

**2018 LARGE-SCALE APPLIED RESEARCH PROJECT COMPETITION:
GENOMICS SOLUTIONS FOR AGRICULTURE, AGRI-FOOD, FISHERIES AND AQUACULTURE
APPLICATION FORM**

Application Number: 16502

Project Title: FISHES: Fostering Indigenous Small-scale fisheries for Health, Economy, and food Security

Term of Funding (years): 4 YEARS

Total Budget Request: \$14,415,405

Amount Requested from Genome Canada (up to \$4 million): 4,000,000

Amount Requested from Agriculture and Agri-Food Canada, if applicable (up to \$3 million):

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Date	19 mars 2019
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* Please indicate with an (*) which Project Leader will assume the overall administrative and financial responsibility for the Genome Canada funds provided in support of the project.

¹ Signatures confirm acceptance of terms as outlined in the Meaning of Signatures

Lead Organization (CEO, President or authorized representative)

Name of organization	Université Laval Madame Eugénie Brouillet Vice-rectrice à la recherche, à la création et à l'innovation
Name of representative	
Title	
Date	
Signature¹	

Genome Centre CEO(s) or authorized representative(s)

Administrative Centre ²	Genome Quebec	Co-lead Centre (if applicable)	Ontario Genomics
Name	Daniel Coderre	Name	Bettina Hamelin
Date		Date	
Signature ¹		Signature ¹	
Additional Centre (if applicable)			
Name			
Date			
Signature ¹			

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² Administrative Centre for projects which have been identified as being co-led by two or more Genome Centres

RESEARCH AREAS AND KEYWORDS

Select the area(s) that relate(s) to the research proposed. If relevant to more than one area, use numbers to indicate the relative weighting (i.e., 1 = primary focus; 2 = secondary focus, etc.; **do not use the same number more than once**)

<input type="text"/>	Agriculture	<input type="text"/>	Energy	<input type="text" value="3"/>	Environment
<input type="text" value="1"/>	Fisheries/Aquaculture	<input type="text"/>	Forestry	<input type="text" value="2"/>	GE ³ LS
<input type="text"/>	Human Health	<input type="text"/>	Mining	<input type="text" value="4"/>	Technology Development

Provide a **maximum** of five (5) words or phrases for each category that describe the proposed investigation.

CATEGORY	KEYWORDS
Research	Northern Indigenous communities; commercial, recreational and subsistence (CRS) fisheries; definition of conservation units (CUs); bio-indicators for sustainability; enhancing effectiveness of resource management/stewardship
Methods & Technologies	Whole genome (re)sequencing; SNP discovery, annotation and high/low throughput genotyping; population genomics, mixed stock fisheries management; genome wide association studies (GWAS)

Provide a **maximum** of five (5) words or phrases for each category that describe the proposed integrated GE³LS investigation.

CATEGORY	KEYWORDS
Research questions	Traditional knowledge systems; subsistence and small-scale fisheries; food security/sovereignty and social well-being; cultural resilience and adaptation to change; socio-ecological systems
Methods	Co-evolution of knowledge through interviews, surveys and focus groups; participatory mapping and visualization; statistical modeling of food security impacts; and assessment of potential social and economic impacts

Sharing of application and reviews

Where applicable, Genome Canada seeks your consent to share the information included in your application and application reviews, on a confidential basis, with the funding partners referenced in the RFA.

I, the Project Leader **consent** to the sharing of the application and reviews with the organizations indicated above.

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I, the Project Leader **do not consent** to the sharing of the application and reviews with the organizations indicated above.

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I RESEARCH TEAM

Please provide in the table below, a list of the research team members (excluding collaborators), their affiliation, role in the project, time commitment to the proposal research and their responsibilities in the context of the project:

Name, Title and Affiliation	Role ³	Time Commitment (hrs/week)	Description of Responsibilities	Signature ⁴
Dr. Louis Bernatchez, Professor, Department of Biology, Université Laval	Project Leader	15 hrs/week	Project Leader, Team Leader for Act.1 and 4 and Team member for Act 2&3. Canada Research Chair (CRC) in Genomics and Conservation of Aquatic resources, population and conservation genomics	
Dr. Jean-Sébastien Moore, Adjunct Professor, Department of Biology, Université Laval	Project Leader	15 hrs/week	Project Leader, Team Leader for Act.2 and Team member for Act 1, 3, 4 &5. Evolutionary ecology of Northern aquatic resource	
Dr. Dylan Fraser, Associate Professor, Department of Biology, Concordia University	Project Leader	15 hrs/week	Project Leader, Team Leader for Act.3 and Team member for Act 1, 2, 4 &5. University Research Chair in Population Biodiversity and Conservation, Northern fisheries, genomics in conservation biology	
Dr. Stephan Schott, Associate Professor, School of Public Policy and Administration, Carleton University	Project Leader	15 hrs/week	Project Leader, Team Leader for Act.5 and Team member for Act. 2&3. Sustainable development in Arctic, food security, integration of traditional knowledge and science	

³ Role includes: Project Leader, Co-Investigator, Collaborator and User.

⁴ **Signatures of the Co-Investigators and Users are required** and confirm that the application has been reviewed and approved for submission to the Genome Centre and Genome Canada by all investigators. **Signatures of collaborators are not required.**

Dr. Monica Mulrennan, Associate Professor, Department of Geography, Planning and Environment, Concordia University	Co-investigator	7 hrs/week	Social science researcher, community-based conservation in Cree communities, Team member for Act. 3&5	
Dr. Mélanie Lemire, Assistant Professor, Département de médecine sociale et préventive, Université Laval	Co-investigator	7 hrs/week	Social/health science researcher, community-based conservation in Inuit communities, Nasivvik Research Chair in Ecosystem Approaches to Northern Health, Team member for Act. 5	
Dr. Kenny Tiff-Annie, Post-Doctoral Fellow, Corcordia University	Co-investigator	35 hrs/week	Social science researcher, fisheries science, climate change, local knowledge, Team member for Act. 5	
Dr. Louise Chavarie Biodiversity Research Centre and Zoology Department, University of British Colombia	Co-investigator	35 hrs/week	Fishery Biologist researcher in the Western Arctic region. Member for Act. 2&3. for work on Great Bear and Great Slave Lakes.	
Dr. Les Harris, Arctic Fisheries Research Biologist, Fisheries and Oceans Canada, Winnipeg	Co-investigator End-user	10 hrs/week	Arctic research biologist DFO Project liaison with DFO, Central and Arctic Region, Team member for Act. 2&3. for work on Arctic char.	
Dr. Xinhua Zhu, Research Scientist, Arctic Aquatic Research Division, Fisheries and Oceans Canada, Winnipeg	Co-investigator End-user	10 hrs/week	Arctic aquatic, Team member for Act. 2&3 for work on Great Slave Lake. Liaison with Indigenous communities from GSL.	

Dr. Kimberly Howland, Research Scientist, Central & Arctic Region, Fisheries and Oceans Canada, Winnipeg	Co-investigator, End-User	5 hrs/week	Arctic aquatic, Project liaison with DFO, Central and Arctic Region. Liaison with Indigenous communities of Great Bear L. Team member for Act. 2.	
Dr. Ross Tallman, Research Scientist, Division of Arctic Research, Fisheries and Oceans Canada, Ottawa	Co-investigator, End-User	5 hrs/week	Arctic aquatic, Project liaison with DFO, Central and Arctic Region. Team member for Act. 2&3 for work on Arctic char.	
Nadia Saganash, Wildlife Management Administrator, Cree Nation Government	Co-investigator End-user	5 hrs/week	Team member for Act. 2, Collaborator with Cree Nation Government, Coordinate actions in Eeyou Istchee	
Lilian Tran, Fisheries Biologist, Makivik Corporation	Co-investigator End-user	5 hrs/week	Team member for Act. 3, Liaison with Inuit communities from Nunavik.	
Janelle Kennedy, Director, Fisheries & Sealing Division, Department of Environment, Government of Nunavut	Co-investigator End-user	5 hrs/week	Team member for Act. 2&3, Coordinate actions in Nunavut	
Dr. Julien April, Biologist, Ministère Forêts, Faune et Parcs, Québec	Co-investigator End-user	5 hrs/week	Team member for Act. 2&3 Coordinate collaboration of Arctic Char and Atlantic salmon research in Nunavik	
Marc Dunn, Director of Environment, Niskamoon Corporation	Collaborator End-user	2 hrs/week	Coordinate actions with Cree communities for both inland and coastal regions	
Angela Coxon, Wildlife Management Director, Eeyou Marine Region	Collaborator End-user	2 hrs/week	Coordinate collaboration and sampling with Cree communities along James-Hudson Bay coast	

Wildlife Board				
Dr. Julien Mainguy, Biologist, Ministère Forêts, Faune et Parcs, Québec	Collaborator	2 hrs/week	Coordinate collaboration of Arctic Char and Atlantic salmon research in Nunavik	
Laurie Beaupré, Biologist, Ministère Forêts, Faune et Parcs, Québec	Collaborator	2 hrs/week	Coordinate collaboration of Arctic Char and Atlantic salmon research in Nunavik	
Dr. Fraser Taylor, Chancellor's Distinguished Research Professor of International Affairs, Geography and Environmental Studies, Director of the Geomatics and Cartographic Research Centre, Carleton University, Ottawa	Collaborator	3 hrs/week	Collaborator on research activities associated to GE3LS component	
Dr. Marie-Jo Ouimet, Public Health Physician, Public Health Department of the James Bay Cree Territory, Montreal	Collaborator End-user	2 hrs/week	Collaborator on research activities associated with GE3LS component	
Clark Shecapio, Cree Trappers Association, Waswanipi	Collaborator End-user	2 hrs/week	Coordinate collaboration and sampling with the Cree communities from inland and coastal regions	
Pamela MacLeod, Cree Nation of Mistissini	Collaborator End-user	2 hrs/week	Coordinate collaboration and sampling with the Cree for work on L. Mistassini, Albanel, Waconichi	
Steven Blacksmith, Cree Nation of	Collaborator End-user	2 hrs/week	Coordinate collaboration and sampling with the Cree	

Waswanipi			community of Waswanipi for work on L. Waswanipi	
Philippe Poulin, Manager of the Napukkaaliurvik Kuujjuaq Fish Hatchery, Nayumivik Landholding Corporation	Collaborator End-user	2 hrs/week	Provide Nunavik sampling support for work on Arctic char hatchery	
Quentin Steinwand AAROM Coordinator NWT Metis nation	Collaborator End-user	2 hrs/week	Coordinate collaboration and sampling with communities of Slave Lake	
Deborah Simmons, Executive Director, Sahtu Renewable Resources Board	Collaborator End-user	2 hrs/week	Coordinate collaboration and sampling with communities of Great Bear Lake	
George Low, DehCho First Nation Coordinator	Collaborator End-user	2 hrs/week	Collaboration for sampling on Great Slave Lake	
Kathleen Fordy, Coordinator Deninu Kue First Nation (DKFN)	Collaborator End-user	2 hrs/week	Collaboration for sampling on Great Slave Lake	
Edwards Reeves, Manager, Deline Renewable Resource Council	Collaborator End-user	2 hrs/week	Collaboration for sampling on Great Bear Lake	
Ioannis Ragoussis, Responsible for the Genomic Platform Development, MUGQIC Genome Canada Genome Innovation Node, McGill University, Montreal	Collaborator	1 hrs/week	Collaboration for performing Hi-C for the superscaffolding of the Brook Trout genome.	

Mark O'Connor Resource Management Coordinator, Department of Environment, Wildlife and Research, Makivik Corporation	Co- investigator End-user	5 hrs/week	Team member for Act. 5, Liaison with Inuit communities from Nunavik.	
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II PARTICIPATING ORGANIZATIONS' SIGNATURES

To be completed by the organizations in which the research will be undertaken.

The following organizations have reviewed and approved this application and agree to respect the general principles guiding the use of Genome Canada funds, specific guidelines on eligible costs and co-funding, and the specific conditions associated with the release of Genome Canada funds, as outlined in the [Request for Applications for the 2018 Large-Scale Applied Research Project Competition: Genomics Solutions for Agriculture, Agri-food, Fisheries and Aquaculture](#), and Genome Canada's [Guidelines for Funding](#), including adherence to commonly accepted guidelines with respect to ethical, environmental and safety requirements.

In addition, the following organizations agree to respect applicable policy and program guidelines of other funding agencies, which are identified as sources of co-funding in this application.

Organization	Name & Title of Authorized Representative	Signature	Date dd/mm/yy
Université Laval	Eugénie Brouillet, Vice President, Research and Innovation		
Concordia University	Justin Powlowski, Associate Vice-President, Strategy and Operations		
Carleton University	Rafik Goubran Vice-President Research and International		
Fisheries and Oceans Canada (DFO)	Dr. Sen Wang, Regional Director, Science, Central and Arctic Region		
Ministère des Forêts, de la Faune et des Parcs	René Desaulniers, ing., Directeur général		
Government of Nunavut, Department of Environment, Fisheries and Sealing Division	Janelle Kennedy, Director, Fisheries and Sealing Division, Government of Nunavut		
Cree Nation Government	Isaac Voyageur (Director of Environment and Remedial Works Department)		
Makivik Corporation	Gregor Gilbert, Director, Department of Environment, Wildlife and Research		

III LAY SUMMARY

In a maximum of **one-half (1/2) page**, describe the proposed research in a way that can be understood by a lay audience. Be sure to indicate how the proposed research will result in social and/or economic benefits. This summary may be used by Genome Canada to inform the public and other stakeholders about the value of genomics research

Food insecurity is a debilitating problem in Northern Canada: compared to the national average, it is twice as high in off-reserve Subsistence households and four times higher in Nunavut. Moreover, increased shipping, tourism, and mining exploration and development pose serious risks for northern aquatic biodiversity and the fisheries it supports. Climate-induced changes in the geographic distribution and abundance of fish threaten the economic livelihoods of northern communities, their traditional harvesting practices as well as their ability to feed themselves and maintain access to healthy food. Consequently, reducing the potentially negative impacts of these threats on northern fisheries is crucial for communities who are tied to fish for their food security and culture. For these fisheries, the identification of regions important for subsistence and commercial harvesting and whether they comprise genetically distinct groups of populations is a key step towards a sustainable harvest. The project **FISHES (Fostering Indigenous Small-scale fisheries for Health, Economy, and Food Security)** will develop and apply genomic approaches in concert with Traditional Ecological Knowledge (TEK) to address critical challenges and opportunities related to food security and Commercial, Recreational, and Subsistence (CRS) fisheries of northern Indigenous Peoples in Canada (Inuit, Cree and Dené communities). We will develop genomic resources for six species important to northern communities and use these resources to identify genetically distinct populations, assess their vulnerability to future climatic conditions, quantify their contributions to mixed-population harvests, and measure the contribution of fish from developing hatchery programs to subsistence harvests. Using a novel knowledge co-evolution framework, we will braid and bridge scientific information with TEK in support of sustainable harvests of CRS fisheries. FISHES will support the co-generation of knowledge to foster the development and co-management of sustainable fisheries, increased food security, and enhanced social well-being and cultural continuity. FISHES will also contribute to our ability to forecast the response of key fisheries to rapid global and socio-economic changes in northern Indigenous communities.

IV RESEARCH SUMMARY

In a maximum of one (1) page, summarize the proposed research, including integrated GE³LS research activities. Describe the deliverables expected at the end of the project and the social and/or economic benefits anticipated from their practical application.

Overarching goal: To develop and apply genomic approaches in concert with Traditional Ecological Knowledge (TEK) to address critical challenges and opportunities related to food security and Commercial, Recreational, and Subsistence (CRS) fisheries of northern Indigenous Peoples in Canada.

Challenges: Northern fisheries are facing major changes and reducing the negative impacts is crucial for communities tied to the fisheries for their food security and culture (Brander 2010; Islam & Berkes 2016). Improved management practices supported by knowledge co-evolution are urgently needed in the context of a shift across these fisheries, often involving users with competing interests who may place different cultural and socio-economic values on the resource. The identification of regions important for subsistence, commercial and recreational harvesting and whether they comprise genetically distinct groups of populations is a key requirement for adaptive co-management of harvest.

Solutions: Our exceptional team is comprised of researchers, Indigenous and government collaborators who have worked together and combine all the expertise for implementing a novel knowledge co-evolution framework at the interface of genomics, fisheries management and TEK. We will develop genomic resources for six species important to CRS fisheries to; define genetically distinct populations, quantify their contributions to mixed-stock harvests and contributions of hatchery programs to subsistence harvests, assess the impact of overharvesting, and predict the genomic vulnerability of exploited species to climate change. We will bring scientific information into dialogue with TEK towards sustainable harvests of CRS fisheries. Building on our established research partnerships with communities, we will: i) create/sustain appropriate engagement, knowledge exchange and co-learning processes; ii) map food sharing networks to identify the importance of focal species for food security and supplementary income source; iii) use visual map tools and online interactive atlases to share observations (relationships between genetically distinct populations, community preferences and commercial quota and test fishery potential); and iv) merge project data to existing data on fish harvest, stock assessment, diet and population demographics to model links between fisheries, ecological factors, different dimensions of food security, and biodiversity conservation over time.

Deliverables: **D1)** Genomic resources and assays to inform CRS species management for food security and economic development in northern communities; **D2 & D3** : A series of reports and guides for end-users and stakeholders describing how definition of genetically distinct populations (**D2**), and how knowledge of mixed-stock harvests, hatchery supplementation, and quantitative data collected by Indigenous partners (**D3**) can provide guidance on management practices to ensure long-term sustainability of harvests in CRS fisheries; **D4)** A first assessment of genomic vulnerability underlining future climate adaptation, contributing to our ability to forecast the response of key fisheries to rapid global changes in northern Indigenous communities; **D5 (GE3LS):** A forum for the exchange and co-generation of knowledge on CRA fisheries development and co-management, informed by a shared understanding for different contexts, values, and priorities; **D6 (GE3LS):** Implementation strategies of collectively derived objectives and future vision (development of a fisheries policy and its implementation, strategy to enhance the use of fish in certain regions as a food source).

Socio-Economic Benefits (SEB): Socio-economic benefits: 1) Food security/social well-being - Through partnered research, we will co-produce evidence to foster sustainable fisheries, food security, and social well-being; 2) Socio-economic development - We will support the development of sustainable fisheries in Canada's North; 3) Environmental protection - For key CRS species, we will provide the first multi-species pan-Northern assessment of genomic variation underlining climate adaptation in fish, thus contributing to our ability to forecast the response of key fisheries to rapid global and socio-economic changes in northern Indigenous communities, including risks related to increased shipping, tourism, and resource extraction in Canada's North.

V RESPONSE TO PRE-APPLICATION REVIEW

In a **maximum of two (2) pages**, provide responses to the reviewer comments and recommendations provided to you in your Pre-Application Summary of Review.

If these were addressed in your Full Application, please indicate specifically where in the application changes were made. If you disagreed with the reviewers' comments, please explain your point of view.

Weakness 1: *You need to demonstrate the value of genomic research and what it can deliver in direct impact.* **Response 1:** We have emphasized with more details the value of genomic research in Activities 2-4 and the SEB section. In particular, under activities associated with mixed-stock harvests on a variety of the project's focal fish species (Activity 3, p 28-30), we have further emphasized the significance of genomics (cost-effective GBS genotyping) for more accurately quantifying the contributions of different populations to local fisheries harvests. We expect that by providing new information on spatial distribution of different populations and their contribution to CRS fisheries, genetic stock identification (GSI) activities will directly affect quantitative fisheries assessments in the north where data are currently limited, and provide essential information on how to retain sustainable fisheries.

Weakness 2: *There is no strong evidence indicating an appropriately explicit inclusion of quantitative stock assessment, and estimation of key fisheries parameters.* **Response 2:** Unfortunately, northern fisheries are in what are considered data poor situations which limits the use of quantitative stock assessment models. However, we explain in Activity 2 (p.26-27) and Activity 3 (p.28-30) that for each fishery based on one or multiple species of local interest, the applicable FISHERS Indigenous partners or governmental agency (Department of Fisheries and Oceans (DFO) and Ministère des Forêts, de la Faune et des Parcs (MFFP)) will collect information pertaining to basic quantitative stock assessment and fisheries parameters: catch data including number of fish caught/species, size distribution, dates of capture, locations of capture, catch per unit effort, gear type, and otoliths for age validation.

Weakness 3: *The important and challenging part of the co-production process is how the communities TEK aspect will "guide the genomic science objectives for the research process" but there is little or no information on how this will be achieved.* **Response 3:** We are following a knowledge co-evolution process to bring knowledge types together and create new knowledge that is culturally appropriate and empowers knowledge holders. One example of the overlay of TEK and genomic data comes from Activity 3 (p.28) where fisheries parameters described above will be integrated to complementary TEK surveys for each mixed-stock harvest fishery through the GE³LS which will provide information from our Indigenous partners pertaining to longer-term temporal changes to seasonal fish movements and harvest rates. Thus, TEK is instrumental in providing a historical perspective on trends in changes in catch, fish body size etc. for certain spawning populations when considered in tandem with the spatial data on harvest contributions of each population using GSI. For instance, Indigenous partners have informed and determined the specific project goals of FISHERS (e.g. Activity 3.1 for Lake Mistassini Walleye and Brook Trout and Lake Waswanipi Walleye, Whitefish and Brook Trout for coastal James Bay; Activity 3.2 for Arctic Char). Our collective research and knowledge process will provide a foundation for more meaningful and substantial collaboration in the co-management of these species in the future.

Weakness 4: *For a co-production project it seems interesting that DFO members are COIs but none of the First Nation Representatives are COIs.* **Response 4:** We have now included three new co-investigators to represent the three main regions covered in this study, all women: i) Nadia Saganash from the Cree Nation Government; ii) Lilian Tran, from Makivik Corporation, Nunavik; and iii) Janelle Kennedy, Government of Nunavut. Also, to strengthen the interactions with community end-users, each region will have a Regional Advisory Board composed of indigenous members associated with fisheries and food security. The Regional Advisory Boards will be consulted prior to each field season to ensure

the project maintains adherence to the agreed upon project objectives. This will ensure that the knowledge gaps and objectives identified by our Indigenous partners steer the objectives, methods, and outcomes of the project in each region. Finally, all team members have extensive experience working across the regions included in the study.

Weakness 5: *This co-production process needs to be further described as the success of the project is dependent on the validity of the coproduction process.* **Response 5:** In the “Setting the stage” section (p. 16-17), we describe the process in detail and how it is linked to Indigenous partners’ involvement at all stages of the research process in line with our knowledge co-evolution framework. A knowledge-gathering phase will take place prior to sampling, and be used to select which samples are used with respect to any historical samples currently held by government agencies. This will be facilitated by the formation of Regional Advisory Boards described above. As part of the knowledge-gathering phase, the boards will meet to discuss current knowledge, current knowledge gaps, research strategies, capacity building opportunities, desired outcomes and sampling strategies that should be implemented in order to address these objectives. This will include sampling locations and focal species important for the communities. The Regional Advisory Boards will be consulted prior to each field season to ensure the project maintains adherence to the agreed upon project objectives, and as in previous collaborations, we will feed research results back to them.

Weakness 6: *The investigators may wish to consider whether they are being overly ambitious by selecting 7 fish species to evaluate.* **Response 6:** We explain clearly in the Setting the stage section (p. 14) and Activity 2 (p. 25-26) the importance of each species for the different Indigenous communities (Cree, Inuit, Dené) and regions. Not all species are present nor investigated in each region. Quite simply, cutting many species would also mean cutting partners because the identification of species was driven by the specific regional needs of the different Indigenous communities who are partners in this project. However, we agree that our pre-proposal was too ambitious and we have decided to cut one species, the cisco which is globally the least important to our partners out of the 7 species initially targeted. Also, we are now proposing to genotype 20000 fish maximum (instead of 25500, Activity 2&3 combined) which will still be statistically sufficient to reach our goals. We are also proposing that GSI studies for Arctic Char in Nunavut will focus on three specific regions identified as of special interest by our Inuit partners. It is important to note here that the genotyping method we chose (GBS) does not require a long prior step of marker development and that our MFFP and DFO partners already possess about 4000 samples needed for the project such that genotyping will be initiated very soon after the project begins.

Weakness 7: *The project does not have a high risk – high return component that advances the approach of genomics.* **Response 7:** The methods we proposed may not qualify as “novel”, but they are state-of-the-art and their integration with TEK to northern Indigenous fisheries is definitely novel and unique, even possibly worldwide. The new Activity 4 now adds a high risk – high return component that has never been applied in fisheries or any other research context pertaining to food security, therefore being very novel and relevant to FISHERIES. The goal is to investigate which exploited populations might be most vulnerable to future climate change by quantifying the novel metric “genomic vulnerability”. This metric quantifies the mismatch between current and predicted future genomic variation based on genotype-environment relationships modeled across contemporary populations. Moreover, this will be achieved by comparing patterns of genomic variation and quantification of genomic vulnerability based on the analysis of both SNPs variation and Structural Variants (SV) characterized for each individual fish using whole genome re-sequencing (30X coverage). Indeed, while it is becoming increasingly recognized that SV (e.g. inversions, copy number variation, insertion–deletion, sequence repeats) represent a significant source to an individual’s genetic makeup, no project to our knowledge has integrated the analysis of SV in studies pertaining to adaptation to climate change, especially for northern ecosystems.

VI RESEARCH PROPOSAL

Including Research on the Ethical, Environmental, Economic, Legal, and Social Aspects of Genomics (GE³LS)

Maximum thirty (30) pages, including charts, figures and tables (the list of references the list of references can include all types of research outputs and is not included in the page limit). This section must address all relevant evaluation criteria for the competition.

Using a Gantt chart, show project activities, milestones and the timelines for reaching them. Attach the Gantt chart to the end of this section. Please note that the Gantt chart is not included in the page limits above. A Gantt chart template that can be used is attached in Appendix VII.

SETTING THE STAGE

An ambitious goal: The central goal of **FISHES** will be to develop and apply genomic approaches in concert with Traditional Ecological Knowledge (TEK), to address critical challenges and opportunities related to food security and Commercial, Recreational, and Subsistence (CRS) fisheries by northern Indigenous Peoples in Canada (Inuit, Cree and Dené communities). To achieve this goal, we propose an ambitious project that follows a knowledge co-evolution framework, which implies that the purpose and rationale of the research will be jointly determined and coordinated by the research team, including Indigenous partners, and policy makers involved in fisheries management, biodiversity conservation, food security, and community economic development. Thus, our project is located at the interface of genomic sciences, fisheries management, local/Indigenous knowledge and GE³LS objectives.

The challenges of sustainable fisheries and food security

Food insecurity is a debilitating problem in Northern Canada: compared to the national average; it is twice as high in off-reserve Indigenous households and 4 times higher in Nunavut (Proof 2019) (Council of Canadian Academies 2014). Food insecurity in the North remains an urgent social challenge, despite increased spending for food support programmes like Nutrition North Canada, with an annual budget of \$99 million. Moreover, increased shipping, tourism, and mining pose serious risks for northern aquatic biodiversity (Reist et al. 2013; Schindler 2001; Wrona et al. 2013). In the Arctic, warming is occurring at twice the rate of the rest of the planet (Solomon 2007). Climate-induced changes in the distribution and abundance of fish threaten the economic livelihoods of northern communities, their traditional harvesting practices, their ability to feed themselves, and maintain access to healthy food (NWT 2005; Usher 2002). Projected patterns of global climate change are a major concern to northern freshwater and anadromous fisheries (Poesch et al. 2016). These changes will impose new pressures on Commercial, Recreational and Subsistence (CRS) fisheries. Reducing these impacts on food security is particularly crucial for northern communities (Ford et al. 2012) which are in demographic expansion (25% between 2010-2015 for the Cree, Bowles et al. 2017), thus imposing a strain on subsistence resources (Furgal and Seguin 2006). Developing management plans for the fisheries of these ecosystems will require an understanding and anticipation of whether and how northern Canada's freshwater fauna will adapt to such dramatic and rapid changes. While natural resource management and conservation in Canada's North has historically been a site of cultural resistance, fisheries-related research undertaken through the affirmation of Indigenous governance, knowledge, values and practices has the potential to contribute meaningfully to Indigenous food security, resurgence (economies, food systems) and reconciliation. Improved management practices supported by knowledge co-evolution is urgently needed in the context of a shift across CRS fisheries, often involving users with competing interests who may place different cultural and socio-economic values on the resource.

Unfortunately, and despite their immense potential, northern fisheries do not benefit from the same cutting-edge scientific information available to fishery managers in southern Canada, thus creating inequity. Indeed, there are insufficient scientific data to facilitate sustainable CRS management practices in a rapidly changing northern environment, and management/governance issues both represent major barriers to expansion of these fisheries (Poesch et al. 2016).

The socio-economic and food security importance of fish in northern Indigenous communities

While the importance of particular fish species varies regionally, freshwater and anadromous fishes have always been crucial to food security and to the cultural base of northern Indigenous communities in Canada (Tonn et al. 2016) (Fig. S1). Migratory Arctic Char are highly sought after by Inuit throughout Nunavut and Nunavik (Tallman et al. 2016). Chars are not abundant along coastal James-Hudson Bay where Cree communities instead harvest migratory Whitefish and Brook Trout (Schembri et al. 2019). Absent elsewhere in our study areas, Atlantic Salmon represents a significant food and economic resource for the Inuit of Ungava Bay, Nunavik). Fisheries of inland Cree communities in Québec mainly target Walleye, Lake Trout and Brook Trout in large lakes. The inland Dené communities of the NWT rely heavily on two great northern lakes – Great Bear and Great Slave Lakes – for subsistence fisheries targeting resident populations of Whitefish and Lake Trout (Tallman et al. 2016). **Because of this diversity of harvested species and their varying occurrence and/or importance among communities, FISHERS will develop and apply genomic approaches in concert with TEK to address critical challenges and opportunities related to the exploitation of each of these six species.** These six species also offer a major opportunity for economic development and employment creation throughout Canada's North, a region with limited economic options and lack of employment. However, the full potential of northern CRS fisheries has yet to be reached, in part because insufficient scientific data to support sustainable management is a major barrier to expansion (Tallman et al. 2018). Table S1 provides details on species exploited, fisheries governance and harvest per region. **In Nunavut**, the yearly quota for 1,775 Arctic Char is available but rarely reached. **In Nunavut**, the demand for Char far exceeds the current supply. **In Great Slave Lake**, commercial harvest of Whitefish and Lake Trout have been much less than estimated available quotas. **In Great Bear Lake, James Bay and northern Quebec**, basic information is available for subsistence fisheries only.

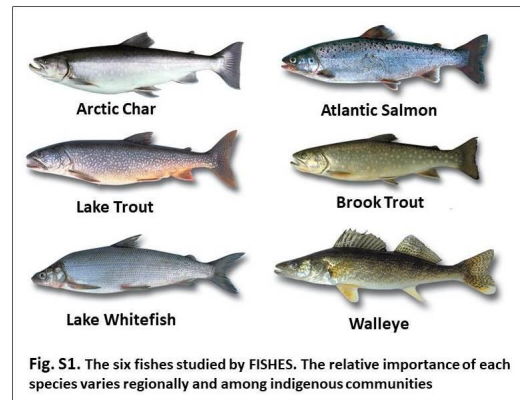


Table S1. Details on species exploited, fisheries governance and harvest per region.

Region	Species	Fishery type	Governance	Commercial quota available vs. actual commercial catch	Commercial value	Estimated subsistence harvest
Nunavut	AC	C,S	Co-management ¹ (DFO, GN, local HTOs)	790 mt/yr ² vs. 85 mt/yr ²	\$18 million/yr ²	532 mt ³
Nunavik	AC,AS	R*,S	Provincial (MFFP)	0	NA	233 mt (59 kg/capita/yr) ⁴
Great Slave Lake	LW,LT	C,R*,S	Federal (DFO)	Up to 1.3 T/yr vs. < 0.5 T/yr ⁵	\$3.9 million/yr ⁵	700 mt/yr (~75kg/capita/yr) ⁴
Great Bear Lake	LW,LT	R*,S	Federal (DFO)	0*	0*	900 mt/yr ⁶
James-Hudson Bay	LW,BT	S	Eeyou Istchee	0	0	320 mt/yr (51 kg/capita/yr) ⁴
Mistassini Lake	BT,LT, W	R*,S	Eeyou Istchee	0*	0*	NA

AC=Arctic Char, AS=Atlantic Salmon LW = Lake Whitefish, LT = Lake Trout, BT = Brook trout, W = Walleye

C=commercial, R=recreational, S=subsistence. *Total economic value of the recreational fishery is unknown but significant when accounting for direct value and indirect value to local economies and communities. 1 While officially co-managed, actors recognize that imbalance regarding data generation/ownership is a barrier to meaningful co-management. 2 Nunavut Fisheries Strategy 2016-2020. 3 Priest and Usher 2004 (number of fish harvested converted to weight assuming 2.7kg/fish). 4 Berkes 1990. 5 NWT 2017. 6 Muir et al. 2013

Quotas for northern CRS fisheries were typically developed more than 30 years ago, and have not been revisited in light of contemporary realities – including community needs and opportunities (i.e. to enhance economic development and food security), tools (i.e. with the benefit of genomic technologies in fisheries management), and co-management structures (involving local Indigenous organizations and public governments from federal and provincial/territorial scales) which mandate the inclusion of Indigenous knowledge, in concert with scientific assessments in decisions regarding quotas and harvest allocations. For example, Arctic Char quotas in Nunavut were determined ~30-40 years ago. Any updates, emerging fisheries applications and new stock assessments are done directly between local Hunters and Trappers Associations and DFO, with limited input by regional wildlife organizations due to the predominantly local stock characteristics (Boudreau and Fanning 2016). Fisheries quotas for Whitefish on Great Slave L., have been determined by DFO by averaging commercial catch over 3-5 years, on the basis that only one population unit was exploited because Whitefish population structure is unknown (X. Wang, DFO, pers. comm.). As emergence of revitalization of NWT commercial fisheries by 2021, a new fish plant will be built, which stimulated the development of integrated fisheries management plan associated with needs of mixed stock fisheries management of Lake Whitefish in GSL. New knowledge from FISHERIES on Genetic Stock Identification will be crucial toward this goal. In Eeyou Istchee, recreational harvesting quotas for non-Cree fishers were determined by the provincial government ~30 years ago. In light of recent signs of Walleye overharvesting in the southern part of Mistassini Lake, and the transmission of fisheries management control of the territory to the Cree in 2017, there is strong political momentum within the Cree Nation to revisit existing non-Cree quotas, whilst factoring in local Cree community harvesting (A. Coon, pers. comm.). Finally, there has never been any quota or fisheries management along the James Bay Coast, so new knowledge from FISHERIES will be instrumental toward implementing a first management plan in concert with the Cree Nation and governmental partners.

Overall, FISHERIES research activities will involve a sharing of Indigenous and scientific knowledge in support of knowledge co-evolution for sustainable development and management of CRS fisheries that are worth tens of millions annually in local northern communities of Canada, and much more socio-culturally as essential sources of subsistence.

Scientific knowledge gaps and the need for knowledge co-evolution with Traditional Ecological Knowledge (TEK) and local knowledge

Although government biologists have been working for decades in some regions of Canada's North on fisheries biological characteristics (age, growth, distribution, catch data), important knowledge gaps relevant to sustainable fisheries development and management remain. Indeed, the lack of rigorous monitoring programs for CRS fisheries is a major concern for local communities (Bernatchez and Bernatchez 2018). Fisheries management requires knowing whether harvests target genetically distinct groups of populations to maximize the conservation of genetic diversity needed for adaptation to changing environments and for sustainable fisheries (Schindler et al. 2010; Bernatchez and Bernatchez 2018). Genetic delineation of distinct populations in mixed-stock fisheries is critical for enabling managers to decide on areas and timing of harvest, and is vital for refining quotas and monitoring success of hatchery supplementation (Bernatchez et al. 2017). Recent studies show that protecting fine-scale diversity can help promote food security for Indigenous peoples (Rogers and Schindler 2011; Schindler 2010). In particular, the scales of environmental assessments need to match the scales of the socio-ecological processes that will be affected by anthropogenic-driven environmental change.

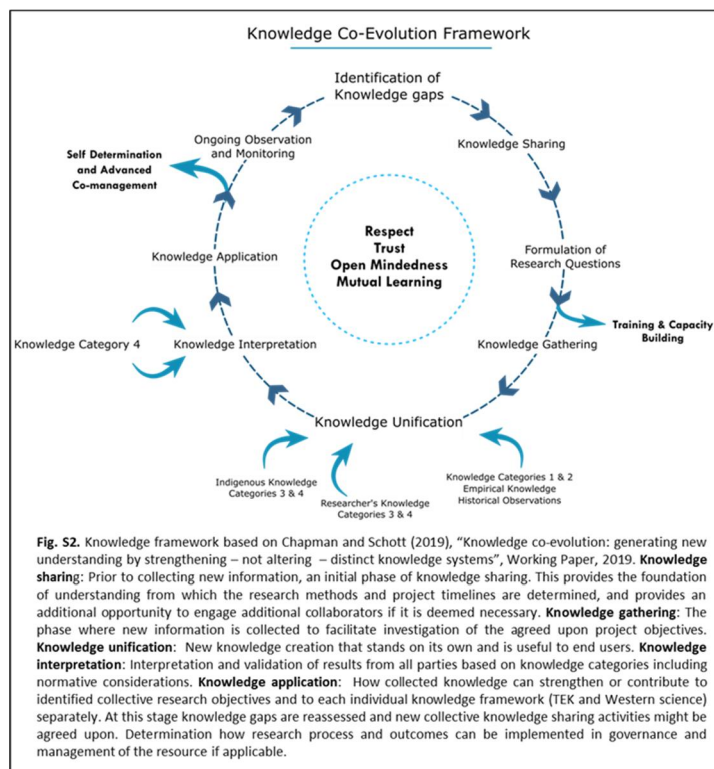
While genetic/genomic information has been used for decades to manage salmonid fisheries elsewhere (Bernatchez et al. 2017), such data have rarely been incorporated into northern CRS fisheries management. Thus, little is known about the number and geographic scale of distinct populations for freshwater and coastal species harvested by Inuit, Cree, and Dené communities. Furthermore, the evolutionary potential of CRS fish species to adapt to a changing climate or to respond to increased and/or selective harvesting is simply unknown. Multidisciplinary approaches that avail of

both western science and TEK – defined as the “cumulative body of knowledge, practice, and belief, evolving by adaptive processes and handed down through generations by cultural transmission about the relationship of living beings (including humans) with one another and with their environment” (Berkes et al. 2000) – are essential for sustainable fisheries co-management and conservation (Armitage et al. 2011; Dale and Armitage 2011; Thornton and Scheer 2012). Conventional management and monitoring based solely on western science has been limited by logistical and financial constraints as well as local legitimacy. At the same time, northern communities recognize that the extensive local or traditional ecological knowledge (TEK) they hold can benefit from western knowledge and technological inputs as they grapple with unprecedented changes to natural and social environments. As clearly laid out in their 16 letters of support (attached), our Indigenous partners are looking for solutions that will allow improving CRS fisheries management and sustainability. This will be best achieved by promoting and supporting the development of community-based monitoring grounded in an adaptive knowledge co-evolution process, which requires comprehensive management initiatives predicated on traditional and user knowledge, local cultural values, and the most up-to-date scientific methodologies.

A knowledge co-evolution process uniting TEK, genomics and fisheries science.

The underlying foundation of FISHERS is a commitment to work closely with our Indigenous partners to create an ethical, responsible, and culturally appropriate space for greater dialogue and shared learning for fisheries genomics research. **Thus, integrated into Activities 1-4 described below are the outcomes of Activity 5 (GELs) which will allow the team to integrate the knowledge and priorities of the Indigenous partners.**

Following a Knowledge Co-Evolution framework (Chapman and Schott, in prep; Fig. S2), the project will include the establishment of culturally-appropriate protocols and standards of engagement from the onset of the project, for academic researchers and other end-users involved in the project (e.g., Fisheries and Oceans Canada (DFO), Ministère des Forêts, de la Faune et des Parcs Québec (MFFP), Government of Nunavut and Nunavik, Cree Nation Government, Regional Advisory Boards representing our Indigenous partners from the different communities) as well as an equal voice governance structure for the research process. Relevant Northern agencies and community members will be included as partners, with capacity building and progress towards enhanced self-determination as central objectives. Beyond fundamental equity, our goal is to open a space for knowledge co-evolution that fosters trust and long-term learning to support community-driven application of research results to enhance stewardship of fishery resources, strengthen food security, and assist in preserving cultural identity and the transfer of traditional knowledge. Local Indigenous authorities representing the Cree, Inuit and Dené communities involved in FISHERS have already been centrally involved in the development of the proposed research objectives and will continue to be involved for the duration of the project through the Regional Advisory Boards, hiring of local



collaborators for sample collection, end user implementation and mapping of observations, interpretations, assistance with interviews, and workshops. As concrete examples of involving Indigenous communities right from the onset of the project, Moore met in April 2018 with Nunavut representatives at a Government of Nunavut (GN) Fisheries Workshop. In fact, the development of a Nunavut fishery policy with a strong emphasis on Arctic Char is a current mandate of the GN (Nunavut Fisheries Strategy 2016). Bernatchez and Fraser also met multiple times with representatives of Cree end-users who identified their most pressing fisheries management issues. We also included in our team three co-investigators who represent the three main northern regions covered by FISHERS: i) Nadia Saganash from the Cree Nation Government; ii) Lilian Tran, from Makivik Corporation, Nunavik; and iii) Janelle Kennedy, from the Government of Nunavut. We met with MFFP and DFO representatives in order to align research objectives identified by local communities with government priorities in terms of northern fisheries management that they are responsible for. The knowledge co-evolution process includes a distinct knowledge-gathering phase that will guide genetic sampling, and be used to select which samples are used with respect to any historical samples currently held by DFO. To facilitate this, each region will have a Regional Advisory Board (RAB) that is made up of members closely associated with fisheries and food security. As part of the knowledge-gathering phase, the RAB will meet to discuss current knowledge and knowledge gaps, research strategies, capacity building opportunities, desired outcomes and sampling approaches that should be implemented in order to address these objectives. This will include sampling locations and focal species important for the communities, while attempting to sample all source populations where Genetic Stock Identification studies are targeted (see Activity 3). The RAB will be consulted prior to each field season to ensure the project maintains adherence to the agreed upon project objectives. We will follow a knowledge co-evolution process that strives to bring knowledge traditions together to create new knowledge that is culturally appropriate, empowers knowledge holders and seeks to strengthen both knowledge streams. For example, the overlay of TEK and science data is well illustrated in FISHERS' proposed Activities dealing with population genomic structure and bio-monitoring for maintaining Indigenous fish food security in strategic northern regions/fisheries. Here, TEK is instrumental in providing a historical perspective on population trends (changes in catch, fish body size, timing of migration, spatial distribution, etc.) for spawning populations when considered in tandem with the spatial data on harvest contributions of each population estimated from genomic information. The RAB that will be formed in the first stage of our research process will guide the ongoing research efforts of these governmental partners who have collected standard fisheries assessment data (e.g. age structure, growth data, catch data) for years in specific regions to implement sound management actions. Our collaborative research process is intended to create more community and regional capacity in managing and governing fishery resources, to establish even stronger links in data collection and co-management decisions to ensure sustainable use of fishery resources for enhanced food security, cultural identity and regional economic development options.

An exceptional team: To achieve our central goal, we have formed an exceptional and diverse team. **All members have extensive experience working with our key Indigenous and governmental partners and on the six fish species included in the proposal.** Together, we combine the necessary expertise to successfully develop and implement a novel knowledge co-evolution framework at the interface of genomics, fisheries management and TEK. The team comprises eight academic researchers (4 men, 4 women), and four with a background in fish biology (genomics/ecology) and four with a GE³LS related background. L. Bernatchez is a senior scientist with 30 years of experience in fish population genetics/genomics. In particular, he is a project co-leader in a currently funded LSARP fisheries-focused project ending in 2019 (EPIC4: Enhancing Production in Coho: Culture, Community, Catch; <http://www.sfu.ca/epic4/index.html>) and will transfer his lead expertise and experience to FISHERS. D. Fraser is an early-mid career with 15+ years of inter-disciplinary expertise in combining fish genetics and ecology with TEK; J.-S. Moore has a similar profile but is an early career scientist while L. Chavarie, also early-career, brings to the team a unique expertise in fish phenotypic analyses. Together, the four GE³LS

members combine an exceptional range of expertise on sustainable development and knowledge processes of TEK and science (S. Schott), approaches to northern health related to food security (M. Lemire), Indigenous institutions of environmental stewardship and community-based conservation (M. Mulrennan), and fisheries modeling, climate change, and TEK (T. Kenny). In order to ensure that the research goals will be aligned with the needs of our Indigenous partners through the entire project, we have included in our non-academic team three co-investigators (N. Saganash, L. Tran, J. Kennedy) to represent the three main regions covered in the project. The academic team is also supported by five co-investigators from government agencies who will bring to FISHERS strong expertise in the assessment and management of northern fisheries (L. Harris, X. Zhu, J. April, R. Tallman, K. Howland). Our team is completed by 15 collaborators representing either government agencies or Indigenous communities from throughout the studied regions and bringing additional expertise and support for TEK surveys, sample collections, community liaison activities and local fisheries management.

An extensive track record of collaborations: FISHERS will not be the first experience of collaboration among its academic members. For more than 15 years, we have engaged with Indigenous communities, the Government of Nunavut, Makivik Corporation (Nunavik), the Cree Nation Government, DFO, and MFFP in many synergistic and successful collaborations in the form of local projects and syntheses of TEK towards ensuring northern food security and sustainable CRS fisheries. As selected examples; (i) Moore and Schott have been collaborators in another LSARP (Genome Canada) project (TSFN; Towards a Sustainable Fishery for Nunavummiut) in the Kitikmeot region; (ii) Moore, Harris, Lemire and Bernatchez have been involved in projects funded by Sentinel North and Polar Knowledge Canada and involving partners from many Inuit communities in Nunavik and Nunavut (e.g. Kuujuaq, Salluit, Cambridge Bay, Iqaluit, Pangnirtung, Kugaaruk); (iii) Chavarie, Zhu, Howland, and Schott have been involved together in fisheries management and TEK projects involving Dené communities from Great Bear and Great Slave lakes, and (iv) Fraser, Bernatchez, Mulrennan and Schott have long been involved in collaborative fisheries management and TEK projects with Cree communities both from inland (Mistissini), and coastal James Bay (e.g. Wemindji, Eastmain, Waskaganish, Moose Factory, Moosonee).

A successful delivery of tangible benefits: Our previous studies provided tangible benefits to Indigenous communities, in particular as part of long-term collaboration established with the Cree community of Mistissini 20 years ago by Bernatchez and now led by Fraser. Through integrative TEK-science research, these benefits comprise: (i) setting community-based management options for Mistissini Lake Walleye; (ii) protecting spawning habitat of Brook Trout populations that contribute most fish to annual harvests in lake or coastal habitats from certain forestry or mining practices; (iii) facilitating annual monitoring of genetically-distinct populations through Cree-operated outfitting camps; and (iv) providing scientific evidence relating to issues of concern to local community members about harvested fish populations, such as overharvesting, changes in types of fishing gear used, environmental changes impacting fish populations observed, etc. In turn, these tangible benefits have contributed to the establishment of sustainable fishing practices in the local Indigenous community of Mistissini and local Cree-operated tourism outfitting camps, to ensure the long-term economic benefits of fisheries resources in Mistissini Lake. More broadly, these past research collaborations in Mistissini Lake typify the challenges related to fishery resources and conservation planning in other isolated or northern regions of the world. In particular, our collaborations have illustrated that both western science and TEK are required to recognize and maintain fish population diversity (and threats facing this diversity), and to implement practices necessary for achieving a balance between biodiversity conservation and sustainability for food security and local economy.

Our past collaborations have also culminated into many, often well-cited research publications (Fraser et al. 2006, 2013; Moore et al. 2013, 2016, 2017) and outreach activities that foster development of local co-management or Indigenous-led fisheries conservation planning (Marin et al. 2017; Cambridge Bay H, TO & aRTLeSS Collective 2017). Our past ecological, phenotypic, life history, and microsatellite DNA research on some of the species supporting northern fisheries will provide a baseline in certain

regions to advance genomic understanding of population structure, adaptation to environmental change, and population bio-monitoring necessary for sustaining local food security (Fraser and Bernatchez 2005, Chavarie et al. 2013). For example, previous work and consultation with Indigenous fishers strongly suggested that distinct population structure is more pervasive than currently recognized (Marin et al. 2016; Chavarie et al. 2015), or that mixed-stock harvest assessments require greater genotypic resolution as well as temporal re-assessment (Dupont et al. 2007; Moore et al. 2017). These collaborations also provided crucial information about patterns of migration and identified critical habitats for foraging, spawning and overwintering (Fraser et al. 2006; Moore et al. 2017).

In summary, FISHERS offers positive assets to support the structure, capacity-building, and local empowerment necessary for effective co-management or Indigenous-led management models of food security and socio-economic development related to fisheries, and will generate tremendous opportunities for comparative genomics, fisheries science and TEK research synergies across regions.

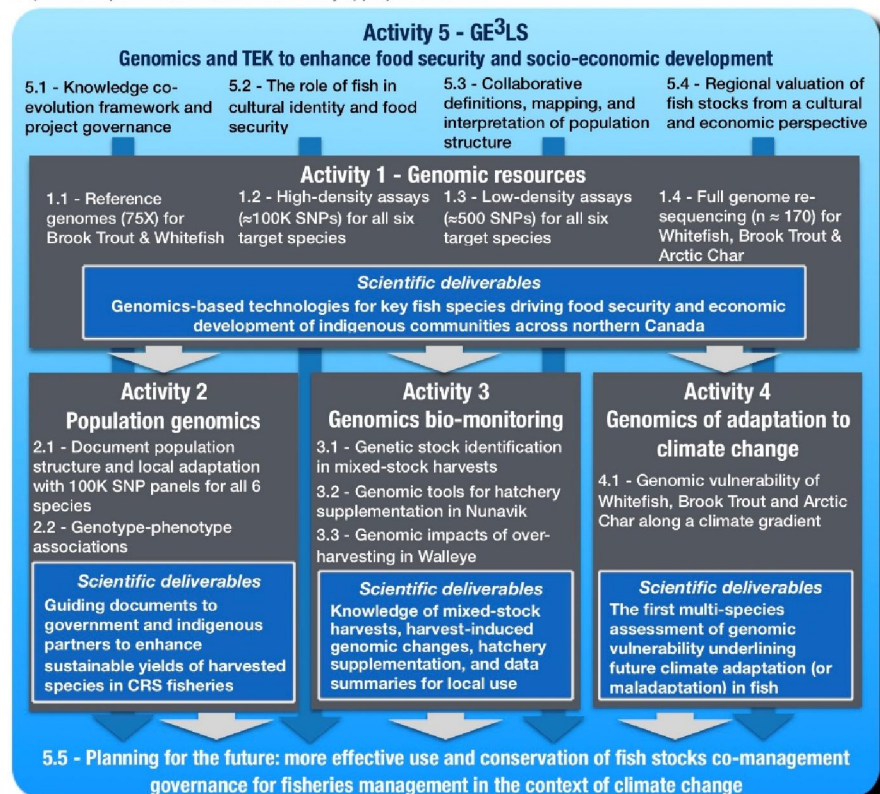
As shown in the chart below, FISHERS comprises five inter-related research Activities that will produce scientific deliverables for the direct Socio-Economic Benefits of multiple end-users.

FISHERS in a page: Fostering Indigenous Small-scale fisheries for Health, Economy, and Security

FISHERS addresses important socio-economic challenges facing northern Indigenous communities to provide solutions that are in tune with local needs and that respond to existing opportunities:



The genomic work performed through FISHERS (Act. 1 to 4) will be guided by the GE³LS (Act. 5) to ensure the science directly responds to specific local needs in a culturally appropriate manner:



Activity 1. Team: Bernatchez (Leader), Moore, Fraser.

Genomic resources for high and low throughput genotyping.

Meeting our objectives proposed in Activities 2-4 will require the development and use of four types of genomic resources described below.

Sub-activity 1.1: To produce publicly available reference genomes for Brook Trout and Whitefish.

Context: A well-annotated genome sequence provides the ultimate resource for genomic approaches; it is the backbone against which the genotyping data generated in the different proposed activities will be mapped to obtain crucial positional information (Fuentes-Pardo and Ruzzante 2017). For Activity 2, which will require the identification and genotyping of ~100,000 single nucleotide polymorphisms (SNPs) for each species (justified below and in Activity 2), a reference genome will greatly improve our efficiency in i) identifying high quality SNPs (Rochette and Catchen 2017), ii) locating and annotating SNPs, and iii) revealing the gene content in the neighbourhood of these markers, thus providing candidate genes for adaptive traits of interest (Ekblom and Wolf 2014). For Activity 3 which will require genotyping fish using a low-density assay (~500 SNPs) for population and parentage assignment, the reference genome will allow performing the optimal selection and design of PCR primer pairs for each SNP, and thus defining the best set of markers for each species. For Activity 4 which will require whole genome re-sequencing of 500 fish representing three species, the reference genomes will allow the most complete account of individual genomic variation (e.g. structural rearrangements, copy number variation, insertion–deletion, single nucleotide polymorphisms (SNPs), sequence repeats) (Ellegren 2014). This will also provide the basis for haplotype information, genome-wide estimates of linkage disequilibrium and a powerful foundation to screen for signatures of selection (Hohenlohe et al. 2010).

Of the six species targeted in FISHERS, high-quality (chromosome level assembly), functionally annotated reference genomes are available for Atlantic Salmon (Lien et al. 2016) and Arctic Char (Christensen et al. 2018). These facilitated exceptional progress in understanding and resolving many of the complexities inherent to the whole genome duplication event arising in salmonids from a spontaneous auto-tetraploidization event (SWGD) 100-80 MYA (MacQueen and Johnston 2014). In addition, the genome of the closest non-SWGD species (Northern Pike) provides comparative mapping information particularly important in some of the more difficult duplicated salmonid chromosomes (Rondeau et al. 2014). A chromosome level assembly (long-reads PacBio and Hi-C) is being completed for Walleye by the Great Lakes Genomic Center (R. Klaper, UW-Milwaukee, pers. comm.), as well as for Lake Trout which is being done by L. Bernatchez in collaboration with I. Ragoussis (McGill U.). Thus, at least a draft version of these other four species will be available by the time FISHERS begins and we anticipate that the first draft version of both Brook Trout and Lake Whitefish genome assemblies, usable for aligning GBS reads, will be available within 12 months from the start of the project and a polished version of both genomes will be completed within two years.

Objective: We propose to sequence the genomes of the two remaining non-sequenced species: Brook Trout and Lake Whitefish, ~3 gigabases each.

Methodology: The starting material will be double haploid individuals produced from aborted haploid gynogen individuals. This has already been achieved for Brook Trout progeny this year (with help from R. Devlin, DFO) and will be done in fall 2019 for Lake Whitefish. The process will allow differentiating between highly similar paralogous duplicated regions from allelic sequences. Very high molecular weight DNA will be obtained from fresh tissues to ensure the production of quality long read sequencing libraries. Using PacBio (Sequel) sequencing technology performed at the McGill University - Génome Québec Innovation Centre, we will aim to sequence both species at 75X coverage which will ensure high quality genome assemblies based on our experience with the Lake Trout genome. Eight sheared gDNA large insert libraries (SMRTbell Template Prep Kit 1.0, size fractionation of 15–20 kbp) will be prepared per species and sequenced on 114 Sequel SMRT cells. Genome assembly using all raw reads will be done using a combination of software most often used for PacBio assembly (e.g. Canu, FALCON, wtdbg2) and draft genomes will be polished with the Arrow software. Chromosome-level genome assembly will be

achieved by our collaborator I. Ragoussis (see letter of support) using Dovetail™ Hi-C technology and HiRise™ Scaffolding Software. Super-computing resources from Compute Canada and IBIS (U. Laval) will be available for performing genome assembly. High density genetic maps are available for Brook Trout (Sutherland et al. 2017) and Lake Whitefish (Gagnaire et al. 2013) which will be used to place the scaffolds onto chromosomes, along with synteny information between the scaffolds and the already published genomes for other salmonid species. Genome annotation will be performed using transcriptome database available for both *Salvelinus* and *Coregonus* genera (Carruthers et al. 2018). All data will be put into public databases (e.g. NCBI) as soon as they are validated.

Milestone 1. The production of a publicly available reference genome for Brook Trout and Whitefish.

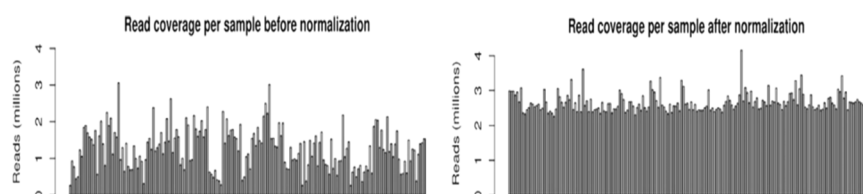
Sub-activity 1.2: To develop high-density Genotype-By-Sequencing (GBS) assays for 6 species.

Context: Based on previous genotype-phenotype/environment studies in salmonids (e.g. Barson et al. 2015, see further explanation in Activity 2), and standards being set in the literature, we believe that ~100,000 SNPs will be necessary for rigorously defining locally adapted fish populations in FISHERIES. Various high-density genotyping assays could be adopted, each with their pros and cons. For example, we could develop a 100K SNP chip for each species (e.g. Affymetrix or Illumina array platforms) but we decided not to go that way for the following reasons. First, developing such arrays takes time, especially considering six species, which may overly increase the time needed to reach our milestones. For instance, in a previous Genome Canada project that Bernatchez was involved in, it took 1.5 years (including the time to collect samples and screen variation to identify SNPs) to develop a 200K SNP chip for one species. Also, SNP chips cannot provide haplotype information, which will be required for enhancing resolution of genetic stock identification (Activity 3). Therefore, the 7 000 samples analysed in Activity 2 and 500 Walleye samples in Activity 3 (Sub-activity 3.3.) will be genotyped using the cost-effective and standardized Genotype-By-Sequencing (GBS) protocol performed using the Ion Torrent sequencing technology for which Bernatchez' lab and the IBIS sequencing platform at U. Laval have six years of experience (e.g. Bernatchez et al. 2016; Perreault-Payette et al. 2017). GBS offers advantages over the other methods that make it optimal for FISHERIES. Because GBS does not involve any development steps, genotyping can start at the beginning of the project since many samples will be readily available from our partners, which is a hugely positive asset. Another major advantage over SNP chips is that GBS data can be analysed as haplotypes, which will be extremely valuable for performing GSI in Activity 3 (McKinney et al. 2017a). Also, we will acquire four sequencers of the latest Ion Torrent GeneStudio S5 generation (2 bought, 2 in donation) that will each generate 125 million reads and a median length ~150 bp in about two hours. These will be used in priority for FISHERIES which will ensure speed in processing and avoid long queuing for sequencing our samples. GBS will not cost more than using SNP chips which are estimated at 105\$/sample for a 90K SNP chip by the McGill – Genome Quebec Innovation Centre.

Objective: We will apply a GBS protocol to genotype up to 100,000 SNPs for each of the six species.

Methodology: Following DNA extraction, testing for sample quality, and normalising for concentration, double-digest libraries will be constructed. Each sample will be barcoded with a unique 6-nucleotide sequence and pooled in 96-plex and cleaned up. The libraries will be amplified by PCR and sequenced on the S5 sequencers. Each pool will be sequenced on a first chip. Following this first round of sequencing, variation in coverage among individuals will be checked and DNA volumes for each individual will be normalised in order to obtain a more even coverage on the next chips being sequenced (Fig. 1.1). This has proven extremely efficient for us in order to increase the number and the quality of SNPs being genotyped, and substantially reduce the number of missing data (Prince et al. 2017).

Figure. 1.1. Example of sequence coverage variation before and after DNA volume normalization in the EPIC4 Genome Canada LSARP project on Coho Salmon.



Based on our previous experience with the older Ion Torrent Proton technology, we estimate that 8 chips (96 individuals/chip) on the Ion Torrent GeneStudio S5 technology (125M reads/chip) will allow the genotyping of ~100,000 SNPs. The latest version of the program STACKS (Rochette and Catchen 2017) will be used with standard filtering steps to call genotypes at non-duplicated loci. A catalog of putative non-duplicated loci will be created (cstacks) based on alignment position on the reference genomes and the “populations” module will be used to call genotypes, applying several filtering steps to ensure quality of the data. Because they have been shown to play an important role in local adaptation in other salmonids (e.g. Waples et al. 2016; Limborg et al. 2017), we will use the method of Limborg et al. (2016) to identify duplicated loci and we will retain a representative proportion (tentatively 15%-20% of all markers retained) of these genomic regions in our marker panels. Allele frequencies at non-duplicated markers will be estimated using the R package PolyFreqs (Limborg et al. 2016).

Milestone 2. The production of a ~100,000 SNPs GBS assay for each of the 6 FISHER species.

Sub-activity 1.3: To develop low-density (500 SNPs) genotyping assays (Rapture) for 6 species.

Context: Performing Activity 3 will require genotyping 12,500 fish with a low-density SNP assay for quantifying; i) mixed-stock harvests which require identifying the populations of origin of harvested fish by means of genetic stock identification (GSI) and ii) contributions of hatchery fish which will require identifying parents of origin using the Parentage Based Tagging (PBT) method. Both of these applications necessitate the genotyping of several 100s SNPs and a common set of markers can be designed for both (Beacham et al. 2018). Our recent GSI study on Arctic Char showed that a population assignment success of 90% could be reached with 500 SNPs (Moore et al. 2017). Developing an assay of ~500 SNPs for each species should allow an exceptional level of confidence in performing both GSI and PBT. Different low-density genotyping assays could be used in FISHER, each with their pros and cons. Among these, and while not compromising on quality of the data, methods based on amplicon sequencing are the most cost-efficient when genotyping ~500 SNPs or less on 1,000s of individuals (Meek and Larson 2019). A first option is the “genotyping-in-thousands by sequencing” protocol (GTseq, Campbell and Narum 2015), which requires conducting several rounds of primer testing to ensure that all primer pairs for the GTseq panel produce appropriate numbers of reads. With six species, this could take many months of development with some uncertainty of the final outcomes. Alternatively, we could outsource the primer development (e.g. Illumina TruSeq® or ThermoFisher AgriSeq) and use these companies’ kits but our estimates show that this would be the least cost-efficient approach. Given this, we propose to use the “Rapture” method, combining a sequence capture enrichment step to the GBS protocol described above (Ali et al. 2016). The main advantage is that the SNP selection is made directly from the GBS data obtained for source populations (Activity 2). Secondly, the time of development will be substantially shorter than alternative methods, thus reducing the time needed to reach our milestones. Both Bernatchez’ group and the personal of the IBIS sequencing platform have developed a solid expertise in Rapture (e.g. Dorant et al. 2019), thus reducing the uncertainty of the outcomes.

Objective: We will fine tune the Rapture protocol in order to genotype ~500 SNPs for each of the six species. (Exact number could vary among species based on the outcomes of simulations (see below)).

Methodology: For each species, and in order to reach the final number of loci, ~700-800 custom probes will be selected from a *de novo* SNP reference catalog genotyped on a subset of about 200 fish (part of Activity 2) which will provide reliable allele frequency quantification. Probes will be selected based on several criteria: i) the quality observed in GBS; ii) the minor allele frequency (MAF) of each SNP which should be > 0.15; iii) the level of information content estimated by on training holdout leave-one-out simulations (Anderson 2010); iv) include as many loci as possible with multi-SNP haplotypes to increase power to resolve populations (McKinney et al. 2017a); v) ensure to include duplicated loci in a proportion representative of their occurrence in salmonid genome (~15-20%, McKinney et al. 2017b).

The probe library will be purchased from Arbor Biosciences™ and we will follow the Mybait protocol supplied with their capture kit. Each sample will be barcoded with a unique 6-nucleotide sequence and a total of 768 individually tagged fish will be pooled on a same sequencing chip to obtain a minimum of 100X coverage/fish to ensure sufficient coverage for all SNPs while minimising the sequencing cost/fish (16\$/sample), including library preparation by the personnel of the IBIS sequencing platform.

Milestone 3. The production of a ~500 SNPs Rapture assay for the 6 FISHES species.

Sub-activity 1.4: To sequence ~ 170 genomes (500 total) for Whitefish, Brook Trout and Arctic Char.

Context: This Sub-activity will provide the genomic resources for Activity 4 that aims at: i) comparing patterns of adaptive variation across a climatic gradient among the three main salmonids from eastern James-Hudson Bay (Kemp et al. 1989), and ii) investigating which populations might be most vulnerable to climate change based on predictive modeling of “genomic vulnerability” (Bay et al. 2018). Although SNPs were initially thought to contribute the majority of genomic variation, structural variation (SV) (e.g. inversions, copy number variation, insertion–deletion, duplicated regions) represents a significant, yet often poorly understood source of genetic variation. For instance, we recently showed that in the marine Australasian snapper, SV outnumber variation caused by SNPs by 3-fold in terms of total bases affected (Catanach et al. 2019). Recent studies also revealed that SV may play an important role in local adaptation (Wellenreuther and Bernatchez 2018; Wellenreuther et al. 2019). For instance, Pearse et al. (2018) found a large inversion in rainbow trout that contains key photosensory and circadian rhythm genes varying in frequencies with latitude and temperature, thus revealing environmental dependence and suggesting local adaptation. Yet, the relative role of SV vs. SNP variation in maintaining evolutionary potential in the face of a changing environment has never been rigorously investigated. To rigorously compare genome-wide patterns of SNP vs. SV variation, genotyping methods such as GBS or SNP chips are insufficient. Instead, Whole Genome Resequencing (WGR) offers an unprecedented marker density and allows surveying all types of genetic variation, including the different types of SV (Ellegren 2014).

Objective: Our objective will be to produce a detailed inventory of SNP and Structural variants for Whitefish, Brook Trout and Arctic Char, the three species targeted for Activity 4.

Methodology: For each three species, we will sequence ~25 fish/population x 7 locations for a reliable representation of genomic variation (sample sizes similar to Bay et al. 2018) along the latitudinal gradient for each species (500 fish sequenced in total) representing populations spread from southern James Bay to northern Hudson Bay. Sequencing will be performed at the McGill U. - Génome Québec Innovation Centre using HiSeqX sequencing platform. This technology offers an overall accuracy >99.5%, but it remains difficult to distinguish true genetic variation from technical artefacts unless a minimum coverage of 30X/individual is done for the correct identification of variants (Fuentes-Pardo and Ruzzante 2017). This will be achieved by sequencing two samples/lane (PE 150) thus producing 60 Gbp/fish. FASTQC will be used to remove low-quality bases (PHRED quality score < 20). High-quality reads will be mapped to the reference genomes using BWA and/or Bowtie2, and GATK indelrealigner will be used to realign reads to the reference genome. Short variants (SNPs and small indels) will be called using the latest version of GATK and large structural variants (duplications, deletions and inversions) will be called for each sample in parallel using alignment (bam) files and the LUMPY algorithm as the caller.

Milestone 4. Production of ~ 170 whole genome sequences for Whitefish, Brook Trout and Arctic Char.

Deliverable for Activity 1. D1: Genotyping assays for stock conservation & management that includes:

- **a:** A comprehensive inventory of SNP and SV variation in Whitefish, Brook Trout and Arctic Char to assess the genomic vulnerability of these exploited species to future climate change;
- **b:** Genomics-based technologies (high & low-density genotyping assays) to conserve and manage CRS species for food security and economic development of Indigenous communities throughout northern Canada and elsewhere (achieved within 6 months);
- **c:** Genomics-based technologies to managed hatchery-supplemented fisheries of Arctic Char by Inuit communities in Nunavik and elsewhere achieved within 6 months).

Activity 2. Team: Moore (Leader), Bernatchez, Fraser, Chavarie, Harris, Zhu, Howland, Tallman, April, Schott, Saganash, Kennedy

Population structure, local adaptation, and genotype-phenotype associations in key CRS fisheries

Identification of genetically distinct populations (or fish stocks) and the scale of local adaptation within the distribution of a species is a key step towards conserving the genetic diversity needed to adapt to environmental changes (Waples and Gaggiotti 2006; Allendorf et al. 2010; Garner et al. 2016). For fisheries, the presence of multiple genetically and phenotypically distinct stocks can buffer against locally detrimental environmental conditions and thus have a positive impact on their long-term economic value (Schindler et al. 2010; Nesbit and Moore 2016). Traditionally, quantifying population structure has been accomplished through surveys of a few markers such as microsatellites (Schwartz et al. 2007). These tools have been the workhorses of fishery managers for two decades, but the small number of markers typically used (< 20) lacks resolution in situations of weak genetic structuring (Puttman and Carbone 2014) and cannot identify genomic regions that are underlying locally adaptive traits (Allendorf et al. 2010). The use of thousands of genetic markers (e.g. in the order of 100,000, Barson et al. 2015) such as SNPs increases the precision of population parameters of interest for fisheries management (e.g., genetic distinctiveness of stocks, effective population size), and also offers an opportunity to document the genomic regions underlying adaptations to variable environmental conditions (Allendorf et al. 2010). Such genomic regions that correlate with environmental factors (e.g., temperature, precipitation, anadromous migration length) can provide powerful tools to managers tasked with maximizing the long-term yields of fisheries (Bernatchez et al. 2017).

Genotype-environment associations, however, do not reveal the phenotypes underlying adaptation. With phenotype-genotype association studies, which combine genome-wide genetic variation with individual phenotypic data, it is possible to interpret the adaptive nature of patterns of variation in the genome in terms of their effects on ecologically-relevant phenotypes (Laporte et al. 2015; Bernatchez et al. 2016; Perreault-Payette et al. 2017). The genetic architecture of divergent traits can then help guide management and conservation actions, which may differ depending on whether traits have a simple genetic basis or are underpinned by large numbers of sites distributed throughout the genome (Kardos and Shaffer 2018). For instance, Prince et al. (2017) found that migration timing in Pacific salmon is mainly controlled by a single gene (*GREB1L*) and their results demonstrated that Salmon Conservation Units reflecting overall genetic differentiation can fail to protect evolutionarily significant variation that has substantial ecological and societal benefits.

Genomic tools are used extensively to define management units for fisheries in southern Canada (e.g., Lobster; Benestan et al. 2015; Atlantic Salmon; Moore et al. 2014; Lake Trout in Southern Québec; Bernatchez et al. 2016) but are not yet available to northern Indigenous people for managing their own fisheries. Yet, there are many unique aspects of northern Canadian CRS fisheries that make genomic approaches to documenting population structure and local adaptation particularly critical. First, low aquatic species diversity in the North means that within-species variation is an extremely important component of the total biodiversity (Reist et al. 2013; Chavarie et al. 2014; Fraser et al. 2011; Moore et al. 2014). Second, the very recent demographic upheavals related to the re-colonization of northern Canada following the last glaciation (< 10,000 years ago in some regions) have left important genetic signatures. These are critical to maximize the preservation of key region-specific alleles or traits (Bernatchez and Wilson 1998; Moore et al. 2015). Third, unlike several major marine fisheries in Canada, freshwater and anadromous northern CRS fisheries target populations which are largely genetically-isolated from one another and therefore have the potential to accumulate significant adaptive genetic or phenotypic differences on small geographical scales. Finally, in a few geographic regions targeted by FISHERIES, we previously performed regional assessments of genetic variation for the documentation of population structure (Moore et al. 2017; Fraser and Bernatchez 2005; Dupont et al. 2007), but such an exercise has never been attempted in Canada's North at a larger geographical scale.

While fishery managers tasked with managing equivalent species in southern Canada make extensive use of powerful genomic data (e.g., Coho Salmon; EPIC4; Atlantic Salmon; Moore et al. 2014; Lake Trout in Southern Québec; Bernatchez et al. 2016), similar tools and data have not, as yet, been made available to northern Indigenous people for managing their own fisheries, creating inequity in access and application of the latest state-of-the-art management tools.

Sub-activity 2.1: To define genetically distinct populations based on genomic data.

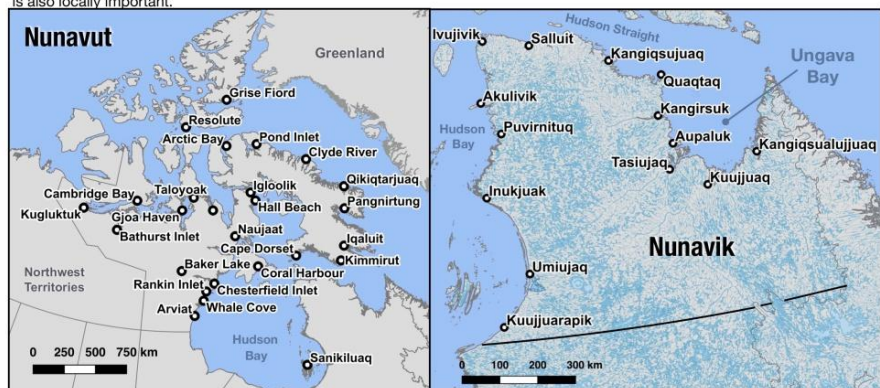
Context: Large-scale assessments of population structure based on genomic data are lacking for freshwater and anadromous fishes in northern Canada. To fill this knowledge gap, we will guide FISHES sampling efforts according to the specific needs of our Indigenous and government partners, for which the relative importance of each of the six species targeted by FISHES varies regionally (Fig. 2.1).

Inuit (Nunavut and Nunavik) –

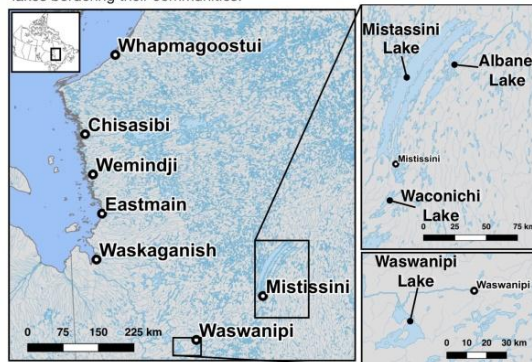
The Inuit have relied on Arctic Char as an abundant, high-quality resource for thousands of years (Friesen 2004). To this day, Arctic Char remains the second most-harvested species of wildlife in both Nunavut (182 tons harvested annually; Nunavut Fisheries Strategy 2016-2020) and Nunavik (Lemire et al. 2015). In addition, Arctic Char stocks support commercial fisheries (Tallman et al. 2018), which provide local employment to harvesters who can sell their catches to one of three fish processing plants in Nunavut: Cambridge Bay, Pangnirtung, and Rankin Inlet. Many other communities have expressed the wish – and in some cases taken concrete steps – to develop local, commercial fisheries. Yet the absence of basic data remains a major obstacle (access to market is another, addressed in Activity 5). Local partner involvement (Government of Nunavut, Makivik Corporation, Regional Advisory Boards) will ensure that our sampling responds to local needs and directly contributes to new fishery development in the short-term. For instance, FISHES will take advantage of the highly successful Nunavut Community Aquatic Monitoring Program (N-CAMP) of the GN to help establish priorities for its sampling efforts. Aside from a recent local assessment (Moore et al. 2017), genomic tools have never been used to define large-scale population structure of Arctic Char in Northern Canada. In Nunavik, several large rivers draining into Ungava Bay also harbour Atlantic Salmon populations which support subsistence harvesting, generate substantial revenue through recreational fishing (MFFP 2016), and will be part of FISHES through collaboration with MFFP and local communities.

Figure 2.1 - FISHES will use cutting-edge GBS genotyping for the management of major northern fisheries by its Indigenous partners. For all 6 species, we will identify genetically distinct populations and genomic regions underlying local adaptation. Genotype-phenotype associations will also be performed to understand the genetic basis of ecologically relevant phenotypes. This data can be used side-by-side with TEK to ensure that management is based on the best available knowledge.

Inuit territories of Nunavut and Nunavik. Its residents rely extensively on **Arctic Char**. In Ungava Bay, Nunavik, **Atlantic Salmon** is also locally important.



Eeyou Istchee is the Cree territory of Québec. Residents on the coast of James-Hudson Bay rely mainly on anadromous **Brook Trout** and **Whitefish**. Inland communities rely on **Brook Trout**, **Lake Trout** and **Walleye** in the large lakes bordering their communities.



In the Northwest Territories, the Dené communities around Great Slave L. and Great Bear L. rely extensively on Whitefish and Lake Trout.



Cree (Eeyou Istchee) – The Cree people of Eeyou Istchee have relied on abundant fish and wildlife resources for generations (Berkas 1990; Fraser et al. 2006, 2013; Marin et al. 2016, 2017). Fishing remains a culturally and economically important activity throughout Eeyou Istchee, and the species and fishery practices differ between inland and coastal areas. On the James Bay-Hudson Bay Coast, anadromous Whitefish and Brook Trout are the main species harvested (Bernatchez and Bernatchez 2018, Berkas 1990; Dewan 2016). Inland, subsistence and recreational fishing takes place in several large lakes. For instance, the community of Waswanipi relies on Walleye from nearby Lake Waswanipi for subsistence and recreational fishing. The community of Mistissini relies on Brook Trout, Lake Trout, and Walleye found in Lake Mistassini, Lake Albanel and Lake Waconichi, for subsistence fishing and operation of Cree-owned fishing camps (e.g. Osprey Excursions); the latter are important seasonal employers. The provincial government of Quebec recently devolved management of the Mistassini-Albanel-Waconichi wildlife reserve – a territory of several 1000s km² - to the Cree Nation of Mistissini in 2017, now operated through the Nibiischii Corporation. FISHER activities in this region will help to provide the evidence-base required by the Nibiischii Corporation to fulfill its mandate by providing the same high-resolution genomic tools available to fishery managers in other larger jurisdictions in conjunction with traditional ecological knowledge to guide local management initiatives.

Dené (Great Bear and Great Slave Lakes) – FISHER will focus on Dené communities living near the two great lakes of the Northwest Territories (NWT): Great Slave Lake (GSL) and Great Bear Lake (GBL). Up to 50% of NWT residents rely on wild-caught animals for > 75% of their meat and fish. For most species, subsistence fishing has a considerably higher economic food-replacement value than their commercial counterparts (NWT 2005). The recreational fishing industry also generates > \$7 million/year in NWT from non-resident anglers (St-Louis 2006). Production of commercial freshwater fisheries in the NWT is estimated at 1000 tons per year with an economic value exceeding \$1.5 million (Tonn et al. 2016). The need to revitalize the NWT commercial fishery was recently highlighted by the NWT Government, and the GSL commercial fishery was identified as a priority to advance regional economic development and diversification, especially for aboriginal communities bordering the lake (NWT 2017). GSL accounts for roughly 90% of commercial landings in the NWT; 80% of GSL landings are of Lake Whitefish (Tonn et al. 2016). Given the dominance of Lake Whitefish, FISHER will focus on this species in GSL where, despite its importance, management is based on the assumption that it is supported by a single management unit because the Whitefish population structure in GLS is simply unknown, a crucial gap that FISHER will fill.

There are no commercial fisheries in GBL, but recreational fishing is an important contributor to the local economy and the community of Déline relies extensively on Whitefish and Lake Trout fisheries for their subsistence (TSÁ TUÉ Biosphere Reserve 2018). DFO has collaborated with Déline over the past 18 years to survey biological characteristics of these populations (Chavarie et al. 2013; Howland et al. 2014). However, assessments of population structure have been limited to a few microsatellite markers for Lake Trout (Harris et al. 2015) and have never been done for Lake Whitefish. An added complexity for fishery managers in GBL is the presence of extensive within-species phenotypic variability for both Lake Trout (Chavarie et al. 2014) and Whitefish, which will be addressed directly in Activity 2.2.

Objective: Genotype 7,000 fish from 6 different species with ~100,000 SNPs for all critical CRS fisheries identified by our local government and Indigenous partners in Inuit, Cree and Dené territories targeted by FISHER to define population structure and local adaptation based on genomic variation.

Methodology: *Sample collection:* We will genotype 7,000 fish samples from all 6 species targeted by Activity 2 (details in Table 2.1). Specific sampling locations will be based on their importance for local CRS fisheries, as determined by local partners in GE³LS Activity 5 (Sub-activity 5.1); estimated numbers of sampling locations are based on existing scientific knowledge of populations and ecotypes within each region, species, and Indigenous group (Fig. 2.1, Table 2.1). For Arctic Char, the species with the widest distribution in FISHER, sampling will further be guided by a recent broad-scale survey of microsatellite and mtDNA (Moore et al. 2015) to ensure that all known genetically distinct regions are represented.

Table 2.1. FISHES will broadly sample in partnership with local communities to include the relevant number of samples per species and sampling locations in order to inform the definition of genetically distinct populations. These samples will be obtained from local resource harvesters whenever possible and the exact sampling locations will be determined based on the priorities of the specific local indigenous partners. Species and regions where GWAS will be performed (Activity 2.2) are also indicated in this table.

Indigenous group	Region	Number of communities involved	Species	No. of sampling locations	Total no. of samples	Genotype-phenotype association
Inuit	Nunavut	18	Arctic Char	40	1600	No
	Nunavik	12	Arctic Char	20	800	No
		3	Atlantic Salmon	5	200	No
Cree	Mistassini L, Albnel L, Waconichi L	1	Lake Trout	10	400	Yes
		1	Brook Trout	10	400	Yes
		2	Walleye	20	800	Yes
	Mistassini L, Albnel L, Waconichi L, Waswanipi L, James Bay-Hudson Bay coast	5	Whitefish	20	800	No
			Brook Trout	15	600	No
Dené	Great Slave L.	5	Lake Whitefish	10	400	Yes
	Great Bear L.	1	Lake Trout	5	500	Yes
			Lake Whitefish	5	500	Yes
			6 Species	160	7000	

About 3,000 samples covering all target regions are already available, thus reducing potential risks associated with sample acquisition and allowing laboratory work to start quickly. Most samples, however, will be obtained by sampling programs put in place specifically for FISHES in collaboration with local partners (DFO, MFFP, GN, Makivik Corp, various Cree and Dené organizations) to train and employ local fishers whenever possible. Biological information of relevance to management (e.g., length and weight, catch-per-unit-effort, and otoliths for age determination), will be collected for all new samples.

Genotyping: We will genotype up to 40 fish per targeted sampling location using the ~100K SNP GBS assay developed for each species in Activity 1, a sample size sufficient to generate robust estimates of allele frequencies per population (Ruzzante 1998). Indeed, our previous work on Arctic Char has shown that 6,000 SNP and 40 individuals per sampling location provided sufficient power to detect population structure at a small scale despite low F_{ST} values (avg F_{ST} = 0.011; avg N = 43; Moore et al. 2017).

Bioinformatic and data analysis: Bioinformatic analyses will be performed by the bioinformatics team at IBIS using pipelines streamlined over 6 years of working with GBS data. Population structure will be inferred using model-based Bayesian clustering (ADMIXTURE) and model-free multivariate statistics (DAPC) (Moore et al. 2017). SNPs under divergent selection will be detected using monogenic (BAYESCAN, OUTFLANK) and polygenic (Additive polygenic scores) outlier methods (Babin et al. 2017). We will use redundancy analyses (db-RDA) to investigate the relative contribution of spatial distribution vs. environmental variables to both neutral and adaptive genetic variation. Environmental and climatic variables will be obtained from public databases (e.g., WorldClim, Fick and Hijmans 2017; Bio_ORACLE v 2.0, Assis et al. 2017). Neutral and putatively adaptive genomic variation will be combined for the definition of management units according to the framework of Funk et al. (2012).

Milestone 5. A reference database of neutral and adaptive SNPs for 6 species supporting CRS fisheries throughout northern Canada.

Sub-activity 2.2: Phenotype-genotype association among sympatric and allopatric populations

Context: Many of the northern lakes on which Indigenous people rely for fishing harbor significant within-species population diversity, probably as a result of low overall species diversity leaving many ecological niches unfilled (Schluter 1996). For instance, both scientific data and TEK recognize the presence of multiple Lake Trout ecotypes in Lake Mistassini (Marin et al. 2017), and in Great Bear Lake up to four Lake Trout ecotypes coexist (Chavarie et al. 2014). These ecotypes display variation in morphology, life history, ecology, and habitat use, with potentially important population-level consequences. For example, many ecotypes differ in term of growth rates, and growth plays a pivotal

role in impacting fish survival, longevity, and reproduction, which can in turn influence demography and fishery productivity (Chavarie et al. 2015). Understanding the genetic basis of divergent phenotypes adds a powerful layer of information when compared to surveys of genomic variation alone (Shafer et al. 2015), which can be achieved through phenotype-genotype associations (Nichols and Neal 2010).

Objective: Perform phenotype-genotype associations to identify the genomic basis of phenotypic variation within selected harvested populations to help refine fishery management on the basis of genetically-based variation in morphology, life-history, and ecology.

Methodology: We will document morphological and life history trait variation for a total of 3,000 fish (Table 2.1) among sympatric, parapatric, or allopatric populations previously described or that will be identified in this study. For phenotypic variation, and with the involvement of our local partners, we will collect age and size data to estimate growth rates for each population (Morissette et al. 2018). Morphological variation will be assessed using geometric morphometric methods (Chavarie et al. 2018). We will combine phenotypic and genotypic data to perform Genome Wide Association Studies (GWAS) to assess the genomic basis of phenotypic variation and infer their putative adaptive nature. This will be achieved using the polygenic framework provided by Random Forest, a machine learning algorithm to identify genomic regions that co-vary in association with measured phenotypes (Laporte et al. 2015).

Milestone 6. A reference database of SNPs associated with phenotypic variation for 5 species supporting CRS fisheries throughout northern Canada.

Deliverables for Activity 2. D2: A series of reports for federal government agencies (CSAS, DFO), Indigenous governments (Government of Nunavut, Kativik Regional Government in Nunavik, Cree Nation Government), provincial government agencies (MFFP) and non-governmental research partners (Nunavut Wildlife Management Board, Regional Wildlife Management Boards of Nunavut, Nunavik and Eeyou Marine Region Wildlife Boards, Makivik Corporation, Nayumivik Landholding Corporation (NLC)) describing how definition of genetically distinct populations in each water body investigated in this project could be used to enhance sustainable yields of harvested species in subsistence, recreational, and commercial fisheries. Given our team's longstanding partnerships with Indigenous communities and government agencies of FISHERIES, we envision that reassessment of similar genomic assays as in Activity 2 will take place 5-10 years post-FISHERIES in conjunction with local partners, to ensure long-term continuity.

Activity 3. Team: Fraser (Leader), Moore, Bernatchez, Harris, Zhu, Schott, April, Mulrennan, Tran **Genomics bio-monitoring for maintaining fish food security in strategic northern regions**

Combined with TEK surveys and traditional fisheries assessments (see Activity 5), genomic tools hold great potential for the accurate monitoring of changes to wild fish populations with direct benefits for northern food security. Activity 3 focuses on three monitoring approaches that have not been assessed for certain species or that in others, require greater genotypic resolution than in previous collaborations with our Indigenous partners and temporal re-assessment (Fraser and Bernatchez 2005; Dupont et al. 2007, Bernatchez & Dodson 1990). The three genomics monitoring approaches involve; i) quantifying mixed-stock harvests in CRS fisheries found within several coastal regions and large freshwater lakes, ii) estimating the contributions of hatchery fish generated by Indigenous-led hatcheries to subsistence harvests, and iii) tracking harvest-induced genomic changes in wild populations. Information on genetically-distinct stock identification (GSI) and parentage-based tagging (PBT) in mixed-stock fisheries is vital for refining quotas, monitoring the success of hatchery supplementation, avoiding overharvest of small populations, and improving other management tools (food sharing, social norms) (Beacham et al. 2018, Bradbury et al. 2014). In addition, fisheries may be size-selective in removing larger fish (Law 2000), so tracking if size-selective harvesting results in changes towards smaller, earlier-maturing fish is critical for preventing negative impacts to food security (reduced fisheries productivity or value; contamination levels in consumed fish) (Hard et al. 2008, Heino et al. 2015, Nussle et al. 2016). Given the complementarity between Activity 3 and 5, they will be undertaken in synergy, and involve close sharing and exchange of data and results as they come along through the FISHERIES project atlas (Sub-activity 5.3).

Sub-activity 3.1. : Contribution of different fish populations to mixed-stocked fisheries

Context: Most harvested fish species are comprised of multiple populations (Dupont et al. 2007, Beacham et al. 2018, Bradbury et al. 2014, Harris et al. 2015). Such populations mix temporally during specific parts of the life cycle where harvesting occurs (Beacham et al. 2018, 2018b; Harris et al. 2016a). The relative contribution of each population to harvest can vary inter-annually (Fraser and Bernatchez 2005; Dupont et al. 2007; Beacham et al. 2018, 2018b); larger populations may consistently provide a greater contribution to annual harvests, but local environmental fluctuations will also influence year-to-year productivity of individual populations (Schindler et al. 2010, Zimmerman et al. 2013). Therefore, there are ample demonstrations that it is critically important for sustainable harvesting and maintaining food security to quantify the relative contributions of discrete populations harvested in mixed-stock fisheries, to prevent overharvesting of small populations and to understand which populations are most productive over time (Schindler et al. 2010, Beacham et al. 2018, 2018b; Bradbury et al. 2014). Northern CRS fisheries regularly occur as mixed-stock fisheries (e.g. Fraser and Bernatchez 2005, Marin et al. 2016, 2017, Dupont et al. 2007, Harris et al. 2016a, Harris et al. 2016b, Moore et al. 2016).

Our Indigenous and government partners have emphasized that the lack of knowledge on the contribution of different fish stocks to the different CRS fisheries (see letters of support) is a major information gap for them to develop and enhance community-based sustainable fisheries management. For instance, it is important for them to know if disturbances in given breeding or rearing habitats of specific populations (e.g. due to hydroelectric dam construction or mining development as occurs in Northern Quebec and the Northwest Territories) will impact the local fisheries or more broadly depending on the scale of dispersal and the importance of the population to the fishery. This crucial information can be obtained by conducting Genetic Stock Identification (GSI) on several different CRS fisheries. Populations defined in Activity 2 will provide the necessary baseline data to perform effective GSI in mixed-stock harvests. In many regions, including Ungava Bay (Nunavik), Nunavut, James-Hudson Bay coast, Great Bear and Great Slave lakes, formal GSI will be conducted for the first time. In Mistassini Lake, past mixed-stock harvest assessments require greater resolution as well as temporal re-assessment in being conducted >15 years ago (Fraser and Bernatchez 2005, Dupont et al. 2007).

Objective: Our main objective will be to monitor the harvest contribution of genetically distinct populations to mixed-stock harvests that support the most important CRS fisheries for our Inuit, Dené and Cree community partners in different regions of northern Canada.

Methodology: During the four project years, and for each mixed-stock fishery based on one or multiple species of local interest (Table 2.1), the applicable Indigenous partners will receive training by FISHERS personnel to collect and properly preserve tissue samples from harvested fish for genomics research. Indigenous and governmental partners will also collect information pertaining to basic fisheries parameters: catch data including number of fish caught/species, size distribution, dates of capture, locations of capture, catch per unit effort, gear type, and otoliths for age validation. Collected data will be kept in databases and shared among all partners. **Complementary TEK surveys for each mixed-stock fishery through GE³LS Activity 5 (Sub-activity 5.3) will provide information from our Indigenous partners on longer-term temporal changes to seasonal fish movements and harvest rates.**

GSI is frequently used to assign harvested fish to large numbers of baseline populations (n=30-200) across large coastal regions, such as in Pacific or Atlantic salmon (Beacham et al. 2018b; Bradbury et al. 2018). **The situation for our CRS fisheries is much simpler:** our own past population genetic or GSI work, TEK surveys and consultation with Indigenous partners suggest that only a few to up to 10 distinct populations will comprise mixed-stock harvests in inland lakes (Great Bear, Great Slave; Mistassini and adjacent lakes) (Fraser and Bernatchez 2005; Fraser et al. 2006, 2013; Dupont et al. 2007; Bowles et al. 2017), along the James-Hudson Bay Coast (Bernatchez and Dodson 1990), or within Ungava Bay for Atlantic Salmon (J. April, MFFP, *pers. comm.*). These modest numbers of baseline populations and their moderate levels of population differentiation (e.g. Mistassini Walleye and Brook Trout $F_{ST} = 0.02-0.09$) will ensure accurate GSI using the 500 SNP Rapture assays developed in Activity 1 (Anderson et al. 2008;

Beacham et al. 2018b; Bradbury et al. 2018). **We do acknowledge, however, that in some unstudied regions or in particular cases, a compromise may need to be struck by conducting GSI at a regional level if population genomic structure is determined to be very shallow (Anderson et al. 2008; Beacham et al. 2018b).** We also emphasize that the focus of GSI of Arctic Char in Nunavut will be to assign harvested fish from CRS fisheries in three small, localized regions: Gjoa Haven and two others to be determined from the advice and consultation with the Regional Advisory Boards and the Government of Nunavut. A good example of how FISHERIES could rapidly contribute to the development of new fisheries comes from Cape Dorset where commercial quotas exist for two rivers located too far from the community for fishing to be profitable. Community members, however, have indicated that the fish they catch for subsistence near the community each summer are probably migrating from these stocks (J. Kennedy, pers. comm.). Genomic data in this case could confirm Char origin and facilitate the design of fishing regulations that promote the economic feasibility of a commercial fishery without compromising the sustainability of the harvest. Involvement of local partners (GN, Makivik Corp, RAB) will ensure that our sampling responds to local needs and directly contributes to the development of new fisheries in the short-term. **GSI in each region will only require several baseline populations because candidate baseline populations and their distributions are either already largely known or highly suspected from previous telemetry and genetic research, and local TEK surveys (e.g. Harris et al. 2015; Moore et al. 2016, 2017).** Proposed sample sizes for each baseline source population (n=40) in Activity 2 is consistent with several recent studies adopting similar numbers of SNPs for conducting GSI with high statistical power (Moore et al. 2014; Beacham et al. 2018b). The proposed sample sizes for each inland lake or coastal mixed-stock fishery (Table 3.1) are critical towards confidently estimating the relative proportion of catch that each fish population contributes to local harvests within each inland lake or local coastal region (Anderson et al. 2008). Across species, 12,500 fish will be genotyped using Activity 1's 500 SNP assays, as well as 500 additional walleye using the ~100K SNP assay for Activity 3.3. The contribution of each population to mixed-stock fisheries will be estimated using a variety of GSI analyses within the Rubias (<https://github.com/eriqande/rubias>) R package that can also accommodate multi-SNP haplotype data. Where applicable, GSI analyses will consider harvest contributions of different populations both in space and in time, which is critical for determining sustainable areas and timing of harvest, refining quota management strategies, and protecting fine-scale diversity that promotes food security (Schindler et al. 2010; Rogers and Schindler 2011).

Table 3.1. Sample size for each species in each region according to local needs and interest.

Species	Nunavut	Nunavik	Great Slave L	Eastern James-Hudson Bay	Mistassini L, Albanel L, Waconichi L, Waswanipi L	FISHERIES partners
Arctic Char	2000 ^a	1500 ^b				Inuit, DFO, MFFP
Atlantic salmon		1000				Inuit, DFO, MFFP
Whitefish			2000	2000		Dené, DFO, Cree
Brook Trout				1000	1000	Cree
Walleye					2500 ^c	Cree

^aGjoa Haven, two other local mixed-stock fisheries (to be determined); ^bActivity 3.2; ^cIncludes n=500 for Activity 3.3 with the 100K SNP array.

Milestone 7. A quantitative estimate of various stock contributions for 5 species supporting CRS fisheries throughout northern Canada.

Sub-activity 3.2: Identifying the origin of Arctic Char in a hatchery supplemented fishery

Context: Canada's North harbours large numbers of wild fish populations but they do not always occur close to Indigenous communities, limiting access to fish resources and exacerbating food insecurity (Nunatsiaq News 2017). Arctic Char do not occupy certain rivers near communities because natural waterfall barriers historically impeded their upstream migration to freshwater watersheds. Recently, the upstream access of Arctic Char to the Nepihjee watershed near Kuujuaq (Nunavik) was facilitated by dynamiting side channels around previously impassable falls. The community constructed a hatchery to facilitate the colonization and production of Arctic Char in the drainage. Considerable

resources are invested annually to stock large numbers of primarily early juveniles (~50,000-100,000 fry, with plans for increased production) and occasionally older juvenile life stages (age 3 months). Arctic Char now return to the Nepihjee watershed each year to spawn and overwinter though their exact numbers are unknown. They are harvested both here and in adjacent bays. It remains unknown whether harvested fish in the Nepihjee watershed originate from hatchery reared fish, fish born in the wild with hatchery ancestry, or from the progeny of wild fish that colonized the watershed from adjacent regions. The apparent success of the Nepihjee hatchery has generated interest in other regions where overharvesting in rivers located near a community has led to stock collapse, or where other opportunities for Char stocking may occur (e.g. isolated lakes adjacent to communities). Supporting the operations of the Nepihjee hatchery through applied genomic-derived solutions would contribute to the sustainable development of similar initiatives in other northern communities.

Objective: We will work with the Inuit community of Kuujuaq, the largest community of Nunavik, to seasonally and spatially identify origins of harvested Arctic Char in a region where Inuit-led hatchery supplementation is now implemented. Our Inuit partners are particularly interested in understanding the relative contribution of hatchery reared Char to the annual harvest of local Inuit, and which hatchery release strategies produce the most viable hatchery fish in the wild.

Methodology: The Arctic Char populations of Nunavik defined in Activity 2 and the Napukaaliuvik fish hatchery broodstock used for supplementation will serve as baseline populations to perform Parentage Based Tagging (PBT) of locally harvested Arctic Char. Our Inuit collaborators will provide samples from 1,300 Arctic Char harvested in fisheries located near the hatchery over successive study years (Kuujuaq area) which will be genotyped using the Rapture ~500 SNP assay, and where feasible, data on individual Char of relevance to fisheries management and assessments (size, sex, catch rates, locations of capture etc.). This sample size is necessary for adequately determining the contribution of hatchery-reared Char to local fisheries over successive years. The hatchery contribution will be quantified with PBT where the genotypes of individuals to be identified are matched to prospective parent genotypes used in the hatchery in previous years (another $n \sim 200$, based on a known number of wild adult males and females whose gametes were used to generate hatchery fish in different years). PBT will be carried out using SNPPIT (Anderson 2012), or COLONY (Wang 2016), which produces parental assignments when the genotype of one parent is missing. Among harvested Char of hatchery origin, we will also quantify the contribution of fish reared up to the early juvenile (fry) stage before release vs. released at 3 months. Such a comparison will provide invaluable information on how to optimize hatchery rearing practices to maximize the number of surviving adult hatchery-reared Arctic Char in the wild.

Milestone 8. A quantitative estimate of hatchery reared Arctic Charr contribution to a subsistence fishery in Nunavik.

Sub-activity 3.3: To identify genotype-phenotype associations for Walleye size-selective harvesting

Context: Fisheries harvesting is generally size-selective in catching faster growing, larger body-sized fish (Law 2000; Hard et al. 2008; Heino et al. 2015; Nussle et al. 2016). Body size, maturation and related traits are genetically heritable in fishes (Van Wijk et al. 2013). Hence, overharvesting induces the evolution of reduced size- and age- at maturation in fishes which in turn can affect the overall productivity and long-term sustainability of wild fish populations (Fraser 2013; Heino et al. 2015) and the food security they provide (Heino et al. 2015). Despite tremendous interest in understanding fisheries-induced evolution, few studies have had the necessary long-term life-history and genomic data to evaluate how rapid and to what extent fisheries-induced evolution may arise in wild populations, or the time required for recovery following a cessation of overharvesting (Heino et al. 2015).

Walleye are important for CRS fisheries across North America, including much of Eeyou Istchee territory within central and northern Quebec. In Quebec's largest lake, Mistassini Lake, our past collaborations with the Cree Nation of Mistissini integrated both TEK and scientific knowledge and have regularly consulted with local fishers for effective sampling and local management solutions (Fraser and Bernatchez 2005; Bowles et al. 2017, 2019). Using microsatellites, these collaborations determined that

several distinct walleye populations spawn in different tributaries (Dupont et al. 2007). Between 2000 and 2015 (about 1.5-2.0 walleye generations), the local human population expanded by 25% and tourism/sport fishing increased substantially (Bowles et al. 2017, 2019). Concomitant with these changes, Cree elders and fishers have consistently reported reductions in body size and catch rates in walleye populations adjacent to human development in southern Mistassini Lake (Bowles et al. 2019). In the most recent collaboration, our genomic work provided practical data for fisheries management by (i) determining the relative abundance of walleye populations; (ii) discovering that at least one local population is small and hence more susceptible to overfishing; and (iii) revealing that rapid genomic change associated with body size reductions is likely occurring in southern walleye populations, whereas northern populations with little harvesting show no life history or genomic change (Bowles et al. 2017; Bowles et al. 2019). Consequently, in consultation with the Cree Nation of Mistissini between 2016 and 2018, the community established a local public awareness program and management plan to reduce overexploitation of walleye in southern Mistassini Lake (e.g. see Cree Nation of Mistissini's Facebook page: <https://www.facebook.com/283179395149064/photos/a.365994666867536/1284147851718875/?type=3&theater>).

Objective: With FISHERS, we have an unprecedented opportunity to use powerful genomics tools to provide the Cree Nation of Mistissini with top-quality long-term population monitoring of southern Mistassini Lake walleye. Using the ~100K SNP assay along with assessments of TEK and life history monitoring, we will assess: (i) the genomic consequences of observed body size reductions in walleye, and (ii) whether recent management and public awareness initiatives within the community are leading towards a rapid reversal or partial reversal of genomic change following overexploitation.

Methodology: Our Cree collaborators will collect catch data (sex, body size, date of capture, tissue samples; catch-per-unit-effort) for Walleye from three southern Mistassini L. walleye populations where rapid, size-selective overharvesting has been documented, and where community-based conservation measures are being implemented for wild population recovery. They will also collect the same data from a northern population with low levels of exploitation for comparison. We will genotype 300 of these fish across population. Genotypic variation will be compared to 200 samples collected ~20 years ago before size-selective overharvesting effects were observed, and before community-based conservation measures were implemented. We will use GWAS to assess the genomic basis of phenotypic variation and to infer their putative adaptive nature using Random Forest as in Activity 2. Because genotype-phenotype associations may be population-specific (Rogers 2012), we will perform a GWAS of each population separately. We will use the Walleye reference genome to position SNPs and identify what potential candidate genes are in their vicinity. Thus, genomic regions in linkage disequilibrium with (or causative) SNPs that overlap with signatures of selection will offer strong evidence that these traits underlie harvesting-induced evolution or reversal from such evolution (Hirschhorn and Daly 2005).

Milestone 9. A reference database of SNPs associated with phenotypic traits impacted by selective harvesting in Walleye.

Deliverables for Activity 3. D3: A series of reports, guides and workshops for end-users and stakeholders (federal, provincial, Indigenous government agencies and non-governmental research partners listed in Activity 2) describing in-depth knowledge of mixed-stock harvests, harvest-induced genomic change, hatchery supplementation, and summaries of quantitative data collected by Indigenous partners for local fisheries assessments. The knowledge generated within these reports will form a critical basis maintaining and enhancing food security and socio-economic activities derived from CRS fisheries. Given our team's longstanding partnerships with Indigenous communities and government agencies of FISHERS, we envision that reassessment of similar genomics bio-monitoring activities will take place 5-10 years post-FISHERS in conjunction with local partners as has been done in specific regions for certain species (e.g. Mistassini L.: Bowles et al. 2017). The acquired new knowledge on Genetic Stock Identification will be crucial toward either; i) readjusting quotas that were established ~30-40 based on very limited scientific information (e.g. Arctic Charr in Nunavut or Whitefish in Great

Slave L., Walleye in L. Mistassini) or implementing the first harvesting quotas for Whitefish and Brook Trout along the James Bay Coast.

Activity 4. Team: Bernatchez (Leader), Moore, Fraser.

Assessing genomic signals of selection to predict fish stock vulnerability to climate change.

Current and projected patterns of climate change are a major concern to freshwater fisheries in Canada (Poesch et al. 2016). These changes particularly threaten the economic livelihoods of northern communities as well as their ability to feed themselves and maintain access to healthy food (NWT 2005; Usher 2002). Consequently, climate change is of major concern for our Indigenous partners. For instance, the Cree have increasingly observed more extreme weather events, unpredictable weather patterns, and seasonal shifts and changes in flora and fauna, and these changes are of utmost concern to them as they have an impact on their land access, food security and infrastructure (Cree Nation of Mistissini and the Cree Nation Government 2018). The latest projections indicate that air temperature will increase by 2°C–11°C by 2070 (depending on region), with greater warming in the north (Fig. 4.1).

In the Arctic, warming is occurring at a rate twice the rest of the planet (Solomon 2007). Precipitation will differ substantially from current patterns (Fig. 4.1) and water budgets will be affected by variations in the seasonal timing and magnitude of temperature and precipitation. These changes will impose new selective pressures to CRS fishes with important influences on their physiology, life history traits, spatial distribution, and survival. To develop management plans for the fisheries of these ecosystems, we need to understand and anticipate whether and how northern Canada's freshwater fauna will adapt to such dramatic and rapid changes. **Currently, the evolutionary potential of CRS fish species for adapting to a changing climate is simply unknown.**

Sub-activity 4.1: Multi-species genomic vulnerability along a climatic latitudinal gradient.

Context: The mismatch between environment and physiology can lead to shifts in species ranges, population declines or extinction (Urban 2015). The difference between these outcomes is determined by the adaptive capacity of different populations within a given species: those that possess standing genetic variation for climate-related traits are most likely to adapt to rapidly changing environments (Aitken et al. 2008). Recent studies showed that climate tolerances vary throughout species' ranges and will influence responses to ongoing climate change (Peterson et al. 2018; Stanley et al. 2018). Understanding the effects and distributions of potentially adaptive alleles associated with climate can therefore aid efforts to accurately predict species responses to future conditions (Bay et al. 2018). For instance, Finstad and Hein (2012) predicted that increases in temperature will impose new selective pressures that could decrease the range of anadromous, larger Arctic Char by 25%-50% relative to sedentary and smaller ones within the next 50 years. Identifying the number and effects of genomic regions underlying the expression of anadromy vs residency would improve our capacity to predict how different Char populations will react to climate changes depending on their genetic make-up.

To investigate which populations might be most vulnerable to future climate change, the metric “**genomic vulnerability**” has been defined as the mismatch between current and predicted future genomic variation based on genotype-environment relationships modeled across contemporary populations. Using this novel approach, a recent study identified genomic variation associated with climate across the breeding range of a migratory songbird (Bay et al. 2018, Fig. 4.2). They found that populations requiring the greatest shifts in allele frequencies to keep pace with projected future climate

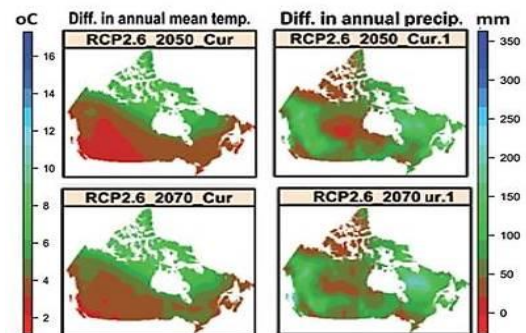


Fig. 4.1. Projected temperature and precipitation for 2050 and 2070 under two Representative Concentrate Pathways (RCP 2.6 Geophysical Fluid Dynamics Laboratory's [GFDL] CM3). (from Poesch et al. 2016).

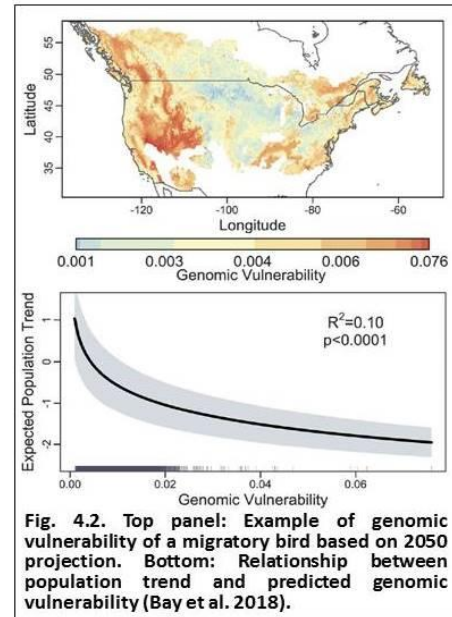
change experienced the largest population declines. This study shows that the integration of genomic adaptation can increase the accuracy of future species distribution models. A complementary approach to infer the adaptive significance of genetic diversity is to compare patterns of variation across multiple species (Stanley et al. 2018). Examination of population genetic variation across climate gradients may clarify the role of selection and adaptive variation as determinants of population structure (Kelley et al. 2016). When present, congruent multispecies spatial patterns may highlight important macro-ecological determinants of population connectivity and provide a window into future population structuring forces in aquatic ecosystems. For instance, this facilitated the identification of a multispecies biogeographic break aligned with a steep climatic gradient in the northwest Atlantic that was driven by seasonal temperature minima (Stanley et al. 2018). Such studies also shed light on constraints that shape adaptation to future environmental conditions (Yeaman et al. 2016).

Objective: We will compare patterns of adaptive variation across a climatic gradient among the three CRS anadromous salmonids inhabiting the east coast of James Bay, Hudson Bay: Whitefish, Brook Trout and Arctic Char. Our ultimate goal will be to quantify the vulnerability to climate change of different populations along this latitudinal gradient based on predictive modeling of “genomic vulnerability”.

Methodology: We will use samples of Whitefish, Brook Trout and Arctic Char from Activity 2 distributed from southern James Bay to the northern Hudson Bay. This represents a latitudinal transect of 1,200 km with a steep climatic gradient. Thus, the fish growing season (the number of degree –days > 5.0°C) varies from 200 to 1,000 from north to south and ice breakup differs by two months. Populations from these species exhibit a north-south gradient in life history traits (growth, fecundity and age at reproduction), suggesting adaptation to local climatic conditions (Morin et al. 1982). For each three species, we will analyse ~25 fish for each of 7 sampling sites/species along the gradient (total of 500 fish). Such sample size/population is comparable to that used by Bay et al. (2018). Patterns of genomic variation and quantification of genomic vulnerability will be analysed for SNPs and SV characterized for each individual fish using whole genome re-sequencing (Activity 1). For each sampling location, we will obtain current environmental data (from publicly available databases, e.g. WorldClim and NOAA World Ocean Database) and environmental conditions projected to 2050 under future climate change scenarios (RCPs) defined by the Intergovernmental Panel on Climate Change. We will use “Gradient forest”, a machine-learning regression tree-based approach to test if a subset of genomic variation can be explained by environment and to visualize climate-associated genetic variation across the study range (Ellis et al. 2012). We will then quantify a “genomic vulnerability” estimate as the mismatch (measured as the Euclidian distance) between genotypes and future environments using associations across current gradients as a baseline (Fitzpatrick and Keller 2015). This will be done for all populations of all three species and separately for SNPs and SVs. This will permit us to i) identify which populations (and which species by extension) are least likely to adapt quickly enough to track future climate shifts, and ii) quantify the relative effect of the two types of genomic variation on genomic vulnerability.

Milestone 10. Publically available genetic markers (SNPs & SV) to enhance our ability to forecast the response of three key CRS fish species fisheries to rapid global changes in northern Canada.

Deliverables for Activity 4. D4: We will provide a first multi-species assessment of genomic vulnerability underlining future climate adaptation (or maladaptation) in fish.



Managing data sets: Genomic data generated during the project will be handled on two Linux servers at the IBIS, with 64 and 148 CPUs and 1 and 2 To of RAM. The data will be managed by E. Normandeau, a bio-informatician with 5 years of experience in managing data from large-scale genomics projects, e.g. the LSARP EPIC4 project, which generated 11 TB of raw data, in the range of what is projected for FISHER (15 TB). Based on our past experience with similar projects, analyses should require an additional 20 TB of intermediate data, bringing the total disk space needed for the project to 35 TB on the local servers, plus 15 TB on a remote server for raw data storage, and two sets of IBM LTO-8 tapes for long term backup of the raw data, including one set of tapes stored offsite from the IBIS. Large datasets will be transferred among project collaborators using Globus (www.globus.org), a world leading large-scale data transfer solution used among others by Compute Canada and deployed on the IBIS servers. At the IBIS, B. Boyle will be leading the sequencing platform responsible for generating all the GBS data of the project (about 5TB). Boyle successfully delivered all of the GBS data for the EPIC4 project and, in collaboration with E. Normandeau and S. Larose, the server administrator at the IBIS, created an automated system for data delivery from the sequencers to the servers used for data analyses. S. Larose and J. Laroche, also bio-informaticians at the IBIS, will both be providing hardware and software support throughout the FISHER project. All the raw reads generated for the genomics activities will be archived on the Short Read Archive (SRA), the gold standard sequenced reads repository hosted by the NCBI. Data release will follow Genome Canada guidelines – see Appendix VI. The phenotype data consisting of morphological information for 3,000 fish analyzed using GWAS will also be backed up along with the genomic data on the local and remote servers as well as the tape archives.

Activity 5 (GE³LS). Team: Schott (Leader), Lemire, Mulrennan, Kenny, Moore, Fraser, O'Connor

Contribution of population genomics, bio-monitoring and TEK for fisheries co-management, and to enhance food security and socio-economic development in northern Indigenous community settings

Activity 5 comprises distinct GE³LS objectives, sub-activities, and deliverables that will collectively contribute to a respectful governance structure, knowledge accumulation process and research protocol for the overall project (Activities 1 through 5). As described above, several GE³LS activities, timelines and deliverables feed directly into the biological activities (namely, Activities 2-4). Therefore, Activity 5 (which spans the entire duration of the project) will be undertaken according to the timing of particular parts of the scientific activities, which will commence and terminate at different times for different regions and species. This project structure will foster genuine synergies and knowledge/data exchange between the genomic and GE³LS dimensions of the project, while ensuring Activity 5 is not restricted to the end of the project to ensure maximum benefits to the communities and knowledge-users involved. To facilitate this exchange, a FISHER Atlas (Sub-activity 5.3) will be created at the onset of the project, as an accessible platform of knowledge exchange and data sharing between GE³LS researchers, scientists, traditional knowledge holders and knowledge-users through all phases of the project. The FISHER Atlas will be used to advise research directions, provide project updates, data validation, and interpretation. An atlas has already been developed through TSFN and the GN NCRI making it feasible to make a similar platform available to all project partners at the onset of the FISHER project (within the first 6 months).

Activity 5 will build on the success of the knowledge co-evolution framework developed during the Genome Canada LSARP project *Towards a Sustainable Fishery for Nunavummiut* and further elaborated by Chapman and Schott (2019). This project engages diverse northern Indigenous regions in a participatory research process and involves the analysis of culturally-sensitive information pertaining to local, genetically distinct fish populations, fisheries harvests, fisheries conservation and management, and community food security. All research will abide by the Tri-Council Policy Statement on research with Indigenous Peoples, ITK's National Inuit Strategy on Research, and adhere to OCAP™ (Ownership, Control, Access, Possession), and all conceptual, methodological, and governance aspects of the project are guided by a commitment to develop and maintain equitable and mutually-beneficial research collaborations and processes (Sub-activity 5.1). The project framework develops a knowledge

coevolution framework that supports the co-generation of new knowledge informed by quantitative and qualitative data related to the biology of aquatic species and ecosystems, fisheries harvest, diet, and food security in addition to Indigenous knowledge and ontologies. Activity 5 will first provide a comprehensive overview and comparative analysis of the current legal, policy, and governance landscape (including customary and traditional institutions of stewardship) for fisheries management/co-management and conservation in each of the regions, existing stock and fishery/harvest assessments, and related harvester income security and food support programmes related to fish and seafood (Activity 5.2). In close partnership with each regional working group, we will examine the relative importance of key fish species for local food security (as defined by each region) within the context of species regional genetic diversity (Activity 5.2) and identify unique populations (as defined by Western scientific and Indigenous knowledge), preferred harvest locations, and harvest timing (Activity 5.3). Furthermore, we will explore socially, culturally, and ecologically sustainable economic development opportunities fisheries that would contribute to generating additional incomes, enhanced food security, business development opportunities, and overall employment (Activity 5.4). Collectively we will use these findings to inform and co-design strategies for each region that will support more effective fisheries co-management, better food security strategies, adaptation to climate change and the potential introduction or expansion of commercial or recreational fisheries (Activity 5.5). Insights and recommendations will address harvester support programmes across the regions, Nutrition North and regional social support programmes that strengthen food security.

Sub-activity 5.1: To formalize the knowledge co-evolution framework and project governance structure by establishing Regional Advisory Boards and the development of Community Research Agreements that clarify protocols, expectations, governance arrangements and intellectual property considerations in a mutually agreed-upon framework.

Context: Knowledge co-evolution requires the establishment of a research governance structure that places Indigenous partners at the centre of decisions about the research process. In response to this, Regional Advisory Boards (see Management Plan) will be setup at the outset to direct all stages of the research, and to make sure our findings are effectively communicated to the end users.

Objectives: To construct Regional Advisory Boards and to identify relevant regional data, policies, programmes and knowledge gaps.

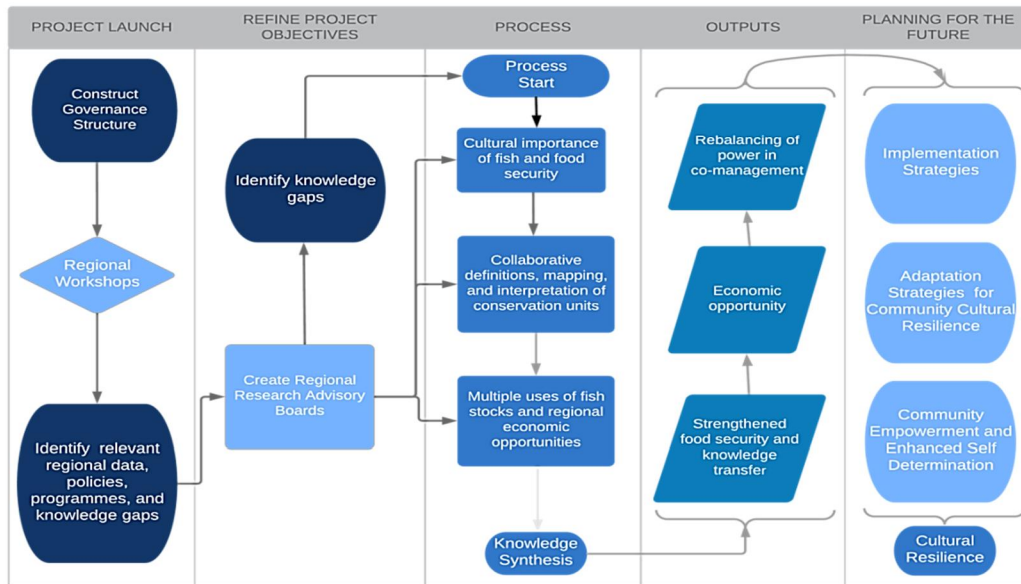
Methodology: We will co-develop the project with a regional advisory board comprised of **Indigenous community members and relevant researchers** in each region to steer joint research objectives and methodologies in the first year of the project. The former will include representatives from multiple sectors such as **the hamlet/Band office personnel, elders, hunters and fishers, health, social services and community wellness officers, educators and youth**. Activities of the regional advisory boards will be led by a remunerated community project coordinator in each region. Representatives of regional and territorial organizations (e.g. Department of Fisheries and Oceans) will participate in a related advisory committee, specifically addressing fisheries concerns in each region. The research governance and knowledge framework will oversee the development of Community Research Agreements and feed into regional food security strategies, cultural programming initiatives, and commercial fishery development plans, and will act as a platform for future co-management implementations.

We will organize four workshops, one for each main region (Nunavut, Nunavik, Great Bear/Great Slave Lakes, and Eeyou Istchee) that include representatives from all organizations relevant for fisheries management and food security in the region. Workshops will assist in identifying appropriate members for regional research advisory boards. Research advisory boards will be consulted on a regular basis on research process, results and changes and will meet with research team members on an annual basis.

All data and knowledge from the project will be collected and documented under the guidance of each regional advisory board and scientists that are partners on the research project. Collectively, we will identify knowledge and data gaps and what knowledge and/or data are of collective interest to be

gathered throughout the research process. Through this process we will advance a dialogic knowledge co-evolution and learning framework that will contribute to: (1) new knowledge creation that is beneficial to end users and for scientific and local understanding; (2) collaborative definitions and interpretations of distinct population structure; (3) better understanding of Indigenous institutions and stewardship to reduce power-imbalances in co-management, assessment and governance of fishery and wildlife resources; (4) understanding of cross-cultural engagement with fish and the role of fish in cultural identity and food security across regions; (5) local capacity-building for strengthening collaboration between regions, researchers, governments, and people.

Research process and steps



Milestone 11. To formalize the knowledge co-evolution framework and project governance structure by establishing Regional Advisory Boards and the development of Community Research Agreements.

Sub-activity 5.2: To document the role of fish in cultural identity and food security across regions

This will be achieved using a richly documented understanding, supported by community videos, of the contribution and significance of different fishes to cultural identity and food security in each region.

Context: Critical to the development of knowledge co-evolution will be the establishment of opportunities for local experts and community members to share their knowledge, perceptions, and concerns about the status and role of fisheries within their respective communities. This must occur in a manner that is founded in respect and is culturally appropriate for all participants. To support this, we will employ participatory methods used in community-based research that have previously been shown to be effective in supporting inclusive, productive knowledge exchange in a meaningful and respectful manner. Food sharing networks and barter systems vary in their contribution to local food security across Indigenous communities. To understand the relative importance of focal species for food security, food exchanges, and local economy, we aim to document the role of sharing and sharing networks and barter systems in and between communities in each region.

Objectives: We will identify what specific research direction is mutually desirable and how to conduct the research together. We wish to create new knowledge on the desirability and importance of any of the 6 in the regional context and what challenges people in the region face with respect to food security.

Methodology: As Judy Iseke (2013: 559) explains “Story is a practice in Indigenous cultures that sustains communities, validates experiences and epistemologies, expressed experiences of Indigenous

peoples, and nurtures relationships and the sharing of knowledge. Storytelling is also a central focus of Indigenous epistemologies, pedagogies, and research approaches.” Here, through local and regional workshops, we will identify the role of focal fish species for food distribution and sharing networks using story-based approaches, focus groups and interviews with key stakeholders. Workshops will be run with each fishery advisory board and with a representative sample of community members (e.g. in terms of gender, age, and household income). Photo-voice methodology and community videos will be used to create safe and productive spaces for engagement, knowledge exchange, and co-learning. Photo-voice methods allow participants to use photographs and stories associated with each photograph to convey issues that are of importance to them, allowing researchers and workshop participants to gain an understanding of the context and conditions of fisheries from the perspective of each participant. This facilitates the identification and articulation of particular obstacles and opportunities to enhancing the role of fisheries in local food distribution and sharing networks. We intend to follow the approach initially developed by Wang and Burris (1994) and subsequently refined for Indigenous community contexts (e.g. Castleden, Garvin, & Huu-ay-aht First Nation, 2008). While the method is not without its challenges (see Nykiforuk et al 2016), it has the advantage of offering an early and engaging approach to hearing local perspectives and voices on the role and status of fisheries and provides a foundation to support community-level discussion of those views.

Subject to the approval of participants, we also hope to use community video (also known as participatory video) to engage, honour and support Indigenous traditions and preferences for oral transmission of stories, histories, lessons and other knowledges. These videos will involve a group or community creating their own videos through a process that enables participants to articulate their personal and collective vision for fisheries to researchers, decision-makers and others. This will involve the collection of individual stories, followed by opportunities for storytellers to review their own story and listen to those of others before coming together to identify common themes and resonances about the shared context and lived realities of fishing today. The final product will be one that arises from an integrated visual collective storytelling process. We see this process as having the potential to invert or disrupt existing power relations (notably between researcher and the researched) by making space for Indigenous participants who hold the most knowledge of their own realities and context (Wheeler 2011). In this respect community participatory videos will be a key methodology in ensuring that Indigenous knowledge is given equal weight in this project.

Milestone 12. A richly documented understanding, supported by community videos, of the contribution and significance of fish to cultural identity and food security in each region.

Sub-activity 5.3: Collaborative definitions, mapping and interpretation of fish population structure, by performing an assessment and comparative analysis of the current and past regulatory environment, co-management regimes, distinct fish populations and market approaches for the distribution of fish through the creation of an online atlas to support knowledge exchange and mobilization.

Context: Scientific understandings and traditional methods of defining population structure may not always align. TEK provides multi-generational knowledge, often supported by customary institutions of stewardship that include guidance on culturally appropriate harvesting and sharing practices. Regional advisory boards will oversee contributions from local knowledge holders which will then feed into dialogue surrounding scientific data and indigenous knowledge. Following collective interpretation and deliberation, the potential for new knowledge outputs will be explored, including the generation of new hypotheses for further consideration. An important aspect of generating shared understandings concerns the communication of knowledge and interpretations across different knowledge systems. Previous research has found that incorporating maps and interactive Atlases has greatly improved knowledge translation in collaborative research projects (Taylor et al. 2006); using map-based data display provides a universal and well-understood medium to transfer and communicate complex information among knowledge systems. Beyond the typical place names, points, and polygons found on typical maps, online atlases (also referred to as cybercartographic maps) are designed to accommodate

various media, including audio-video files and data representations. These unique characteristics create a versatile conduit for knowledge recording and display suitable for all knowledge systems.

Objectives: Create knowledge exchange platforms to identify distinct fish populations and their importance for knowledge holders; compare and share governance/management approaches.

Methodology: Working with the research advisory board in each region, we will actively engage with local knowledge experts and active fishers in each region to gain a better understanding of “fish TEK”, how it has informed institutions of Indigenous stewardship and how (following the long-term, integrative TEK-science research conducted by Fraser et al. (2006, 2013) and Marin et al. (2017) with the inland Cree community of Mistassini) it can enter into dialogue with evolutionary biological knowledge at the population level. Using semi-directive interviews, collaborative fieldwork, focus group discussions, and mapping exercises we propose to extend this integrative approach to other contexts within Eeyou Istchee as well as other northern regions which would benefit from a dialoguing of TEK and scientific knowledge to identify unique populations of focal fish species. Preferred harvest locations, harvest timing, and harvesting techniques will also be established alongside information on the cultural importance of different species and their role in food security, sharing practices and changes in food supply in each region (Activity 5.2).

To facilitate knowledge exchange and mobilization throughout all facets of the project (e.g. genetic relationships between populations, community valuations and preferences, and quotas), and with the collaboration of Dr. Fraser Taylor, we will create a number of online Atlas using the cybercartographic software Nunaliit, developed by the Geomatics and Cartographic Research Centre located at Carleton University. This software is used across the Arctic by numerous academic and community-led research groups including S.Schott in the current LSARP Towards A Sustainable Fishery for Nunavummiut project (S. Schott et al. 2018), as well as by the Government of Nunavut for their Nunavut Coastal Resource Inventory (NCRI (<https://gov.nu.ca/environment/information/nunavut-coastal-resource-inventory>)). These Atlases accommodate a variety of data types, including small- and large-scale observations, place names, audio and video recordings, and documents (Rochette and Blanchet 2007). We will use the atlases to facilitate local and traditional knowledge recording in communities and enhance communication between and among communities and researchers. The ultimate goal is to produce a centralized Atlas that overlays scientific results (Activities 2-4), federal and regional fishery management strategies, traditional and local knowledge, and any other information determined to be of interest for community members and/or end users. This product has the potential to enhance the co-management process by providing a holistic, interactive visualization of information relevant for improved decision-making, by enabling communities to access data previously difficult to obtain and interpret.

In collaboration with the Government of Nunavut’s Department of Environment, we will hold workshops demonstrating the utility of Nunaliit in each region (one in Yellowknife, one in Qikiqtarjuaq (Baffin), one in Eeyou Istchee and one in a community in Nunavik). Each workshop will demonstrate the latest species observation data from the NCRI for the region and discuss how the data could be used for the benefit of regions and communities. We will work with communities to determine how the data collection process could be refined and improved to address the objectives determined for each region. Collaborative research planning will occur in specific communities (determined through activities 5.1, 5.2, 5.3) to identify what information is of interest (e.g. documentation of TEK, subsistence fishing sites, travel routes, areas of rapid change, hazards on the land and ice, etc.). This will inform the development of community-specific atlas platforms. If communities decide they would like to have their own Atlas, a training workshop involving youth and elders selected by community representatives will be held to collect and record information that is deemed important for the community. Youth trained to input data in to the Atlas will have the ability to continue adding information outside of the training workshop such that data collection can occur independently of researchers. All atlases will, however, use the same coding and software so that they can be linked if communities see value in sharing their data. In addition to the community Atlases, we will focus on a unique Arctic char Atlas that will incorporate

population structure and harvest restrictions (e.g. quotas, recreational fishing guidelines and traditional harvest rules), the history and current status of Arctic char fisheries (e.g. open, closed), and locations where research is ongoing (e.g. test fisheries). This type of spatial representation of these data currently only exists for the Gjoa Haven, Nunavut, and is of great utility to communities and fishery co-managers. Based on previous research in Nunavut, many communities, regional or local organizations, and government departments are not fully aware what quotas and data already exists, where it is documented, and how it is spatially distributed.

As described above, the FISHERS project Atlas will be also updated consistently throughout the project, ensuring communities are up-to-date with regards sampling locations, project progress and preliminary results, specifically population structure, which can be layered with fisheries data presented in the Arctic char Atlas when applicable. If communities are interested, local information, such as areas important for subsistence fishing, can be included in the FISHERS Atlas. This atlas will facilitate interpretation of interactions among distinct populations within different species, current and historical commercial fisheries, and subsistence harvest by communities and resource managers. Understanding such interactions allows communities and resource managers to identify areas where distinct populations are suitable for increased harvest, may be vulnerable to over-harvest, or are not well understood, allowing them to better manage fisheries resources in a culturally sensitive manner in their regions.

Milestone 13. A comprehensive overview and comparative analysis of the current and past regulatory environment, co-management regimes, conservation units of fish and market approaches for the distribution of fish through the creation of an online atlas.

Sub-activity 5.4: Perform a regional valuation of fish stocks from a cultural and economic perspective, by providing a comprehensive understanding of how fish are valued by current and potential user groups, including their cultural significance and economic opportunities tied to tradeoffs between subsistence, commercial, recreational, and conservation purposes.

Context: Providing a culturally and economically sustainable development plan for community fisheries requires a comprehensive understanding of how fish are valued by current and potential user groups. This not only includes Indigenous communities but also alternative users such as commercial and recreational fishers and conservation groups, and can be valued in economic and cultural terms. Valuation may also be influenced by new knowledge available from the outcomes of Activities 2-4; updated information on population structure and mixed-stocks fisheries, combined with documented traditional knowledge of historical distributions may reveal trends that affect user group's perspectives of fisheries cultural and economic worth.

Objectives: We will value multiple and alternative uses of fish species in each region for subsistence, cultural, recreational, commercial and conservation purposes.

Methodology: Building on the outcomes of 5.1 and 5.2 we will evaluate the relative value of focal species for different uses that are common and culturally appropriate in each community setting. We will compile information gathered in focus groups and use this to inform the design of specific focus group sessions to better understand past and potential uses of focal species by season and location, and culturally appropriate alternative practices and uses of various fishing grounds by season. We will try to determine how local end users would substitute fishery resources in the context of altered use patterns. To characterize valuation structures, we will use random utility and discrete choice models (McFadden and Train 2000) to estimate values. Surveys and interviews with local and external fishers will be administered concerning the economic and cultural value of different types of fisheries to assess willingness to accept changes (stakeholders) and to pay for alternative use of fishery resources (commercial, increased subsistence, recreational, or conservation) (Ditton and Sutton 2004). The survey will be given to a representative sample of local fish resource users, selected with guidance from the regional research advisory board, who will be asked about their preferred choices of using different fishing areas for subsistence, commercial, recreational, and conservation purposes. Various scenarios and choices will be presented that will allow us to estimate the relative value of tradeoffs (both spatially

and seasonally). To characterize the valuation structures of nonlocal alternative user groups, we will conduct focus group sessions with three different groups: commercial fish buyers, sport fishers, and conservation agencies (e.g. NGOs and government Departments). The purpose of the focus groups will be to understand what the preferences of the groups are in terms of fishery resource use and valuation (Oh et al. 2005). Based on focus group results we will design a web-based survey targeting recreational, commercial and conservation minded stakeholders. The survey will be constructed to elicit the valuation of alternative uses of fisheries resources in various areas of our research project. Participants will be contacted using publically available email addresses listed on their organization's website, on social media, as well as through established networks within the commercial and recreational angling community (e.g. NOAA, American Fishery Society). We will complement stated data from our surveys with revealed data from existing harvest studies (Lysenko and Schott 2019), (Priest and Usher 2004).

Following the completion of initial valuation, a follow-up survey including new information about the sustainability of fish stocks, and climate changes induced vulnerability and changes gathered through Activities 2-4 will be conducted to assess how the new knowledge has impacted each user group's assessment of the value of relevant fisheries. Results from our surveys and focus groups will inform us about overlaps and inconsistencies in the desired uses of fishery resources between local resource users and potential alternative users, and inform local communities about most preferred potential alternative uses and what type of compensation could be expected if they redistributed access to specific locations or in specific seasons. The incorporation of follow-up surveys will allow the assessment of how new knowledge co-generated through a dialogue of genomic assessment and TEK influenced the economic and/cultural valuation of fishery resources. This information can be used to improve study design and safeguard against any perceived negative impacts of new knowledge on cultural valuation in the future. Our unique and novel insights could inform the design of further studies of this kind in Canada and other remote areas worldwide, and be the basis of a framework to evaluate the relative merit and appropriateness of alternative uses of fisheries.

Milestone 14. A comprehensive understanding of how fish are valued by current and potential user groups, including their cultural significance and economic opportunities tied to tradeoffs between subsistence, commercial, recreational, and conservation purposes.

Sub-activity 5.5: Planning for the future for more effective use and conservation of fish stocks co-management governance for fisheries management in the context of climate change.

Context: Sustainable harvest practices are inherently linked to stable food security for communities that practice subsistence harvesting, yet the depth of these links and how they are directly related to the numerous dimensions of food security, support programs, economic development and conservation remains unknown. Past research projects have characterized various aspects of both dietary and health information in three geographically distinct regions of the study area (Nunavut, Nunavik and Eeyou Istchee) creating an opportunity to gain further insight into the nuanced and intricate relationship between fisheries harvest and long-term, ecologically sound conservation practices and food security. In Activity 5.5, we will work with our project partners to co-construct evidenced-based (scientific, local, and traditional knowledge) adaptation strategies to promote food security and sustainable fish harvests in the context of environmental changes.

Objectives: To provide a vision and strategy for sustainable development and food security for each region, to provide insights, lessons for concrete steps moving forward.

Methods: We will integrate project data and genomic knowledge with existing data, traditional and Western science knowledge on fish harvest, stock assessments, local diets, population demographics and contextual factors (Activities 5.2 – 5.4) to examine relationships between ecological and management factors, fish harvest, and different dimensions of food security and sustainability. To do so, we will also leverage existing dietary and health information from three culturally and geographically distinct Indigenous regions (Nunavik, Nunavut and Eeyou Istchee, based on the availability of existing diet/health studies). Scenarios of past (1980 to present) and future (the year 2030 & 2050) changes in

the supply of local fish (i.e. projected changes in biomass, by species and conservation unit) will be explored through the development of dynamic ecosystem models. Dynamic ecosystem models are effective tools to examine past and future impacts of climate change on marine ecosystems and have been applied in hundreds of ecosystems around the world, and used effectively to develop optimal fishing and marine management policies in various global regions (Colléter et al. 2015). These models make it possible to estimate previously unknown ecosystem parameters (e.g. biomass by species).

The methodology for the development of dynamic ecosystem models is described more comprehensively elsewhere (Hoover et al. 2013, Suprenand et al. 2018, Blanchard et al. 2002). Using the ECOPATH with ECOSIM modelling framework (Christensen and Walters 2004), we will use local biophysical and harvest data to examine potential changes to the abundance of fish and fish harvests e.g. the various culturally important fishes included in this study) for each of the participating FISHERIES regions (based on availability of local aquatic species data). The resulting biomass/species from the dynamic ecosystem models will be used as the basis for discussion at the Regional Workshops where the results will be used to develop community-relevant scenarios of future fisheries harvest (e.g. the development of a new local fishery to support food security). To understand what strategies can be used to proactively respond to climate change and to support food security and sustainable harvest and consumption at the community, regional/territorial level over the longer term, we will solicit local perspectives through workshops regarding how the regions would like to respond to projected changes in fish supply to ensure food security in the long term; what policies and programs at regional/territorial levels can support the community in responding to changes to ensure food security over the long term, and identify how community-identified strategies that support food security under climate change can be supported by programs, initiatives, and policies at the regional and territorial levels. We will prepare communities and regions that are interested in commercial fishery development for transitioning to the Northern Integrated Commercial Fisheries Initiative (NICFI) that is managed by DFO in collaboration with the various Regional Advisory Boards. This will lead to the production of a regional lessons learned report for more effective use and conservation of fish stocks and a Best Practice guide for more effective co-management governance for fisheries management in the context of climate change.

Milestone 15. A regional lessons learned overview and guide to plan for more effective use and conservation of fish stocks co-management governance for fisheries management in the future.

Deliverables (D) for Activity 5: D5: A forum for the exchange and co-generation of knowledge and insights on CRA fisheries development and co-management, informed by a shared understanding and respect for different contexts, values, and priorities that includes:

- A knowledge co-evolution framework for northern fisheries development and co-management
- Comprehensive documentation in reports and locally accessible forms, including community videos, images, drawings and recordings of stories and experiences of the contribution of fisheries to food security and cultural identity.
- Interactive online atlas tools to communicate and share information and findings on alternative definitions and values, as well as shared understandings of fish population structure, governance institutions, current and past regulatory regimes.
- Value estimations of CRA fisheries harvest by community and type of fishery including commercial, subsistence and recreational fishery existing and potential opportunities

D6: Implementation strategies for collectively derived objectives (at both community and regional levels) and future visions (such as development of a fisheries policy and its implementation for Nunavut, or a strategy to enhance the use of certain fish species in certain regions as a food source).

FISHERIES will provide the collective genomic and social (GE³LS) knowledge base and tools required to support the sustainability of major inshore/inland CRS fisheries and access to safe, nutritious, and culturally-preferred food for Indigenous people in Northern Canada. It will also generate tremendous opportunities for comparative genomics, fisheries science and TEK research synergies across regions.

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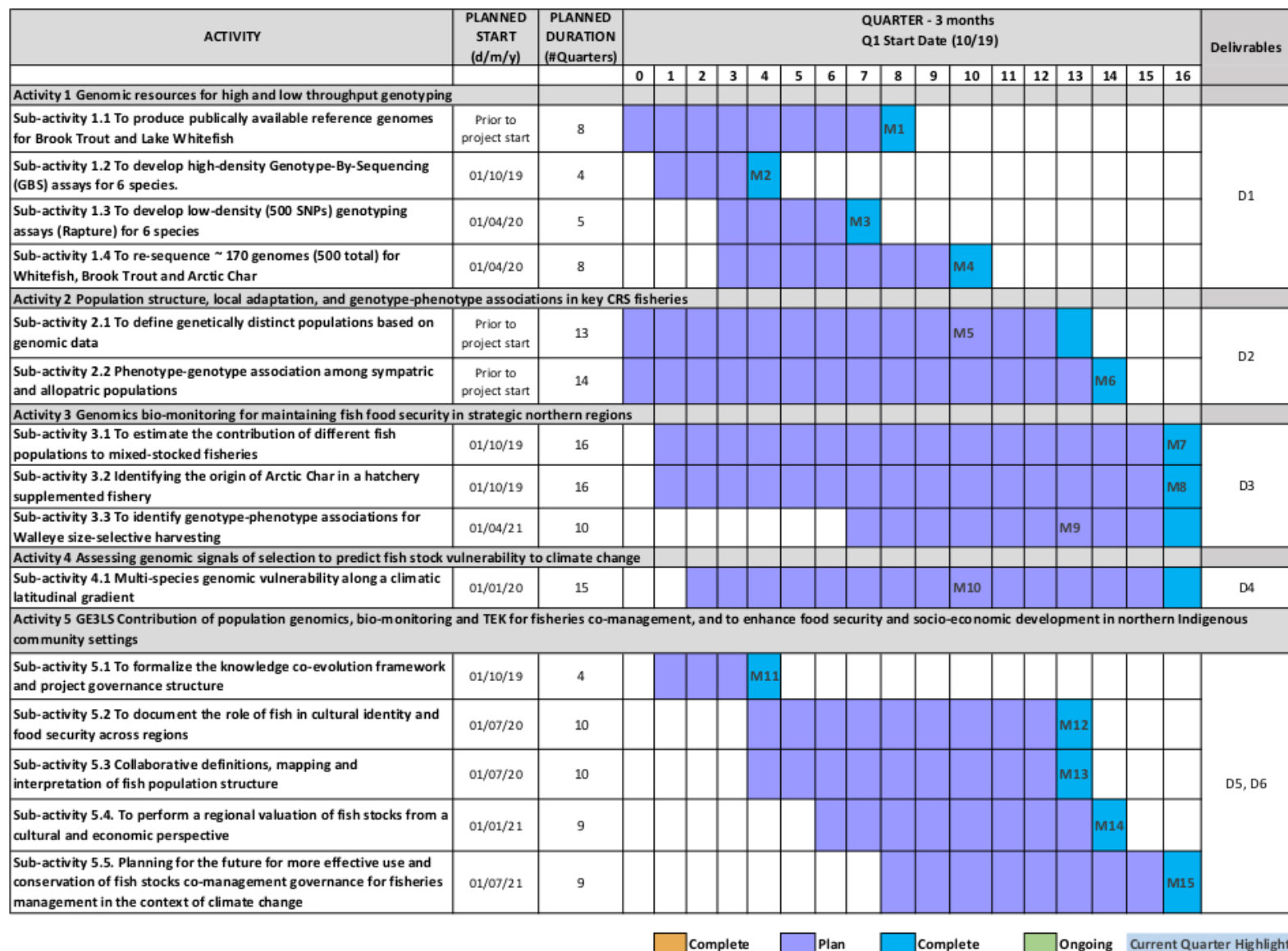
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GANTT CHART

Some of our GE3LS activities feed into the biological activities (namely 2 and 3). Although these Activities span almost the whole timeline of the project, specific activities commence and terminate at different times for different regions and species. Therefore, GE3LS deliverables will fit accordingly in timing to particular parts of the genomics activities when they take place, and they do not have to wait to the end.



Milestones

- M 1.** The production of a publicly available reference genome for Brook Trout and Whitefish.
- M 2.** The production of a ~100,000 SNPs GBS assay for each of the 6 FISHES species.
- M 3.** The production of a ~500 SNPs Rapture assay for the 6 FISHES species.
- M 4.** Production of ~ 170 whole genome sequences for Whitefish, Brook Trout and Arctic Char.
- M 5.** A reference database of neutral and adaptive SNPs for 6 species supporting CRS fisheries throughout northern Canada.
- M 6.** A reference database of SNPs associated with phenotypic variation for 5 species supporting CRS fisheries throughout northern Canada.
- M 7.** A quantitative estimate of various stock contributions for 5 species supporting CRS fisheries throughout northern Canada.
- M 8.** A quantitative estimate of hatchery reared Arctic Charr contribution to a subsistence fishery in Nunavik.
- M 9.** A reference database of SNPs associated with phenotypic traits impacted by selective harvesting in Walleye.
- M 10.** Publically available genetic markers (SNPs & SV) to enhance our ability to forecast the response of three key CRS fish species fisheries to rapid global changes in northern Canada.
- M 11.** To formalize the knowledge co-evolution framework and project governance structure by establishing Regional Advisory Boards and the development of Community Research Agreements.
- M 12.** A richly documented understanding, supported by community videos, of the contribution and significance of fish to cultural identity and food security in each region.
- M 13.** A comprehensive overview and comparative analysis of the current and past regulatory environment, co-management regimes, conservation units of fish and market approaches for the distribution of fish through the creation of an online atlas.
- M 14.** A comprehensive understanding of how fish are valued by current and potential user groups, including their cultural significance and economic opportunities tied to tradeoffs between subsistence, commercial, recreational, and conservation purposes.
- M 15.** A regional lessons learned overview and guide to plan for more effective use and conservation of fish stocks co-management governance for fisheries management in the future.

Socio-economic deliverables (D)

- D1: A set of genotyping assays for stock and conservation management that includes:**
 - a:** A comprehensive inventory of SNP and SV variation in Whitefish, Brook Trout and Arctic Char to assess the genomic vulnerability of these exploited species to future climate change;
 - b:** Genomics-based technologies (high and low-density genotyping assays) to conserve enhance and manage anadromous/freshwater species for food security and economic development of Indigenous communities throughout northern Canada and elsewhere;
 - c:** Genomics-based technologies to develop new aquaculture broodstocks and hatchery-based production of Arctic Char by Inuit communities in Nunavik and elsewhere.
- D2:** A series of reports and guides for end-users and stakeholders describing how adoption of CUs in each water body investigated in this project can inform management practices toward ensuring long-term sustainability of harvests in CRS fisheries in the different areas under study.

D3: A series of reports, guides and workshops for end-users and stakeholders (federal, provincial, indigenous government agencies and non-governmental research partners) describing in-depth knowledge of mixed-stock harvests, harvest-induced genomic change, hatchery supplementation, as well as summaries of quantitative data collected by indigenous partners for local fisheries assessments. The knowledge base generated within these reports will form a critical basis maintaining and enhancing food security and socio-economic activities derived from CRS fisheries.

D4: A report documenting the genomic vulnerability of Whitefish, Brook Trout and Arctic Char along the James-Hudson Bay Coast in the face of future climate change, thus contributing to our ability to forecast the response of key fisheries in northern indigenous communities.

D5 (GE³LS): A forum for the exchange and co-generation of knowledge and insights on CRA fisheries development and co-management, informed by a shared understanding and respect for different contexts, values, and priorities that includes:

- A knowledge co-evolution framework for northern fisheries development and co-management underpinned by Community Research Agreements and overseen by regional Research Advisory Committees.
- Comprehensive documentation in reports and locally accessible forms, including community video, photographic images, drawings and recordings of community stories and experiences to be co-produced with community members, of the contribution of fisheries to food security and cultural identity.
- Interactive online atlas tools to communicate and share information and findings on alternative definitions and values, as well as shared understandings of fish population structure, governance institutions, current and past regulatory regimes, fisheries adaptive co-management arrangements, etc.
- Value estimations of CRA fisheries harvest by community and type of fishery including commercial, subsistence and recreational fishery potential (based on community and regional preferences) and existing commercial quotas, predictions of local or regional fish species availability and stock abundance over time.

D6 (GE³LS): Implementation strategies for collectively derived objectives (at both community and regional levels) and future visions (such as development of a fisheries policy and its implementation for Nunavut, or a strategy to enhance the use of certain fish species in certain regions as a food source).

VII EXPECTED SOCIAL AND/OR ECONOMIC BENEFITS

Maximum of eight (8) pages, including charts, figures and tables (the list of references is not included in the page limit). This section must address all relevant evaluation criteria for the competition. Include a plan for knowledge translation and development of benefits, which outlines the next steps of how the deliverables from the research will be transferred, disseminated, used, and/or applied to realize social and/or economic benefits.

Context. Commercial, recreational and subsistence (CRS) fisheries offer exceptional opportunities to enhance food security, regional/community economic development, employment creation, and capacity building – major social, cultural and economic challenges – throughout Northern Indigenous regions of Canada. Yet the full potential of CRS fisheries has not been reached despite strong political support for their development in many northern Indigenous regions/communities. For instance, most of the commercial fishery development in the Arctic has focused on the offshore sector. A developed inshore/inland sector could provide steady employment and income opportunities for a much more widely distributed population across the entire region, in harvesting, processing, transport and marketing of the fish. In addition, inshore/inland CRS fisheries provide important multiplier effects through indirect benefits such as retail expansion, restaurants and tourism. Inshore/inland CRS fisheries are far more compatible with Northern lifestyles and a mixed economy that depends on a **complex interplay between subsistence and wage-based activities**, with households balancing time and resources derived from each (i.e. elements of a cash-based economy are often required to support harvest such as the purchase of harvesting equipment, gas and supplies). These fisheries also maximize local employment opportunities by allowing fishers to live, work and develop transferable skills in the local economy. For example, respectively, Pangnirtung Fisheries' Arctic Char and Turbot facility and Cambridge Bay Kitikmeot Foods Ltd. provided 35 jobs in 2011–2012 (NDC, 2012) and employed 28 local residents and beneficiaries in support of the Arctic Char commercial fishery in 2012 (DFO 2013). There is, clearly, great potential for local job creation in a number of CRS fisheries across Northern Canada, such as commercial Arctic Char (Senate Committee on Fisheries & Oceans, 2010) and Whitefish in Great Slave and Great Bear Lakes (NWT 2017).

Unfortunately, despite their immense potential, northern fisheries do not benefit from the same cutting-edge scientific information available to fishery managers in southern Canada, thus creating inequity disfavours northern Indigenous communities. Indeed, there are insufficient scientific data to facilitate sustainable CRS management practices in a rapidly changing Northern environment, and management/governance issues both represent major barriers to expansion of these fisheries (Poesch et al. 2016). Increased shipping, tourism, and extractive industries (e.g. mining exploration and development) in the North also pose serious risks for aquatic biodiversity and fisheries, and climate-induced changes will have consequences for the geographic distribution and abundance of fish. Collectively, these factors may threaten economic livelihoods, traditional fish harvesting practices, and healthful food access for northern communities. Thus, mitigating and adapting to, the potentially negative impacts of threats on northern fisheries, while enchainning the social and economic benefits of fish harvests, is crucial for communities who are tied to fish for various facets of life.

FISHES will provide the collective genomic and social (GE³LS) knowledge base and tools required to support the sustainability of major inshore/inland CRS fisheries and access to safe, nutritious, and culturally-preferred food for Indigenous people in Northern Canada. By working in close partnership with end-users from local and regional resource management agencies (comprised of Indigenous, public and governments from community, territorial/provincial and federal levels) the project will contribute directly to tailored and cost-effective solutions to pressing northern fisheries management challenges. We will first establish regional advisory boards to both guide our research team and help local communities to address challenges that they feel are crucially important for social, human and

economic development in their region. The established research process and governance structure will create important capacity for fisheries management and strengthen traditional and local knowledge and cultural identity. State-of-the-art genomics resources for six harvested fish species will then be used to; i) define genetically distinct populations; ii) quantify their contributions to mixed-stock harvests and iii) the contribution of hatchery programs to subsistence harvest; iv) assess the impact of overharvesting, and v) predict the genomic vulnerability of exploited populations to climate change. Genomic information will be considered along with TEK to generate several socio-economic benefits, including a knowledge co-evolution framework that will feedback to: (i) foster and develop sustainable CRS fisheries in Canada's North; (ii) engage, knowledge exchange and co-learning processes for sustainable fisheries developing in northern Indigenous communities and regions; (iii) forecast the response of key fisheries to global and socio-economic changes in northern Indigenous communities, and (iv) model the links between fisheries and different dimensions of food security and biodiversity conservation over time.

As previously noted, the full potential of CRS fisheries has not yet been reached, and insufficient scientific data exist to guide their sustainable economic development in a rapidly changing Northern environment. For instance, demand for Arctic Char far exceeds supply; current commercial harvest averages only 85 mt/y (Roux et al. 2011) but the fishery has an estimated total of 790 mt of potential commercial quota in Nunavut alone (Government of Canada 2018). Quota is simply not taken because of insufficient or outdated scientific information and the lack of support to start fishing operations; most available Char (705 mt) is unharvested and could contribute **\$18 million annually** to Nunavut's economy. In fact, the Government of Nunavut conservatively estimated a **total food replacement value for Arctic Char of at least \$7.2 million**. Based on the *Nunavut Wildlife Harvest Study* (NWHS), **~532t of Arctic char are harvested annually in the territory** (197,000 Arctic char, average mass of 2.7 kg/fish (DFO, 2014)), representing **~\$13M in landed catch for this species alone** (using a commercial shipping price of \$24/kg (Kitikmeot Foods Ltd, Nunavut; DFO 2013)). In Great Slave Lake, commercial harvest of Whitefish and Lake Trout peaked at 3.9 million kg/yr in 1950, but catches have been < 0.5 million kg/yr since 2007 (Tonn et al. 2016). Long important for subsistence (total 700 mt/yr; ~75 kg/yr/person; Berkes, 1990), Great Slave's fisheries are the target of a revitalization to bring commercial production back to historical levels (1.3 million kg/yr by 2021). That is a value of **~\$16.5 million/yr** (~\$24/kg for processed fish, 40% of total lake production; \$5.20/kg for unprocessed fish (NWT 2017)). In Great Bear Lake, past total harvest was 900 mt/yr (3t per family/y), and the lake harbours world-renowned sport fishing lodges that generate substantial revenues (e.g., <https://www.plummerslodges.com/>). Comparable subsistence fisheries data for Cree regions were a total of 320mt (51 kg/capita/yr) for James Bay and 233 mt (59 kg/capita/yr) for northern Quebec (Berkes, 1990). Indigenous fish harvest in the early 1980s was ¼ of the total subsistence food harvest, 6X higher than average Canadian consumption of 7kg/capita/yr (Berkes, 1990). Northern Quebec's major inland lakes (e.g. Mistassini, Albanel, Waconichi) are also important centers for Indigenous-operated sport fishing camps and lodges (e.g. Osprey Lodge: <https://www.escapelikeneverbefore.com/en/members/osprey-lodge/81/outfitters/>; Nibiischii Wildlife Reserve: <http://www.nibiischii.com/>). These seasonally employ dozens of Cree fishing guides and community members. In Mistassini L. alone, visiting recreational fishers generate >\$0.6 million/yr through direct/indirect purchases in Cree communities (C Mianscum, Cree Tourism, *pers. comm.*).

Deliverables. FISHES comprises **six deliverables** that are organized into scientific (genomic) and social (GE³LS) categories, though these are inseparably linked through the fisheries co-management process: **D1)** Genomic resources and assays to inform CRS species management for food security and economic development in northern communities; **D2 & D3:** A series of reports and guides for end-users and stakeholders describing how knowledge of genetically distinct populations (**D2**) and mixed-stock harvests, hatchery supplementation and quantitative data collected by Indigenous partners (**D3**), can provide guidance on management practices to ensure the long-term sustainability of CRS fisheries; **D4)** A first assessment of genomic vulnerability underlining future climate adaptation, contributing to our

ability to forecast the response of key fisheries to rapid global changes in northern Indigenous communities; **D5 (GE3LS)**: A forum for the exchange and co-generation of knowledge on CRA fisheries development and co-management, informed by a shared understanding for different contexts, values, and priorities; **D6 (GE3LS)**: Implementation strategies of collectively derived objectives and future vision (development of a fisheries policy and its implementation, strategy to enhance the use of fish in certain regions as a food source).

Detailed genomics deliverables. Our first deliverable (**D1**) will be the generation of four types of genomic resources and genotyping assays to conserve and manage CRS species for food security and economic development of Indigenous communities throughout northern Canada, for local Indigenous and government-based managers and related end users. First, we will develop well-annotated reference genomes of Brook Trout and Lake Whitefish for the public and scientific community, the first such whole genomes for these species. Second, we will develop high-precision ~100K SNP assays and a low-cost ~500 SNP assays for each of the six harvested species of FISHERIES; these resources will also be beneficial for management agencies and researchers focusing on the same species outside FISHERIES study regions. Our SNP assays from **D1** will enable us to generate the scientific knowledge of subsequent FISHERIES deliverables that are necessary for long-term sustainable development and management of often untapped northern fisheries. For example, our second and third genomic deliverables (**D2, D3**) will be a series of final reports, community-accessible guides and community-based workshops for end-users, stakeholders and fisheries managers describing (i) precisely each species' genetic population structure (**D2**) and (ii) accurately estimating the contributions and spatial distributions of different populations (or new hatchery-based production strategies for Arctic Char) from respective species to mixed-stock harvests (**D3**). As we have done in our past, longstanding collaborations with Indigenous communities in FISHERIES regions, we will co-produce the knowledge generated from these scientific deliverables with TEK surveys (discussed in GE³LS deliverables section below). Not only will this help to facilitate two-way communication with our partners, but it will ultimately contribute to the socially responsible and diverse knowledge base required towards better conserving, enhancing, and managing anadromous/freshwater species facing a rapidly changing environment in Canada's North.

Our fourth genomics deliverable (**D4**) will be a first multi-species assessment of genomic vulnerability underlining future climate adaptation, contributing to our ability to forecast the response of key fisheries to rapid global changes in northern Indigenous communities. We will specifically develop a comprehensive inventory of Single Nucleotide Polymorphism (SNP) and Structural Variants (SV) variation in Whitefish, Brook Trout and Arctic Char along a latitudinal coastal gradient. This novel assessment will contribute to the ability of scientists to forecast the responses of key fisheries to rapid global changes in northern Indigenous communities. Hence, it will help communities to implement their recently developed proposals for climate change adaptation in relation to future harvesting and food security needs (e.g. Cree Nation of Mistissini and Cree Nation Government 2018; Nunavut Fisheries Strategy 2017). We will combine forecasting insights from **D4** with community-based participatory modeling to devise implementation strategies for collectively derived objectives (**GE³LS D2**, below) at both community and regional levels (such as development of future fisheries policies, or strategies to enhance the use of certain fish species as a food source in specific regions). This will be of tremendous value for communities to prepare and plan for future changes in food sources and fisheries.

Detailed GE³LS deliverables. The first GE³LS deliverable (**D5**) will provide a forum for the exchange and co-generation of knowledge and insights on northern CRS fisheries development and co-management. We will create a knowledge co-evolution framework for fisheries development and co-management underpinned by Community Research Agreements and overseen by Regional Advisory Boards. The framework is intended to produce important new knowledge. It can be used for future research processes, to strengthen traditional knowledge through increased knowledge transfer, and to empower indigenous communities in co-management and the governance of their land. In a Canadian context,

this is an exceptionally important aspect of FISHERIES as it meets the objectives of the *Truth and Reconciliation Committee Call for Action* and the *National Inuit Strategy on Research*. We will create comprehensive documentation of the contribution of fisheries to food security and cultural identity in reports and locally accessible videos, photographic images, drawings and recordings of community stories and experiences (to be co-produced with community members). Interactive online atlas tools will also be used to communicate and share information on alternative definitions and values, as well as shared understandings of fish population structure, governance institutions, current and past regulatory regimes. Our atlas tools can be used by regional/federal governments and communities to exchange and store important data throughout the project. They will also facilitate implementation and monitoring of CRS fishing strategies, enable the collection and illustration of bio-monitoring data, and be an essential component of empowering local communities in the co-management of harvested fish populations. We will also conduct a detailed economic and multiple objective analysis (including cultural, social aspects) to determine the relative values of using fisheries for CRS purposes. Some communities and government agencies that have already approached or worked with us already have some preferences for certain types of fisheries. We will work closely with them to determine the opportunities, net benefits and risks of recreational and commercial fisheries. This information will be crucially important in determining alternative uses of fish species for specific areas and seasons.

The second GE³LS deliverable (**D6**) will develop implementation strategies for collectively derived objectives (at both community and regional levels) and future visions, such as development of CRS fisheries policies or strategies to enhance the use of certain fish species as a food source in certain regions. Here we will connect all of our scientific knowledge and TEK to create viable scenarios for sustainable development in each region. The scenarios will inform adaptive co-management strategies, economic development plans and community business plans. They will also inform regional and local food security strategies as well as national policies such as Nutrition North.

Socio-economic benefits.

Genomic resources and GE³LS-related tools of FISHERIES will provide tremendous new knowledge for sustainable harvesting and management of major anadromous/freshwater northern fisheries. They will enable end users responsible for local fisheries management – i.e. Indigenous communities, governmental agencies such as DFO, MFFP etc. – to set appropriate fisheries management targets, quotas and regulations in specific regions. The genomics resources and GE³LS-related tools of FISHERIES will also help to ensure the availability of high-quality and healthy food for Indigenous people in Northern Canada. These benefits will be derived from an inclusive knowledge co-evolution and co-management framework, economic and cultural valuations of the six focal fish species of FISHERIES, fishery implementation strategies, local capacity planning, and from interactive communication and planning tools. We expect the benefits to create new employment positions in a more effective communication, co-management and continuous stock assessment process among regional partners.

To this end, FISHERIES will develop genomic resources to provide crucial information on the population structure and mixed stock harvest contributions of six focal species supporting Inuit, Cree and Dene fisheries found in different coastal regions and large inland lakes. Our reports, guides and workshops developed from application of these genomic and related resources will be key in providing science advice on sustainable harvests through stock assessments either to (i) our Indigenous end users in regions where fisheries management is Indigenous-led and community-based (e.g. Cree coastal communities along James Bay and Hudson Bay and in the Indigenous-managed Nibiischii Wildlife Reserve that encompasses Lakes Mistassini, Albanel, Waconichi) or to (ii) our government partner end users in regions where federal or provincial agencies oversee fisheries assessment and management activities (e.g., Nunavut, Nunavik, Great Bear Lake, Great Slave Lake: Government of Nunavut, DFO, MFFP).

For example, we will convey to those responsible for setting management targets and quotas in each region (see Table S1, p.14) how knowledge of distinct populations and their contributions to mixed-stock harvests can enhance sustainable yields of harvested species in CRS fisheries, and substantially improve local fishery management and assessment practices (e.g. population-specific quotas, timing and spatial distribution of harvesting). In turn, we expect these deliverables to form a critical basis for maintaining and enhancing food security and socio-economic activities derived from CRS fisheries. In addition, knowledge capacity from certain research activities will inform the enhancement of Indigenous-led hatchery supplementation programs of Arctic Char to maximize their efficiency and productivity in terms of biomass captured on an annual basis. This in turn has potential value for not only enhancing or stabilizing food security, but may also generate economic spin-offs, such as the development of new aquaculture development in Inuit or Cree communities. Knowledge capacity from FISHERS genomics monitoring will inform decision-making on whether locally implemented management practices in response to overharvesting (e.g. Mistassini Lake Walleye) are achieving their desired outcomes. Knowledge generated from the application of our genomic resources will also inform the enhancement of both Indigenous-led hatchery supplementation and Indigenous-implemented harvesting management practices such as to achieve their desired outcomes for local communities. Finally, we will also provide the first multi-species, latitudinal perspective on genomic vulnerability underlining climate adaptation in northern fishes, thus facilitating the capacity of end users responsible for fisheries management in FISHERS regions to better forecast the response of key fisheries resources to rapid global and socio-economic changes in northern Indigenous communities.

For each of FISHERS' species and regions, we will also provide a reliable estimate of the commercial potential and value of fisheries, as well as provide direct input for the development of evidence-based Northern food security (e.g., Nutrition North) and hunter support policies and programs. For example, current commercial harvests of Arctic char in Nunavut are far lower than the allowable quota (705 mt remains available – estimated to represent \$18 million annually). Yet demand for Arctic char far exceeds currently supply. Having a local commercial fishery in certain regions (e.g. Pangnirtung, Cambridge Bay, Rankin Inlet) and enhanced recreational fisheries in others (e.g. Mistassini, Albanel, Waconichi Lakes) will provide more steady supply and access to nutritious and culturally important food resources. Indeed, for several decades, Indigenous Peoples in northern Canada have indicated that they cannot afford to purchase sufficient food to meet their family's needs. The average cost to feed a family of four is estimated to cost over twice (CAD \$410 vs. CAD \$192 per week) as much in Arctic communities, relative to the capital City of Ottawa (Kenny et al. 2018). Money is important, since the production of traditional foods very much depends on the means to purchase and operate the equipment that harvesting from a centralized village requires. Finally, we note that an aquaculture working group between Nunavik and the Cree of Eeyou Istchee has already been established. Our collaborative work on hatcheries and Arctic Char stocks will inform this working group and might lead to the first Northern Arctic Char aquaculture programme with tremendous potential market value and employment opportunities. A comparable programme in Iceland has an export value of \$ 30.25 million (of which 25 % is exported to the U.S.) (FAO, 2019).

In sum, FISHERS will shed light on the interactions between cumulative impacts of CRS fisheries development and changing socioeconomic conditions, as they relate to biodiversity conservation, susceptibility of harvested fish populations, sustainability of fisheries production and fish-centred food security over time. FISHERS will contribute to income supplementation, food security, business development opportunities, strengthening of cultural ties and employment derived from fisheries resources.

Though it is challenging to estimate the entire social and economic contribution of FISHERS research, it is clear that it has a high potential to amount to millions of dollars with direct benefits for tens of thousands of Indigenous people throughout Canada's North. The exact valuation of local inshore (and inland) fisheries in terms of cultural importance, commercial potential, recreational opportunities and as a healthful, sustainable, culturally relevant nutritious food source is not fully understood and accurately valued. **FISHERS represents a unique opportunity to fill this crucial knowledge gap. Indeed, FISHERS will be the first project of its kind to actually try to measure and value multiple uses of fisheries for the maximization of local benefits.** Moreover, we will conduct an analysis of governance and sharing of best practices across regions to support the participating regions in optimizing their choices, management and use of local fishery resources. We anticipate that the contribution of several years of research for the six focal species through FISHERS could very well spur the establishment of new fishing plants (as currently under discussion in Gjoa Haven, Nunavut) or substantial expansions of current plants in Cambridge Bay or Rankin Inlet. This clearly is in the interest of several communities that are asking for commercial fishery development, the GN Department of the Environment and the GN Department of Economic Development. **A new processing company employing 25-35 persons would make a substantial economic and social impact on a rural or coastal community with 1000-2000 persons.** A more detailed analysis of harvesting effort for CRS fisheries will provide a more accurate analysis of the connection between local food security and access to country food. **FISHERS will thus contribute to sustainable economic development and employment options in a renewable resource sector.**

A plan for transferring, disseminating and applying the deliverables to realize the benefits.

The FISHERS project team and governance structure includes university-based researchers, Indigenous partners and other knowledge users from the aquatic resource management sector. This structure directly implicates key decision makers in all phases of the project stage – from ongoing research development, to sampling, to data analysis and dissemination of research results to local communities – to ensure the effective transfer and application of the deliverables. For example, our team's (co-investigators) members N. Saganash (Cree Nation Government), J. Kennedy (Nunavut), L. Tran (Nunavik) are key decision makers in their respective regions. Furthermore, we will engage community partners, local resource management agencies, local fishers and elders (e.g. Cree talismen), and wherever applicable, provincial, territorial, and federal governments through various research and knowledge dissemination activities through the project. For example, we will carry out regular, ongoing dissemination of genomic research results and basic fisheries data that will be collected to resource managers in the form of public outreach presentations in northern communities, the interactive online atlas tools, radio interviews translated in Indigenous languages, and translated poster boards and reports with project summaries placed in hunters and fishers association buildings, Band Council offices, Indigenous-operated outfitting camps and local tourism offices. Such activities will allow Indigenous decision makers to fully benefit from the genomic research results. Through participatory modelling and direct involvement of local resource users/managers, the research benefits associated with assessment of conservation units, biomonitoring and food security will be fully transferred to local communities.

Finally, we will ensure that the dissemination of final management recommendation reports to decision makers and co-government bodies is based on a mutually approved bridging of scientific and traditional ecological knowledge, to facilitate: (i) the optimization of sustainable harvesting quotas and fishing locations/times; (ii) equitable harvest allocation between local community members or different stakeholders; (iii) harvesting enhancement (easing harvesting pressures on smaller populations to under harvested populations); (iv) bio-monitoring of fish population health indicators (e.g. wide age and size structure of adult fish, including very large individuals); (v) optimizing hatchery practices to improve survivorship and returns of adult fish to coastal fishing areas; and (vi) conservation measures to accommodate the quantities and quality of critically important spawning habitats to mixed-stock fisheries.

Expertise for realizing the benefits. As reflected in the project governance structure, our exceptional team comprises university-based researchers, Indigenous partners and government collaborators who have previously, worked, and/or are currently working together. **Collectively, the FISHERS team represent all the respective disciplinary expertise (spanning genomics and biodiversity conservation to fisheries, food security, and Indigenous knowledge and worldview) and long-term practical experience working in partnership with communities representing the different geographic regions encompassing FISHERS activities, for implementing a novel knowledge co-production framework at the interface of genomics, fisheries management and TEK.**

Our genomics/fisheries/science team (L Bernatchez, D Fraser, J-S Moore, L Chavarie) bridges basic and applied research on fishes of management interest, with frequent collaborations involving government agencies and Indigenous communities. They have a long history of collaboration together with Indigenous communities of FISHERS. For example, L Bernatchez and D Fraser conducted a pioneer study on the conservation benefits of integrating TEK and scientific knowledge of fish population diversity below species levels (*Ecology and Society* 11: 4 (2006)). They have since followed up with several collaborative TEK and science publications/reports on multiple FISHERS species as part of a longstanding collaborative relationship (since 2000) with the Cree Nation of Mistissini. J-S Moore and L Chavarie have >10 years of experience working on collaborative projects involving Inuit or Dené harvesters and government resource managers, to provide the scientific basis for Arctic Char and Lake Trout management in Nunavut, Nunavik and the Northwest Territories. Collectively, Indigenous communities and FISHERS end users in the aforementioned regions (e.g. Cree Nation of Mistissini, Pangnirtung, Cambridge Bay, Sahtú Renewable Resources Board) have used knowledge bases developed by our science team's past collaborations to (i) influence decisions about forestry and mining locations (to prevent impacts on important spawning sites for populations contributing to mixed-stock harvests), (ii) establish park boundaries that protect key fish populations, and to (iii) implement community-based fisheries management strategies and develop public awareness programs. Furthermore, as main PI of FISHERS, L Bernatchez has >30 years of experience in the commercialization of products and realization of applied benefits derived from the cutting edge genomics research. He is a project co-leader on a currently funded LSARP fisheries-focused project (EPIC4 ending 2019) and will transfer his lead expertise and experience to FISHERS.

With expertise in community economic development and livelihoods, Indigenous knowledge, use, and stewardship of aquatic environments, and food security, our GE³LS team members (S Schott, M Mulrennan, M Lemire, T Kenny) has the expertise to engage with the communities that stand to realize potential benefits from the project. They also have the ability to work effectively across natural and social sciences and to bridge the genomics research and community knowledge through participatory, mixed-method (quantitative and qualitative) approaches. S. Schott is currently a co-PI and GE³LS lead on a Genome Canada LSARP project in Gjoa Haven, Nunavut (ending 2019). His main role is to ensure an appropriate and respectful knowledge co-evolution framework that allows research partners to produce and share new knowledge that is beneficial to end users. He is collaborating closely with Carleton University's Geomatics and Cartography Centre in developing specific interactive atlas tools to document and share traditional knowledge, harvest study information, food security concerns and commercial fishery quotas and opportunities. M. Mulrennan currently directs the Indigenous Resource Management Research Group (IRM lab) at Concordia University. She has worked heavily with James Bay Cree and is centrally involved in research supporting the creation of community-led protected areas in Wemindji. M Lemire is titular of Nasivvik Research Chair in Ecosystem Approaches to Northern Health and is leading several research initiatives in Nunavik related to local/country food consumption and food security in several communities in Nunavik. T Kenny has worked in close partnership with northern and coastal Indigenous communities from the Arctic to the Pacific Northwest on matters of food security, public health, wildlife harvest and biodiversity management/conservation. Together Lemire, Kenny, Schott and Moore are working with the community of Qikiqtarjuaq and other Quebec coastal

communities on several emerging projects to actively promote the consumption of seafood while adapting to global changes and fostering food sovereignty and cultural continuity. Collectively, their work will generate the discussions necessary to create informed decision-making about the adoption of the newly developed technologies within larger governance systems and specific governmental regulatory frameworks. The expertise of the GE³LS team will ensure that, during the course of the project, informed discussions will take place among all stakeholders about the potential uptake of genomics-based knowledge into complex governance realities within local northern communities. It will also explore with stakeholders the potential future positive impacts from the research that extends beyond the time course of its initial funding by Genome Canada.

Our genomics and GE³LS team will work together with local fishers, local and regional-level Hunter and Trapper Associations (HTAs), regional and territorial wildlife organizations and governments, DFO and the Northern Integrated Commercial Fisheries Initiative to develop a shared vision and coherent strategy for fisheries development in Canada's north. This includes the possibility of new or alternative co-management arrangements, revisions to existing commercial fishery strategies, adjustments to fishing quotas, the development of business plans including marketing and market options, and the identification of opportunities for fish plant expansions or new fish plant investments. With the Government of Nunavut Health Board, regional health centres in Nunavut, the Nunavik Health Board, the Eeyou Istchee Health Board and the NWT Health and Social Services Authority we will develop fishery strategies that prioritize health and nutrition in each region. Together with HTAs and regional wildlife organizations, we will discuss how our collectively derived results and insights can improve hunter and fisher income support programmes, subsidies and other supports for country food provision, and the potential for local fish markets and distribution beyond the sharing economy. With the input of elders, youth, active fishers, health boards and research partners in regional and territorial government agencies, we will develop recommendations for improved food security support programmes and policies (such as Nutrition North) for both store-bought food and country food. Finally, we will share our research results on recreational fisheries with sport fishers, Economic Development Departments in interested regions and communities that would like to engage in developing or strengthening recreational fishing activities in order to find pathways for marketing, guiding and outfitting capacity building, as well as potential investments into lodges and further accommodation capacities.

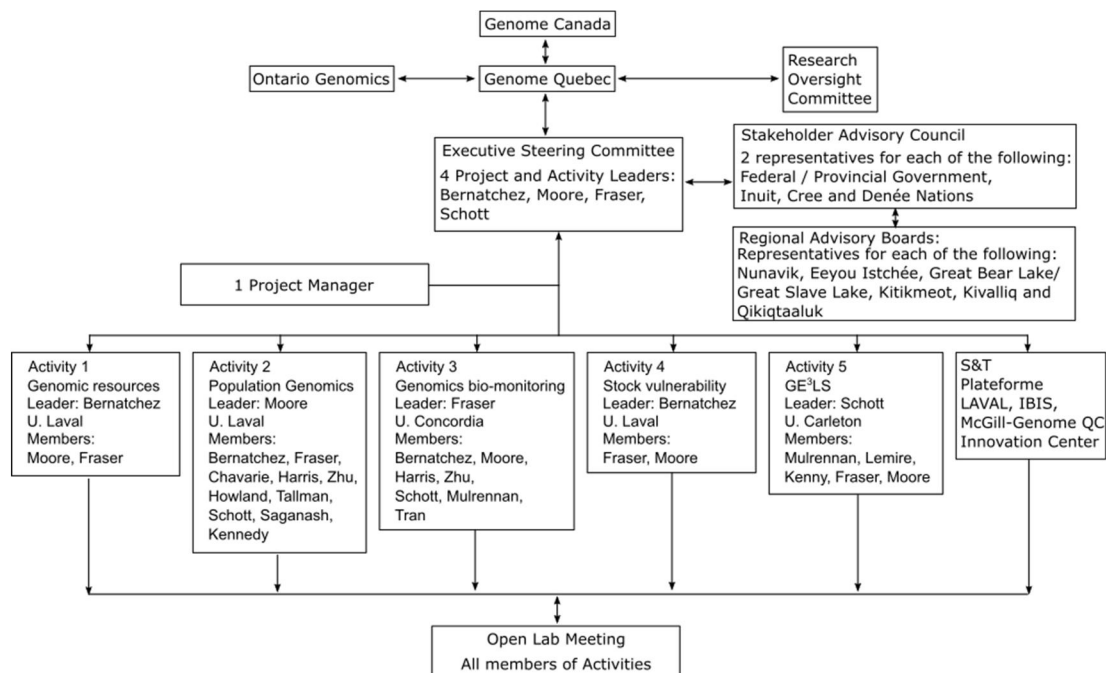
Broader implications. FISHER research will contribute extensively to Canada's role as a world leader in fisheries genomics. But FISHER is also an outstanding and timely opportunity to generate the co-evolution framework of scientific and local knowledge necessary for fostering and developing sustainable CRS fisheries in Canada's North. In turn, we expect FISHER to provide a foundation on which coastal and Indigenous communities can enhance their economic activity through fisheries, improve their food security and empower their own resource management decision-making with the best available knowledge from the most current technologies and tools. Due to past colonialism, a co-production framework that strongly engages Indigenous peoples is fundamentally essential for improving fisheries management in northern Canada and for deriving the full economic and social benefits of fisheries. It is indeed consistent with the mandate of Canadian society to restore (through reconciliation) economic self-sufficiency of its Indigenous peoples and to develop a respectful relationship with them. This can only be achieved through local collaboration from the beginning. Our team understands the importance of the local institutions in place to complete the different deliverables of FISHER and to execute the co-management framework. We have many Indigenous community partners on board that support the FISHER endeavor. We recognize that our project is high risk because how the mechanisms underlying the co-management framework will evolve over the project's four years cannot be predicted with certainty. Yet, FISHER represents a unique opportunity of one of exceptionally high reward in truly fostering local fisheries management and empowerment for local Indigenous communities throughout northern Canada.

VIII MANAGEMENT

Maximum of four (4) pages, including charts, figures and tables. This section must address all relevant evaluation criteria for the competition. Please include an organization chart and project management plan.

FISHES (Fostering Indigenous Small-scale fisheries for Health, Economy, and food Security) is an ambitious, transdisciplinary project that will use genomics to assist Indigenous and governmental management of 6 fishes critically important to food security and CRS fisheries. Our team comprises 4 project leaders (L. Bernatchez, J.S. Moore, D.J. Fraser, S. Schott) who lead the following Activities: Bernatchez (Act. 1 & 4), Moore (Act.2), Fraser (Act.3), Schott (Act5, GE³LS). The team also comprises 12 co-investigators, including 4 academic researchers (M. Lemire, T. Kenny, M. Mulrennan, L. Chavarie), 5 from the government sector (L. Harris, X. Zhu, J., R. Tallman, Howland, April), and 3 Inuit and First Nations co-investigators (J. Kennedy, N. Saganash, L. Tran). In addition, FISHES includes 15 other collaborators representing either governmental agencies or Indigenous communities from throughout the studied regions that bring additional expertise and support for TEK surveys, sample collections, community liaison activities, local fisheries management, etc. Altogether, 18 partner organizations and stakeholders are represented on our team, including: i) Department of Fisheries and Oceans Canada (DFO), ii) Ministère des Forêts de la Faune et des Parcs du Québec (MFFP), iii) seven organizations from the Cree Nation (Cree Nation Government, Niskamoon Corporation, Cree Trappers Association, Eeyou Marine Region Wildlife Board, Cree Nations of Mistissini and Waswanipi, Public Health Department of the James Bay Cree Territory); iii) two organizations from Nunavut (Inuit) (Government of Nunavut and Gjoa Haven HTA) and (iv) two organizations from the Government of Nuvavik (Inuit) (Makivik Corporation and Nayumivik Landholding Corporation); v) five organizations from Northwest Territories (Dené) (Deline Renewable Resource Council, Sahtu Renewable Resources Board, Northwest Territory Metis Nation, DehCho First Nation, Deninu Kue First Nation).

Management structure: The management structure has been developed to ensure milestones and deliverables are achieved on time and within the budget limits. As this project is a collaboration between academia, government agencies, and Indigenous communities, project administration and facilitation are organized to ensure cooperative and effective working relationships and sharing of responsibilities throughout the project's duration. Our project organization chart is as follows:



1. Governance, accountabilities of personnel and finance, and processes for decision making

1.a. Executive Steering Committee (ESC): Bernatchez will chair an Executive Steering Committee, which will also comprise all Activity Leaders (who are also Project Leaders): Fraser, Moore, Schott. The Project Manager will serve as an *ex officio* member and as a secretariat for the Executive Steering Committee, coordinating meetings, preparing reports and monitoring budget expenditures. The chair of the Stakeholder Advisory Council will be *ex officio* members of the Executive Steering Committee. This will allow for direct flow of information among the governance committees. The Executive Steering Committee will follow up on scientific sub-activities, budget allocations and will function in an advisory, consultative, coordinating and communicative capacity whilst centralizing information. Objectives of the Executive Steering Committee will be to avoid unnecessary duplication of effort and to maximize the coordination between the Activities. This committee will have monthly teleconference meetings in the ramp-up period and have quarterly teleconference meetings for the rest of the project. The primary resources for the Executive Steering Committee will be a Stakeholder Advisory Council. The Executive Steering Committee will report directly to a Research Oversight Committee established by Genome Canada, and Genome Québec. The Research Oversight Committee will play the major governance role on behalf of Genome Canada and the two regional genome centers.

1.b. Activity Leaders: Activity Leaders will be responsible for ensuring that the Activity each leads stays on schedule, as laid out in the Gantt chart, and keeps within its allotted budget. Activity Leaders will have monthly conference calls with the Activity Team Members who include the representatives from Nunavut, Nunavik and Cree government but also DFO and MFFP representatives. The Activities are not stand-alone projects. Each Activity is connected with at least one other Activity, including strong, integrated links between “genomics” activities and GE₃LS. The Activity Leaders will ensure that the cooperation is fully exploited and will generate synergy among all team members. Each Activity Leader will report on the Activity progress to the Executive Steering Committee at the teleconference meetings.

1.c. Open Lab meetings: Members of all Activities will have bi-monthly teleconference meetings. In these meetings, one member (student, post-doctoral fellow, research assistant, or Activity Team Member) will give an informal presentation on the progress of his/her work (methods, analysis, results and/or discussion). These meetings will allow a better understanding of each project and maintain the cohesion and synergy connection between the Activities and their members.

1.d. Stakeholder Advisory Council (SAC): The Stakeholder Advisory Council will maintain strong links with the end-users’ representatives of communities that may be impacted by, or stand to benefit from, FISHERIES’ socio-economic deliverables. This council will comprise two representatives from DFO/MFFP, for the Cree, Inuit and Dené Nations. The SAC will elect its own chairperson. The four Project Leaders will be an *ex officio* member of the SAC. The SAC will have full access to the quarterly reports from the Activity Leaders. It will meet at least once a year or more frequently by teleconference if the members deem it necessary or at the request of the Executive Steering Committee to consider a particular query.

1.e. Regional Advisory Boards: To strengthen the interactions with community end-users, each region covered by FISHERIES will have a Regional Advisory Board composed of members closely associated with fisheries and food security. As part of the knowledge-gathering phase, the Regional advisory boards will meet to discuss current knowledge, current knowledge gaps, research strategies, capacity building opportunities, desired outcomes and sampling strategies that should be implemented in order to address these objectives. This will include sampling locations and focal species important for the communities. The Regional Advisory Board will be consulted prior to each field season to ensure the project maintains adherence to the agreed upon project objectives. They will communicate their suggestions/opinions to the Stakeholder Advisory Council.

1.f. Project Manager’s responsibilities and Expertise: There will be one full time project manager (Bérénice Bougas, Ph.D. Biology) located at U. Laval. She possesses strong scientific and management backgrounds, experiences and related qualifications for managing FISHERIES. She has been a half-time manager for four years in another LSARP on fisheries (EPIC4), and therefore very experienced and

acquainted with what the rigorous management requirements of large-scale LSARP projects. B Bougas is bilingual in English and French. She will assist with the project launch, coordination of activities, as well as communication between Activity Teams, end-users, representatives of communities and members of the Stakeholder Advisory Council. She will also liaise with Genome Canada and Genome Quebec, as well as university services at Université Laval which will be the host Institution for FISHERS. She will also coordinate activities with the McGill – Genome Quebec Innovation Center and other S&T platforms located at IBIS. Finally, she will prepare quarterly research and financial reports and will report directly to the Executive Steering Committee on the overall management of the project.

1.g. Decision-Making Authority: The ESC will make decisions regarding the operating of FISHERS based on input from the Activity Leaders and the Stakeholder Advisory Council, as well as feedback from the Research Oversight Committee. The decision making process will be by consensus between the four Project Leaders, but if necessary, L Bernatchez will have the final authority to make go/no-go decisions for the issues pertaining to the genomics-related activities, and S Schott will have the final authority for issues related to the GE³LS. L Bernatchez has extensive experience with genomics projects, being a Project co-Leader with W Davidson of the Genome Canada funded LSARP project *Enhancing production in Coho: Culture, Community, Catch (EPIC4)*. S Schott possesses an extensive experience with research on ethical, environmental, economic, legal and social aspects of genomics, and is also Project Leader of the Genome Canada funded project *Towards a Sustainable Fishery for Nunavummiut*.

2. Project Schedule and Ramp-up

2.a. Ramp-up of Activities: Most of the necessary, more senior personnel for the project (i.e. technical support staff, research assistants, and post-doctoral fellows) have been identified and/or are already in place at each research site (Université Laval, Concordia University, Carleton University, Fisheries and Oceans Canada, MFFP, co-investigators from Inuit and First Nations). Acquisition of major equipment, namely the four Ion Torrent GeneStudio S5 sequencers from Thermo Fisher, is expected to occur within one quarter of project launch. Ramp-up of each Activity and expected completion times for sub-activities are reflected in the project budget and Gantt chart.

3. Coordination of current and future partnerships

3.a. Past and Current Partnerships: FISHERS will not be the first experience of collaboration among its academic members. For more than 15 years, we have engaged with Indigenous communities, Government of Nunavut, Nunavik, Cree Nation Government, DFO, and MFFP in many successful collaborations. As selected examples, (i) Moore and Schott have been collaborators in another LSARP (Genome Canada) project (TSFN; *Towards a Sustainable Fishery for Nunavummiut*); (ii) Moore, Harris, Lemire and Bernatchez are involved in projects funded by Sentinel North and Polar Knowledge Canada and involving partners from many Inuit communities in Nunavik and Nunavut; (iii) Chavarie, Zhu, Howland, and Schott have been involved together in fisheries management and TEK projects involving Indigenous communities from Great Bear and Great Slave lakes, and (iv) Fraser, Bernatchez, Mulrennan and Schott have long been involved in collaborative fisheries management and TEK projects with Cree communities both from inland (Mistissini), and coastal James Bay (Wemindji).

3.b. Future partnerships: We anticipate that existing partnerships and those forged during FISHERS, will be extended in other fisheries genomics and TEK related projects after this four-year project, especially the collaborations developed with Indigenous communities. Chances of future collaborations are very high. ALL of our team members have evidenced their deep commitment to developing and maintaining mutually-beneficial collaborative projects with northern Indigenous communities through their long-term projects and engagements with northern communities. Moreover, we are expecting that close collaborations between FISHERS team members and our end-users will continue over 5-10 years after project completion to ensure effective continuity of the bio-monitoring programs established during the course of the project (e.g. regular GSI analyses of various CRS fisheries based on low cost genotyping with the 500 SNP assays developed during the project).

4. Plans to make research results accessible to the research community

4.a. Accessibility of results of research community: All genomic data will be deposited into public databases as soon as they have been validated. Then all research results will be diffused through peer-review publications, the interactive spatial mapping and communication atlas tools and presentations at conferences. Relevant information will also be circulated on the website which will be built for the project, as well as on a FISHERS Twitter account (for instance to announce new publications).

4.b. Accessibility of results to Stakeholders and public: Besides media relations and public outreach offices from each university, FISHERS will also use the GE³LS meetings (Activity 5) to communicate the research realized by FISHERS and the implications for stakeholders and the public. For instance, through participatory modelling and direct involvement of regional research advisory boards, the research benefits of biomonitoring and food security will be fully transferred to local communities. We will carry out regular, ongoing dissemination of genomic research results to resource managers in the form of regional validation and feedback workshops, interactive online atlas tools, radio interviews translated into Indigenous languages, and translated poster boards and reports with project summaries placed in hunters and fishers association buildings, Band Council offices, Indigenous-operated outfitting camps and local tourism offices. Such activities will allow Indigenous decision makers to fully benefit from the genomic research results. Finally, we will ensure that the dissemination of final management recommendation reports to decision makers and co-government bodies is based on a mutually approved bridging of scientific and traditional knowledge.

5. Arrangement with Technology Services Providers

5.a. S&T Platforms: Statements of Work have been provided from each of the major S&T platforms (essentially McGill – Genome Quebec Innovation Center and IBIS sequencing and Bioinformatics platforms) to ensure that the project can meet its Objectives that require those services. We have considered different genotyping methodologies, and have chosen the most appropriate based on cost, results quality, convenience, including turn-around time, and uptake by potential end-users. Of course, we will remain open to consider alternative approaches should more appropriate, novel methods becomes available during the course of the project.

6. Project Leaders' Experience in Managing Large-scale Projects

6.a. Project leaders: FISHERS is a fully integrated project with a wealth of project leadership and management talent. As mentioned above, both L Bernatchez and S Schott have been involved in successfully leading LSARP fisheries related projects involving Indigenous communities. Bernatchez has also led numerous other large scale collaborative projects (e.g. through NSERC Strategic and RRD grants). Their individual and combined experience in dealing with complex, interdisciplinary projects is not in question. Most of the Activity Team Members also have these qualifications and again they are all leading successful collaborative research projects involving northern Indigenous communities. For instance, D. Fraser has been leading a long term research program with the Cree Nation of Mistissini for more than 10 years. Clearly then, The Project/Activity leaders are used to being in charge of projects that have milestones and that follow closely laid-out Gantt charts (e.g., NSERC Strategic grants; LSARP) as well as providing timely reports on their progress and achievements.

7. Highly Qualified Personnel (HQP)

7.a. Training Opportunities: Team Members have excellent track records in training excellent graduate students and many HQP required for the project (PDF, graduate students) have already been identified. The trainees will have the opportunity to travel to northern Indigenous communities and different research groups to gain a broad training in genomic technologies as well as a better understanding of GE³LS issues, especially pertaining to Indigenous communities in the complex context of a rapidly changing biophysical and socioeconomic environment. **Finally, FISHERS will train qualified persons in Indigenous communities to conduct basic bio-monitoring practices (catch records, measurements, samples collection), effectively enhancing the capacity for Indigenous communities to independently conduct and lead community-based monitoring of aquatic resources even after FISHERS ends.**

IX FINANCIAL INFORMATION

This section must address all relevant evaluation criteria for the competition and must include:

- a description of the financial and budgetary controls (e.g., processes for authorizing purchases, payments and budget adjustments); and,
- a justification for the main budget items including a summary of principal financial assumptions or explanations. If applicable, please include justification and assumptions for the calculation of a general consumable rate per FTE, for consumables commonly utilized in most laboratories. Please refer to budget line number (ref.#) when providing additional explanations. A narrative description of all budget lines is not required.

Budget

- Provide a budget request for up to four years using the budget template provided in Excel 2007 Macro-Enabled (*.xlsm) format.
- It is expected that applicants will work with Genome Centre staff to ensure that the budget meets all requirements outlined in the [Guidelines for Funding](#).
- Please ensure that the research activities are consistent between the research proposal, budget and Gantt chart.
- The budget and supporting documents (e.g., supplier quotes, statements of work (SOWs) from service providers) must be included in Appendix III.

Financial and budgetary control processes

Management of research funds

This project will be undertaken with Université Laval where there are already in place established processes and controls for the handling of grant and project funds. L Bernatchez project leader at Laval, a faculty member, will have the authority to incur expenses on behalf of the Institution. Similarly, D Fraser (faculty member Concordia) and Stephan Schott (faculty member Carleton) will have the authority to incur expenses on behalf of their respective institutions. The Project Leaders are responsible for ensuring that claims for expenses are in accordance with the institution's procedures and are for the project purposes only. Original signatures are required and all original vouchers and invoices are kept for audit purposes.

Research accounts are monitored as follow:

- 1- Laboratory/Project managers are responsible for reconciling all purchases with expenses appearing on the ledgers;
- 2- Activity Leaders are responsible for monitoring the ledgers to ensure all expenses fall within guidelines established by the funding agencies, and that the purchases comply with the institution's purchasing procedures and guidelines. All purchases must have the spending approval of an authorized senior staff member and/or Project Leader and/or Project Manager;
- 3- Project manager monitor the research ledgers on a monthly basis and advise the Activity Leaders of potential spending concerns;
- 4- Financial Services and the project manager ensure that all expenses comply with the granting agency's guidelines.

Université Laval has in place a number of policies and procedures developed to ensure compliance with a variety of funding agency requirements including Tri-Council (SSHRC, NSERC & CIHR). Université Laval has policies governing administration of research funds encompassing purchases, contractors, travels and staff appointments. The Procurement Services department oversees all purchases and all project expenditures must be individually approved by investigators in whose name funds are awarded. All expenditures for the proposed project will be subject to ongoing scrutiny and audit by Université Laval's internal and external auditors as well as any applicable funding agencies.

Accounting and Reporting:

The Project Leaders in conjunction with Université Laval will submit to Genome QC all information and data on a quarterly basis as prescribed by the Center in terms of timing, format and content which will allow for the on-going assessment and monitoring of project performance. Université Laval assisted by the project manager has the responsibility to ensure that all the project Activity Leaders participate in this process. In addition, all co-funding expenditures will be reported to Genome QC and Genome Canada on a quarterly basis. Similar responsibilities will incur to administrative staff involved in the project, either at Concordia (in D Fraser's group) or Carleton (S Schott's group).

Budget adjustments:

Any changes to the scientific, managerial or financial conditions of funding initially approved by Genome Canada will require recommendation from Genome QC and the ROC prior submission to Genome Canada for consideration. All adjustments will be managed according to the principles outlined in Genome Canada's Guidelines for Management of Changes, and others as applicable.

Final Reporting:

Within three months of the completion of the project, the Project Leader will submit to Genome QC a final report that includes a description of the accomplishments of the project relative to the approved objectives as well as a detailed financial report in the format prescribed by Genome Canada.

Justification for the main budget itemsJustification of major equipment items in Budget:

Line item Ref# 17 – Sequencers

The Ion Proton GeneStudio S5 Prime System (sequencers) is particularly suited for this project for following reasons:

- 1) Current GBS expertise in L Bernatchez' laboratory relies on this technology which will be essential to reach FISHERS' research objectives.
- 2) The IBIS platform of genomic analyses has developed a strong expertise in the Ion Proton sequencing technology, which will ensure fast and efficient data delivery. In particular, the IBIS platform offers the production of GBS libraries on sight which is not offered at any other platforms that we are aware of.
- 3) The 4 sequencers requested (two purchased and two in-kind donation) are essential to ensure the rapid, high-throughput necessary to complete the project objectives (namely all sub-activities in Activity 2 and 3) within the proposed timeframe. The cost of purchase and use of the Ion Torrent sequencers is competitive with the cost for sequencing elsewhere, including the Genome Quebec Innovation Centre at McGill.

A quote from ThermoFisher is included in Appendix III that details the best academic discount of the two Ion Proton GeneStudio S5 Prime System for 2019 as \$493,000 CAD (+6.94%: \$529,209).

Line item Ref# 147 – Automated dispenser

An automated dispenser, here the model epMotion 5075tC NGS solution, will be crucial toward enhancing our capacity to reach our Milestones in time. This piece of equipment will essentially be used for performing the 20,000 fish DNA extraction and the library preparations planned in the overall project. A quote from Eppendorf is included in Appendix III that details the best academic discount of the epMotion 5075tC NGS solution for 2019 as \$199,253.55 CND (+6.94%: \$213,082).

Justification of major Consumable items in Budget:

1-DNA extraction

Line item Ref # 15, 19 #20 #22 & #39 – DNA extraction and Quality Check- Act. 2 & Act.3 & 4 (Units: 17,500; \$8 cost /unit; total cost: \$140,000)

Description		Unit Cost	Sub-Total
Extraction	Extraction Kit NucleoMag Macherey-Nagel (for robot)	3.5	
	Tips eppendorf for robotEPMotion	1.5	
	Plate UV star WWR, Axygen	0.2	
	Other (RNase, tubes)	0.7	
			5.9
Quality check	Accuclear kit	0.4	
	Plate WWR	0.2	
	Tips BiotiX	1.5	
	Other		
			2.1
TOTAL			8\$

2- Travel Field work

Ref #16,#18,#36,#41,#65,#66,#67,#72,#73,#83,#135,#136 #143 Act. 2, 3, 4 and 5 (Total = \$1,001,500)

Line item Ref # 41– travel for field work Cree Territory Year 1 - Act.3 (Units: 1; \$89,000 cost /unit; total cost: \$89,000)

Description		Unit Cost	Sub-Total
Travel Mistassini, Albnel, Waconichi, Waswanipi Year 1- 5weeks of field work, Price for 2 5weeks in May and 5 week in September	Cabine rental /month	1500	3,000
	Hotel / night	165	5,115
	Meals / week	700	8,400
	Flight	3500	10,500
	Transportation Truck location, gas		6,000
	Miscellaneous: tent, satellite phone, tent		2,985
Travel Mistassini brook trout, lake trout, walleye and Waswanipi walleye Year 1- 8 weeks of field work in June, Price for 2	Hotel / night /person 300\$ and 165 \$	300	28,500
	Cabin rental /month	1500	4,500
	Meals / week	700	9,800
	Transportation Truck location, gas	5000	5,000
	Miscellaneous: tent, satellite phone, tent		5,200
TOTAL			89,000

Line item Ref # 135– travel for field work Cree Territory Year 2- Act.3 (Units: 1; \$53,000 cost /unit; total cost: \$53,000)

Description		Unit Cost	Sub-Total
Travel Mistassini brook trout, lake trout, walleye and Waswanipi walleye Year 2- 8 weeks of field work in June, Price for 2	Hotel / night /person 300\$ and 165 \$	300	28,500
	Cabin rental /month	1500	4,500
	Meals / week	700	9,800
	Transportation Truck location, gas	5000	5,000
	Miscellaneous: tent, satellite phone, tent		5,200
TOTAL			53,000

Line item Ref # 136 #83– Act.3: travel for field work Cree Territory Year 2- and Act.5: travel for field work Nunavut, Nunavik, NWT; (Units: 13; \$15,000 cost /unit; total cost: \$195,000)

Description		Unit Cost	Sub-Total
Travel fisheries-induced evolution: Mistassini walleye Year3- 5 weeks of field work in May, Price for 2	Hotel / night 165 \$	165	3,465
	Cabin rental /month	1500	1,500
	Meals / week	700	3,500
	Transportation Truck location, gas	3500	3,500
	Miscellaneous: tent, satellite phone, tent		3,035
TOTAL			15,000

Line item Ref #16 #18 #36 & #143– Act. 2 & 3 & 4: Travel for field work - Year 1: 1 travels for 2 persons for 7 areas, Year 2: 1 travels for 2 persons for 5 areas, Year 3: 1 travels for 2 persons for 5 areas, and Year 4 : 1 travels for 2 persons for 3 areas); (Units: 40; \$10,000 cost /unit; total cost: \$400,000)

Description		Unit Cost	Sub-Total
Travel Nunavut - Nunavik 10 days of field work	Hotel / night	200	2,000
	Flight	5000	5,000
	Meals / day	100	1,000
	Transportation Truck location, gas	1500	1,500
	Miscellaneous: tent, satellite phone		500
TOTAL			10,000

Line item Ref # 65, # 66, # 67, #72– Act.5. Travel for field work – Lemire Lab and Mulrennan Lab (1 travel by year for 3 persons for 4 areas) (Units: 48; \$5,000 cost /unit; total cost: \$240,000)

Description		Unit Cost	Sub-Total
Travel Nunavut – Nunavik – Eeyou Istchee 5 days of field work	Hotel / night / person	200	1,000
	Flight / person	3500	3,500
	Meals / day/ person	100	500
TOTAL			5,000

Line item Ref #73– Act.5 Travel for field work –Eeyou Istchee south area - Mulrennan Lab (Units: 7; \$3,500 cost /unit; total cost: \$24,500)

Description		Unit Cost	Sub-Total
Travel Nunavut – Nunavik – Eeyou Istchee 5 days of field work	Hotel / night / person	200	1,000
	Flight / person	2000	2,000
	Meals / day/ person	100	500
TOTAL			3,500

3-Sampling program Ref#96 \$300,000 in-kind from DFO

See Co-funding commitment letter from Fish. & Oceans Canada, Document 3a.

4-Field support Ref#95 \$340,000 in-kind from DFO

See Co-funding commitment letter from Fish. & Oceans Canada, Document 3a.

X CO-FUNDING STRATEGY

Maximum of three (3) pages including tables. Refer to Section 5.2 of the [Guidelines for Funding](#) for details on co-funding requirements.

Please provide a well-developed and feasible plan which demonstrates the project's potential to secure at least 75% of the co-funding prior to the release of Genome Canada funds. All co-funding must directly support the objectives of the project. Co-funding must also be for eligible costs specifically requested in the Genome Canada budget in order to be considered as an eligible co-funding source.

In the format below, please provide details of the co-funding sources. For each source, include the organization name, amount that directly supports the objectives of the Genome Canada proposal, contribution type (e.g., cash or in-kind), expected receipt date, status of co-funding and a description of how the funds will directly support the objectives of the project. Documentation supporting secured or proposed co-funding must be included in Appendix IV (Supporting Documentation for Co-Funding).

Funding Sources

#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
1	Genome Quebec	\$3,732,423	Unrestr. Cash	October 2019	Committed
Genome Quebec will fund 35% of activities conducted in Quebec					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
2	Universities	\$247,144	In-Kind & Restr. Cash	October 2019	Committed
2a Carleton \$191,144: Restricted cash and in-kind contributions to support grants for salary, and workshop and conference. 2b Concordia \$56,000: Cash contributions to support grants for salary.					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
3	Govern Agency	\$1,400,000	In-kind	October 2019	Committed
3a Fish. & Oceans Canada \$1,000,000 and 3b MFFP \$400,000: In-kind contribution for salary, sample acquisition, support and equipment.					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
4	Ressources Aquatiques Québec	\$160,000	In-kind & Restrict. Cash	October 2019	Committed
Cash: to support salary of a research assistant; In-kind value for salary					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
5	IBIS (U. Laval)	\$262,596	In-Kind	October 2019	Committed

⁵ Types of co-funding include: unrestricted cash, restricted cash (e.g., salary support, research grant support) and in-kind contributions

⁶ Status includes: yet to apply, awaiting response, committed and received

In-kind contribution in terms of salary equivalent for bioinformatics, computing, server maintenance and genomic analyses support for the entire project.					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
6	ThermoFisher	\$529,209	In-kind	October 2019	Committed
Donation of 2 Ion Torrent GeneStudio S5 Prime systems. (+6.94% Tax: \$529,209)					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
7	Public Health Dept of the James Bay Cree Territory	\$40,000	In-kind	October 2019	Committed
In-Kind contribution for participation with project activities, professional expertise from a public health perspective and collaboration with project partners.					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
8	Cree Communities	\$1,992,685	In-kind	October 2019	Committed
8a Cree Nation Government \$180,000; 8b Niskamoon Corporation \$400,000; 8c Eeyou Marine Region Wildlife Board \$160,000; 8d Cree Trappers' association \$240,000; 8e The Cree First Nation of Waswanipi \$100,000; 8f Cree Nation Mistissini \$140,000; 8g Nayumivik Landholding Corporation \$239,885; 8h Makivik Corporation \$532,800. In-kind including workforce, travel expense, equipment and supplies for fish sampling and data collecting.					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
8a	Cree Nation Government	\$89,250	Unrestr. cash	October 2019	Committed
Unrestricted Cash contribution for salary (\$105,000 less 15% of Indirect cost)					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
8i	Niskamoon Corporation - Mitacs	\$170,000	Unrestr. cash	October 2019	Committed
Unrestricted Cash contribution for salary (\$200,000 less 15% of Indirect cost)					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
8c	Eeyou Marine Region Wildlife Board	\$85,000	Unrestr. cash	October 2019	Committed
Unrestricted Cash contribution for salary (\$100,000 less 15% of Indirect cost)					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
9	Nunavut Government	\$300,498	In-kind & Restr. cash	October 2019	Committed
Cash: \$60,000: Fisheries economic analysis of existing data In-kind: \$240,498: workforce, travel expense, equipment and supplies for fish sampling and data collecting.					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶

10	Nunavut Communities	\$178,000	In-kind	October 2019	Committed
Gjoa Haven HTA In-kind contribution including workforce, travel expense, equipment and supplies for fish sampling and data collecting					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
11	Dene Communities	\$796,000	In-kind	October 2019	Committed
11a Dehcho First Nations \$192,000; 11b Sathu Renewable Res. \$120,000; 11c Deline Renewable \$5,000; 11d Deninu Kue First Nation \$192,000; 11e NWT Metis Nation \$272,000; In-kind contribution including workforce, travel expense, equipment and supplies for fish sampling and data collecting					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
12	Réseau Québec Maritime	\$25,000	Restrict. Cash	October 2019	Committed
Cash to support workshops for knowledge transfer					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
13	McGill University Innovation Centre	\$10,000	In-kind	October 2019	Committed
In-kind Bioinformatics assistance in genome assembly and cost of Hi-Ci scaffolding.					
#	Name of the organization	Amount	Type ⁵	Expected Receipt Date	Status ⁶
14	Ontario MEDJCT	\$192,271	Restrict. Cash	October 2019	Committed
Contribution for post-doctoral fellow salary					