B. Furey
University of New Hampshire

Temperature is considered the ecological master factor, controlling fish metabolism and, when integrated with prey availability, growth. Quantifying relationships between water temperature and fish respiration, consumption, and growth is thus central to understanding fish biology in a variety of contexts, particularly as warming waters increase energetic demands. In response, species-specific bioenergetics models have been constructed for a variety of fishes with the Wisconsin model framework being among the most popular. However, the research required to parameterize a model for species-specific performance requires intensive and rigorous experimentation that is costly and time-consuming at best or impossible for endangered species or those found in hard-to-access environments. For this reason, we conducted a meta-analysis of Wisconsin fish bioenergetics models to identify potential geographic, environmental, taxonomic, and biological correlates to their variation that might allow future researchers to estimate growth and consumption quickly and easily for a new species. We gathered parameters from existing Wisconsin bioenergetics model for 70 species from 15 orders pairing them with species' taxonomic relationships, preferred habitats and foraging, and anatomical or physiological features. Parameters defining temperature preferences for consumption were highly variable across species, such as optimal feeding temperatures which range from 8°C to 35°C (mean = 21.83°C), but were significantly associated with taxonomy as order explained 61.6% of deviance in optimal temperature (GAM, $p < 0.001$). Future steps include using our results from these and other significant drivers of parameter values to construct predictive models for Spiny Dogfish (*Squalus acanthas*) and Silver Hake (*Merluccius bilinearis)* for which bioenergetics models have not been parameterized but are otherwise data-rich species for validation purposes. Ultimately, we are assessing the potential to translate existing knowledge on fish bioenergetics to data-poor species, increasing our ability to estimate and predict fish consumption and growth in a variety of fundamental and applied contexts, including under climate change.

Seasonal Residency and Overwintering Behaviour of Striped Bass Morone saxitilis in The Annapolis River, Nova Scotia

Keeler J. Colton[1], Samuel N. Andrews[1], Levi Cliché[2], Micheal J.W. Stokesbury[1], Trevor S. Avery[3]

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Striped Bass (*Morone saxitilis)* was considered extirpated from the Annapolis River (COSEWIC, 2011); however, individuals from other spawning populations occur and are seasonally resident. Striped Bass in the northern extent of its range migrate to overwintering habitats where they aggregate, assume a state of torpor, and remain until water temperatures warm the following spring. In the Bay of Fundy, Striped Bass may spend nearly half of their lives in aggregated dormancy, making them vulnerable to anthropogenic changes in their environment and interactions with fisheries. Therefore, understanding the overwintering behaviour of Striped Bass is critical to their conservation and management. To examine the seasonal residency and overwintering behaviour of Striped Bass in the Annapolis River, 23 Striped Bass ranging 55.0–72.5 cm TL were caught by angling and surgically implanted with acoustic transmitters. Ten of these fish were tagged prior to the winter of 2022-2023 and have provided data on overwintering. Movements of these fish were monitored by a receiver array in the Annapolis River and Annapolis Basin in 2022 and 2023. Acoustic tracking, seasonal sampling, and measurements of water temperature were used to characterize winter thermal refugia and habitat use, seasonal movement, and annual residency. Five fish demonstrated year-round residency, and an additional 3 fish remained distributed in the river over winter. Winter habitat included a strong halocline. We highlight

previously undescribed overwintering aggregations of Striped Bass in the Annapolis River and year-round residency of sexually mature individuals.

Development of a high-thoroughput SNP panel for individual identification and mixed stock analysis of Striped Bass

Nathalie LeBlanc
University of New Brunswick

The Striped Bass (Morone saxatilis) is an anadromous fish that experienced population crashes and then recoveries throughout its range from the 1960s to present-day. While many fisheries have re-opened since the crash, ongoing monitoring is required to ensure numbers remain stable in the long-term. Central to this is the need to determine the extent to which major spawning locations contribute to coastal stocks. With next-generation sequencing, researchers have been able to successfully discriminate among closely related regions along the Striped Bass native range, allowing for assignment of unknown individuals back to spawning region and mixed stock estimates from genetic data. However, cost per sample of the next-generation methods used is too high to be useful in large-scale or long-term projects moving forward. In this presentation I describe the development, optimization, and evaluation of a GT-Seq panel: a small panel of highly informative single nucleotide polymorphism (SNP) loci able to assign large numbers of Striped Bass back to six genetically distinct regions across the Striped Bass migratory range at lower cost than traditional NGS methods. The final panel of 236 loci was able to assign 95% of reference individuals back to region of origin, and had <5% error across all simulations when estimating mixing proportion of a stock. To date, this panel is being used in ongoing characterizations of Striped Bass along the Massachusetts coast and the eastern coast of Nova Scotia. As researchers try to better track migration of Striped Bass throughout their native range, this panel provides a low-cost method of genetically characterizing stocks at specific locations and times that can be easily modified as new genetic data is discovered.

The Role of Atlantic Salmon (*Salmo salar*) in Ecological Restoration: Insights from Five Atlantic Canadian National Parks

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Historically, rivers in Atlantic Canada have experienced nutrient limitation. Atlantic salmon (*Salmo salar*) are important vectors of marine-derived nutrients (MDNs) to rivers leading to increased freshwater productivity. With salmon populations in decline, the magnitude of freshwater productivity change is unknown due to a lack of data characterizing the current state of riverine ecosystem function. Across five Canadian National Parks, this study explores how freshwater ecosystem productivity and function vary along a gradient of MDN inputs from ongoing Atlantic salmon restoration initiatives. We evaluate the influence of salmon restoration on riverine primary production through biofilm community response and use stable isotope analysis of Carbon ($\delta^{13}C$) and Nitrogen ($\delta^{15}N$) to characterize MDN uptake in community trophic structure. Early results illustrate that when spawning Atlantic salmon are present in biologically relevant numbers, there is a marked increase in primary production, and in MDN uptake into freshwater food webs. These trends can be seen both across parks and sampling periods. With a robust assessment of the impact salmon and their MDN subsidies can have on ecosystem function, we can more accurately measure and adaptively manage ecological restoration initiatives.

The Decline and Impending Collapse of the Atlantic Salmon Population in the North Atlantic Ocean

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Adult returns to many Atlantic salmon wild and hatchery stocks of the North Atlantic have declined or collapsed since 1985. Enhancement and angling restrictions in North America and Europe and commercial fishery closures on both continents and at sea after 1984 have failed to halt the decline. Human impacts such as dams, pollution or overexploitation were responsible for some stock declines in the past, but adult returns to river and hatchery stocks with no obvious local impacts have also declined or collapsed since 1985. The decline and collapse of stocks has common characteristics: 1) cyclic annual adult returns cease, 2) annual adult returns flatline, 3) adult mean size declines, and 4) stock collapses occurred progressively from south to north on both continents. Cyclic annual adult returns were common to all North Atlantic stocks in the past that were not impacted by anthropogenic changes to their natal streams. A flatline of adult abundance and reduction in adult mean size are common characteristics of many overexploited fish stocks and suggest illegal, unreported, and unregulated (IUU) fisheries exploitation at sea. By-catch of post-smolts and adults in paired-trawl fisheries off Europe and intercept adult fisheries off Greenland, in the Gulf of St. Lawrence, and off Europe remain sources of marine mortality but seem unlikely to be the primary cause of the decline. Distribution in time and space of former, legal high-sea fisheries indicated fishers were well acquainted with the ocean migratory pattern of Atlantic salmon and combined with lack of surveillance since 1984 outside Exclusive Economic Zones or in remote northern regions suggests high at-sea mortality occurs because of IUU fisheries. The problem of IUU ocean fisheries is an acute worldwide problem and has collapsed numerous stocks of desired species (whales, tuna, sharks, etc.), and is probably linked to the decline and impending collapse of the North Atlantic salmon population.

An Assessment of Inner Bay of Fundy Atlantic Salmon (*Salmo salar*) Spawning Success in Fundy National Park

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Atlantic salmon (*Salmo salar*) have declined precipitously throughout most of their North American range. As a result, many strategies have been implemented to try and restore Atlantic salmon populations. One such restoration strategy, implemented by the Fundy Salmon Recovery project, involves the collection of endangered inner Bay of Fundy salmon smolts from their natal rivers to be reared at the world's first marine conservation farm to maturity. This strategy includes both an open net ocean pen and freshwater hatchery components. Upon maturity, these salmon are returned to their natal rivers as adults. This release may be done by hand, by carrying the sexually mature salmon to the water, or by carefully lowering them into pools using a helicopter, so they can naturally spawn. In our study, we aim to determine whether these differences in rearing and release strategies led to significant changes in offspring production from adult salmon in two Fundy National Park rivers. Single nucleotide polymorphisms (SNPs) at 185 loci were used to match parents with the next year's offspring using Colony, a parentage analysis software. Using a fixed effects linear model, we found that there was no significant effect on offspring production caused by release strategy in both rivers. On the Point Wolfe River, rearing strategy was found to have a significant effect on offspring production – with marine-reared adults producing 4 times more juveniles than their freshwater reared adult counterparts. An effective population size of 65.2 was assessed when including all adults spawning in Fundy National Park, and 57.1 when only considering adults in the traditional freshwater rearing program. These results suggest that the marine-rearing strategy, implemented by the Fundy Salmon Recovery project can outperform the traditional freshwater rearing strategy in terms of releasing high-fitness adult Atlantic salmon.

"All Hands in the Tank": Analyzing the social networks of captive rearing and stocking programs for Atlantic salmon conservation in Nova Scotia, Canada

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In the Canadian Maritime region, limited information exists on the social and human dimensions (i.e., values, perspectives, and experiences) of captive rearing and stocking and the contested use of these tools for conservation purposes. We present a qualitative study on Atlantic salmon conservation through captive rearing and stocking programs in Nova Scotia, Canada. The study aims to explore the knowledge gaps within the human dimensions of cultivation-based Atlantic salmon conservation and understand the social structures that support it. In this study, we conducted 20 interviews across two case studies centered around salmonid hatcheries and stocking programs in Nova Scotia, Canada. Study participants included people involved in Atlantic salmon conservation, captive rearing and stocking programs (i.e., hatchery managers, volunteers, anglers, etc.), and individuals and groups critical of using hatchery and stocking programs for conservation. Through ongoing analysis, our preliminary findings indicate that Atlantic salmon conservation via captive rearing and stocking programs requires the functional support of individuals and groups achieved through complex relationships and social networks. Moreover, study participants viewed these programs as important, if not well-defined, components of Atlantic salmon conservation in climate-driven ecological uncertainty. This work is anticipated to contribute to socio-ecological considerations of Atlantic salmon management-via-cultivation in the region.

Stable isotope and lipid assessment of Atlantic salmon (*Salmo salar*) smolts across regional populations in Eastern Canada

Erin McCavour
University of New Brunswick

Atlantic salmon are a significant species environmentally, economically, and culturally in many Indigenous communities, used as a diet staple and symbolic species in social and cultural ceremonies. They play a vital role environmentally by connecting freshwater and marine ecosystems through facilitating nutrient transport and trophic interactions. However, Atlantic salmon are a species at risk listed as endangered, threatened, or of special concern in multiple populations across Eastern Canada. Exploring the energy source and food web of Atlantic salmon can provide information about how they are gaining their nutrients and the overall function of the ecosystem. This project will examine the stable isotope composition of Atlantic salmon smolts collected from various rivers throughout Eastern Canada. Isotopic data will include carbon ($\delta^{13}C$), nitrogen ($\delta^{15}N$), and C:N ratios from archived data (2000- 2019) and new (2021-2023) smolt samples collected from smolt wheel mortalities. The stable isotope data will be used to examine regional differences among Atlantic salmon populations and changes over time. The aim is to see if isotopic differences among smolts can be related to the state of their population and are due to a population-wide genetic component or the productivity of their freshwater habitats. In addition, condition measurements such as length, weight, and lipid content will be assessed to examine differences in the physiology, diet, and freshwater-rearing habitats among Atlantic salmon. The purpose of this study is to determine differences in the trophic ecology of Atlantic salmon smolt populations to give us insight into their environments and their pre-oceanic state, which will help implement future protection and management protocols.

Impact of Restoration on Smolt Age Class Distribution and Growth Rates in a recovering Atlantic Salmon (Salmo salar) Population

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The inner Bay of Fundy (iBoF) Atlantic salmon are a genetically distinct population of Atlantic salmon residing within the Bay of Fundy and northern Gulf of Maine, listed as endangered under the Species at Risk Act. Located in Fundy National Park (FNP), the Upper Salmon River is listed as critical habitat for iBoF salmon and has been the site of several restoration strategies: primarily, release of salmon though traditional (juvenile) and Fundy Salmon Recovery (FSR) models (natural spawning from adult releases). Age at smoltification and annual growth rates are two metrics that are commonly used to assess the iBoF and many other salmon populations. This study aims to evaluate the efficacy of adult releases to maintain a wild-like population, via interpretation of archived smolt scales. Aided by a novel scale-analysis script, we evaluated scales from 4850 individuals sampled between 2002-2022 to assess age distributions of smolt cohorts and annual juvenile growth rates. We observed a shift towards smolt cohorts with more 2+ and 3+ smolts following implementation of FSR release strategies and promotion of natural spawning. So far, we have seen a threefold increase in growth rate variance, and increased instances of high growth outliers following implementation of FSR release strategies and promotion of natural spawning. The results of this study provide insight into the impact of this restoration strategy on annual smolt cohorts, which are a key aspect of maintaining a wild population.

Linking the environment with environmental DNA: modelling environmental dynamics alongside quantitative eDNA data for the enumeration of Atlantic salmon (*Salmo salar*)

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Inferring the abundance of organisms using environmental DNA (eDNA) is a major goal, and challenge, of eDNA research. Across freshwater fish, studies have demonstrated positive relationships between quantitative eDNA signals in collected water samples and fish abundance, yet there is often substantial noise in these relationships that make them difficult to interpret. In natural systems, it's hypothesized this noise is in part attributed to environmental factors influencing the input and output of eDNA in an ecosystem over space and time. Modelling these environmental dynamics alongside quantitative eDNA data could therefore drastically improve our inferences of abundance with eDNA. Expanding upon a prior eDNA investigation, our study is taking advantage of a multi-year (2020-2023) eDNA sampling design centered around juvenile Atlantic salmon (Salmo salar) in two rivers in Fundy National Park, New Brunswick. Our objectives are: 1) to model the influence of environmental variables on quantitative eDNA data during the summer as salmon abundance remains relatively constant; 2) to model how the inclusion of environmental dynamics alongside quantitative eDNA data could strengthen inferences of salmon abundance during their spring seaward migration; and 3) evaluate the spatial and temporal transferability of these models. Summer eDNA samples and environmental covariates were collected once per week over 8-9 weeks in one (2020) or both (2022) rivers, while spring eDNA samples and environmental covariates were collected twice per week over 6-8 weeks in one (2021-2022) or both (2023) rivers around a rotary screw trap that captured and quantified seaward migrating smolts. Our initial results suggest a clear importance of modelling environmental dynamics alongside quantitative eDNA data as it relates to salmon abundance. We expect our findings to provide an important step toward quantitative applications of eDNA for the enumeration of Atlantic salmon.

FISHERIES MANAGEMENT Special Session

Keeping it Real
Kathryn Collet, DNRED/MRNDE

Maine's wild Brook Trout: Building a conservation strategy and fostering resiliency for an iconic native coldwater fish species

Merry Gallagher, Native Fish Conservation Biologist
Maine Department of Inland Fisheries & Wildlife

Maine's extensive and robust wild Brook Trout (Salvelinus fontinalis) population is world renowned however known stressors for this species and other coldwater fishes are immediate and profound. Like anywhere else, Maine is facing statewide land use and climate shifts that cause concern for the future conservation of this iconic species. Subsequent to recent large-scale planning efforts resulting in Maine's Wildlife Action Plan and a recently updated Strategic Fisheries Management Plan, it is clear that the people of Maine place a very high regard on the sustainable management of our iconic Brook Trout resources considerate of the growing stressors caused by changes in land use and climate to further species resiliency in these uncertain times. Hence, statewide conservation efforts are expanding into fields and venues not previously considered or routinely used as areas for enhancing wild Brook Trout habitat priorities and needs. In addition to sustainably managing Maine's wild Brook Trout sport fisheries, MDIFW's Fisheries Division has initiated a focused effort towards fostering and enhancing Maine's wild Brook Trout conservation and habitat needs through invasive species programs and mitigation, land protection strategies and efforts, riparian stewardship and management, environmental research and monitoring, technical assistance on habitat improvement and stream connectivity enhancement projects, and a diversity of partner-driven prioritization efforts across the board to build awareness and a sense of shared stewardship for a fishery resource of statewide significance.

Uncertainties Related to Minnow Trap Bycatch in Vermont

Jud Kratzer and **Levi Brown**
Vermont Fish and Wildlife Department

The use of live fish as bait is a long-standing tradition for many Vermont anglers. According to the 2020 statewide angler survey, just over 50% of respondents used baitfish, and of the anglers that used baitfish, 41% did at least some of their own baitfish harvest (Responsive Management 2020). Personal baitfish harvest provides an economical, locally sourced option that some anglers consider part of the larger angling experience. These benefits are why Vermont allows personal baitfish harvest, despite the inherent risk of capturing non-target fish species as bycatch, the main driver of Vermont's more long-standing baitfish regulations. By design, Vermont's baitfish regulations restrict anglers' harvest of bait, though the portion of these regulations that are intended to reduce bycatch of game species has never been evaluated for efficacy or need. The purpose of this study is to evaluate different minnow traps and determine if trap size and season restrictions are necessary to protect salmonids and other game species from capture and mortality by minnow traps. To begin determining this, we fished minnow traps in 14 northeastern Vermont waterbodies from 23 May to 11 July in 2023, using different opening sizes (1" vs. 2.25") and overall trap lengths (17.5" vs. 31"). Sample sites were categorized into coolwater streams, coldwater streams, and warmwater ponds to evaluate bycatch of coldwater (i.e., salmonids) and warmwater species (e.g., Centrarchids, Percids). Preliminary results suggest that larger trap opening size nor overall length incur more bycatch relative to standard trap sizes legal to use in Vermont. This project will continue in November 2023 as well as in another VT Fisheries District in 2024. If these regulations are not necessary, they can be changed to provide more and better opportunities for anglers to harvest their own baitfish with little additional risk to non-target fish species.

Fisheries Management in New Hampshire

John Magee
New Hampshire Fish & Game Department

Fishing for Likes: Why social media is a double-edged sword for fisheries managers

Rosanne MacFarlane
PEI Department of Environment, Energy and Climate Action
Forests, Fish and Wildlife Division

POSTER PRESENTATIONS

Marijune Tiamzon	Gut it out: Using metabarcoding to reveal the diet of larval American lobsters (*Homarus americanus*) in Southwest Bay of Fundy	UNB
Gabriel Cassoni	Validating a Method to Predict Hatch Time of American Lobster (*Homarus americanus)* In Southwest Bay of Fundy	UNB
Laken Devost	I'm Still Standing: Investigating Success of Conserving Genetic Diversity among Atlantic Salmon (*Salmo salar*) Using Marine Conservation Strategies	UNB
Mia Francis	Effects of experimental nutrient enrichment on intertidal soft sediment chemistry and infaunal invertebrates	UNB
Benjamin Gowell	Investigating linkages between otolith chemistry and warming in the Gulf of Maine	UNE
Clayton Nyiri	Assessing the efficiency of microprocessor-based bycatch reduction devices (MB-BRDs) for the Atlantic spiny dogfish (*Squalus acanthias*) in a recreational fishery	UNE
Emma Christopher	Exploring stable isotope analysis of Atlantic bluefin tuna, *Thunnus thynnus*, eye lenses to determine life history shifts	UNE
Cameron Solda	Riverine and coastal minimum survival estimates for Gaspereau River Inner Bay of Fundy Atlantic Salmon (*Salmo Salar*) Smolts.	Acadia University
Rachel Pomerleau	Quantifying Total Mercury in Bay of Fundy Striped Bass	Acadia University
Hunter Hogan	Gonadosomatic Index and Fecundity in Atlantic Tomcod	Acadia University