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Conservation genomics from a practitioner lens: Evaluating the research-implementation gap in a managed freshwater fishery

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ABSTRACT

Fish and wildlife managers are faced with the daunting task of making informed and sensible decisions in the face of conflicting objectives and rapid environmental change. Conservation genomics – the use of new genomic techniques and genome-wide information to solve biological conservation problems – is an emerging scientific field that holds much promise in delivering practical knowledge to inform decisions, policies, and practices for conservation and management. However, the impact of genomics on conservation and management has been rather limited to date, described as the "conservation genomics gap". We set out to identify perceived benefits and existing barriers supporting or limiting the use of conservation genomics in conservation practice by analyzing how potential knowledge users (conservation practitioners) perceive and evaluate genomics using the case of managed Rainbow Trout (*Oncorhynchus mykiss*) fisheries in the Canadian province of British Columbia. We interviewed 33 government employees and 32 representatives from nongovernmental stakeholder groups involved in fisheries management. We found that very few knowledge users were familiar with genomics or understood the difference between genetics and genomics. Despite low genomics familiarity, respondents generally view conservation genomics favorably, as a reliable and promising tool that could provide them with novel knowledge that would help them improve management or make better decisions. However, the exact benefits or outcomes genomics could provide in applied contexts are potentially limited by politics, communication, expertise, interpretation, cost, competing conservation practices, and time. Our research suggests that genomics has considerable potential in applied conservation and management *if* clearer communication between researchers and practitioners is achieved. We recommend genomic researchers and funding agencies identify wide-ranging practitioners and instate knowledge and sharing interfaces at project outset focused on practitioner objectives and improving practitioner knowledge and familiarity.

1. Introduction

Fish and wildlife populations are increasingly threatened by rapid environmental change and thus require informed conservation and management decisions, policies, and practices based on the best available knowledge (Nguyen et al., 2017a). However, investments in new science often fail to result in actionable biological conservation and natural resource management outcomes; something well-documented by the emerging literatures on "knowledge exchange" and "knowledge mobilization" (e.g. Fazey et al., 2012; Cvitanovic et al., 2015; Nguyen et al., 2017a). This results in management decisions that are often made without the best quality evidence, thus increasing the probability of inappropriate conservation and management actions (Pullin and Knight, 2003).

Genomics research – a relatively new field of scientific knowledge – is often promoted as a beneficial management tool for the preservation of biodiversity, species, and populations (i.e. conservation genomics) (Shafer et al., 2015; Garner et al., 2016). Whereas, for decades, molecular markers (fragments of DNA) have been used in traditional conservation genetics, conservation genomics uses genome-wide information (complete systematic mapping of DNA) to conserve biodiversity and manage species and populations, which in principle, improves genetic precision and inferences between genotype and phenotype (Shafer et al., 2015). For example, cutting-edge genomics research on

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salmonids, the key model species for applying conservation genomics, is (finally) providing insight on the heritable basis of ecologically relevant traits – the adaptive genomic variation associated with specific phenotypes (e.g. Aykanat et al., 2015; Barson et al., 2015; Pearse, 2016; Waples et al., 2019). However, like other new research, conservation genomics may be difficult to translate into evidence-based conservation and management. This is especially true when there is uncertainty or disagreement among the different actors about the value, relevance, and utility of the scientific knowledge (Roux et al., 2006; Cook et al., 2013; Young et al., 2018); when there are different expectations and preferences of new knowledge (Young et al., 2016a); when organizational structures and culture limit communication (Soomai, 2017); and when conflict exists between scientists and elements of broader society about the ownership of new knowledge (i.e. what knowledge is privately held vs. in the public domain or in the public interest) (Salter and Salter, 2017).

Conservation genomics, in general, has made little advancement towards routine application in conservation practice (McMahon et al., 2014; Grueber, 2015; Shafer et al., 2015; Garner et al., 2016; Shafer et al., 2016). This is likely in part due to a "credibility crisis" as genomics ran into difficulties of political buy-in during the 2000s (Salter and Salter, 2017), to public concern and fear about genetically modified animals (i.e. transgenics) (Check, 2002), and to an implementation 'gap' between fundamental research and applicable solutions for conservation practitioners (Shafer et al., 2015; Taylor et al., 2017). The "conservation genomics gap" is also a result of challenges in generating and interpreting genomic data, tasks that have to date been largely confined to academic researchers (Shafer et al., 2015). Each of these problems is connected to a major barrier identified in successfully mobilizing academic science more generally – the failure of scientists to understand the behaviours, preferences, and viewpoints of potential users of their knowledge, and to also effectively translate their science to potential knowledge users (Young et al., 2016a). Another compounding factor may be, as Shafer et al. (2015) argue, that the core problem is not a lack of knowledge about conservation issues but rather a lack of political will to act appropriately on this knowledge. It is also important to recognize the tension between reducing uncertainty through gaining knowledge from scientific research versus the very urgent concerns faced by practitioners of biodiversity conservation (Wiens, 2008). Conservation genomics of salmonids serve as an excellent example to explore this (Piccolo, 2016).

For genomics to have meaningful impact on fish and wildlife conservation and management, suitable ways to remove or overcome general barriers limiting the use of new scientific knowledge are required (Gibbons et al., 2008; Shafer et al., 2015; Shafer et al., 2016; Nguyen et al., 2018; Young et al., 2018). This is especially the case where the new scientific knowledge is technical in nature and prone to using jargon which may alienate those external to the scientific process (Hoban et al., 2013). We analyze how potential knowledge users (government employees and stakeholders [fish and wildlife managers and decision-makers]) perceive and evaluate new claims of conservation genomics knowledge using the case of managed rainbow trout (*Oncorhynchus mykiss*) fish and fisheries in British Columbia (BC).

Rainbow trout are a native cold-water salmonid fish to BC whose populations (when and where thriving) support recreational and subsistence fisheries, which in turn support cultural, social, and economic well-being. Rainbow trout represent 58% of the annual 7.5 million fish caught in the province translating into $957 million CAD direct (e.g. licence sales, accommodations, packages etc.) and indirect (e.g. sales of equipment, boats, fuel etc.) economic contributions (Bailey and Sumaila, 2012; Freshwater Fisheries Society of BC, 2013). However, hydrological changes linked to climate change (increased summer water temperatures and low flows in rivers; increased pH levels, decline in water oxygen content, and increased hypoxia in lakes) are a primary concern that threaten the long-term sustainability of rainbow trout fisheries.

The near-ubiquitous range of rainbow trout in BC is managed through a complex combination of provincial and federal agencies and processes. The system is decentralized and depends on a range of individual actors (e.g. Biologists, Fish and Wildlife Section Heads, Directors, Resource Managers, Assistant/Associate Deputy Ministers, Deputy Ministers etc.). Sport fishing occurs throughout the entire province of BC and provincial fisheries management is divided into nine resource management regions to cover all areas of the province. The conservation and management of freshwater fish is a provincial responsibility while marine fish are a federal responsibility. The British Columbia Ministry of Forests, Lands, and Natural Resource Operations and Rural Development (FLNRORD) is the primary responsible agency for management of wild freshwater populations of rainbow trout. The Ministry also receives scientific and resource support in management from the British Columbia provincial Ministry of Environment (MOE). The Federal Department of Fisheries and Oceans Canada (DFO) is the primary responsible agency for the management of the anadromous form of *Oncorhynchus mykiss*, Steelhead trout. Many of the lakes within BC do not naturally support fish populations due to a lack of spawning habitat or other limitations and in many lakes in the province annual stocking programs are delivered. The Freshwater Fisheries Society of British Columbia (FFSBC) is a private non-profit organization contracted by FLNRORD to deliver the provincial fish stocking program and to offer a range of conservation services (i.e. outreach activities, education) to protect wild fish by diverting recreational angler pressure to hatchery-raised fish. Some First Nation (indigenous) communities manage indigenous and non-indigenous recreational and subsistence fisheries on their reserve lands (areas set aside for First Nations people after a contract with the Canadian government) and are also building relationships and addressing concerns with land and resource use on asserted traditional territories.

Fish and wildlife managers are thus important potential users of new science and represent an important interface for science and action (Young et al., 2013). It is therefore important to understand the perspectives of potential knowledge users and understand the challenges that may impede the movement of new knowledge into action. Along with Taylor et al. (2017) our research is one of the first contributions to navigating the conservation genomics gap or 'space' (Toomey et al., 2017) by directly identifying preferences, experiences, knowledge of, and viewpoints of potential conservation genomics knowledge users (practitioners). However, like Taylor et al. (2017), our case study represents only one context, but provides further knowledge to the factors that could perpetuate a "conservation genomics gap", the perceived barriers of integrating new genomics knowledge into conservation practice, and potential solutions to bridge or navigate the gap. We conclude by providing recommendations to improve communication between genomics research scientists and potential knowledge users with a focus on increased genomics education and awareness.

2. Methods

This research was exploratory, aimed at investigating and categorizing a set of perceptions and behaviours among knowledge users that were unknown at the outset of the study. As such, this research is intended to be primarily descriptive, and hypothesis-generating rather than hypothesis-testing. The data reported in this article were collected as part of a broader study entitled "*Sustaining Freshwater Recreational Fisheries in a Changing Environment*" that aims to develop conservation genomic tools and policy recommendations to help manage and preserve the genetic diversity of rainbow trout. The study objective is to support and sustain healthy populations of rainbow trout and the recreational fishery that depends on them.

Befitting exploratory research, we developed and employed an interview schedule using a mixed-methods approach with both closed- and open-ended questions (Axinn and Pearce, 2006). The closed-ended questions involved a series of Likert-style opinion statements about

Table 1
Interview questions analyzed in this article.

Question	Type
Are you familiar with genomics research?	Open-ended
What do you think of genomics research?	Open-ended
What are the upsides of genomics research (if any)?	Open-ended
What are the downsides of genomics research (if any)?	Open-ended
Do you see genomics research deriving more benefits (being more valuable) for fish stocking programs or for the management and conservation of wild fish populations?	Open-ended
Please indicate the degree to which you agree or disagree with the following statements about genomics research	Closed-ended (Likert-style) with open-ended follow up

Table 2
Affiliations of the 65 respondents, grouped as government employees and stakeholders.

Government employees	*N*	Stakeholders	*N*
Biologists (FLNRORD)	17	First Nations fishery	4
Fish & Wildlife Section Heads (FLNRORD)	6	Private environmental consultants	6
Directors (FLNRORD)	3	Academia	6
Policy Analysts (FLNRORD)	2	ENGO	5
Human Dimensions Specialist (FLNRORD)	1	Retired Government Employees	3
Conservation Science Section (MOE)	3	Freshwater Fisheries Society of BC	6
Science Branch (DFO)	1	BC Hydro	2
Total	33		32

genomics research (which we define as the use of high-throughput sequencing of genome-wide information (Shafer et al., 2015; Garner et al., 2016)) for which respondents were asked to indicate their level of agreement on a five-point scale (strongly disagree, disagree, neither agree nor disagree, agree, and strongly agree), with the option of answering “I don't know”. Open-ended questions allowed respondents to explain their positions and opinions freely. The set of questions analyzed in this article are provided in Table 1. Respondents were not presented with a definition of genomics, its distinguishing characteristics between “traditional” (conservation) genetics, nor the costs or benefits of genomics research. Qualitative data were analyzed using NVivo 12 software (QSR International Pty Ltd., 2018). Quantitative (Likert) data were analyzed using the ‘Likert’ (Bryer and Speerschneider, 2016) and ‘psych’ packages in R version 3.4.4 (R Core Team, 2018). For open-ended responses a three-step inductive coding process was applied to qualitative data (Thomas, 2006). First, responses were read to identify key words (Fig. S1), which became a list of potential codes. Similar potential codes were then grouped into themes. Responses were read a second time and sorted under these themes to provide a measure of their prevalence. A response may have multiple thematic codes if warranted. All coding was performed by the first author.

We developed the initial population frame for the interviews based on a review of the ‘grey’ (government) literature on fish policy and regulations and the BC Government Directory (https://dir.gov.bc.ca/) searching for: “fish” or “fisheries”. The population frame was then further developed in consultation with three senior managers at FLNRORD, MOE, and FFSBC to ensure that key government employees and stakeholders were identified. The population frame was then supplemented by snowball sampling from voluntary referrals by respondents. A total of $N = 163$ individuals or organizations were contacted to request an interview. This study was conducted in accordance to the University of Ottawa Research Ethics Board (File Number: 02-18-08).

A total of 65 interviews (response rate of 40%) were conducted in-person ($N = 43$) and over the phone ($N = 22$) between April and November 2018 divided between two broad groups: government employees ($N = 33$), and representatives from non-governmental stakeholder groups ($N = 32$) involved in the management of recreational and subsistence rainbow trout fisheries in BC. The two-sample Mann-Whitney U (Wilcoxon rank-sum) significance test was used to compare quantitative (Likert) responses between these two affiliation groups. The government employees group includes a large number of FLNRORD individuals involved in fisheries management (i.e. Directors, Resource Managers, Fish and Wildlife Section Heads, and Biologists), as these are the employees most directly involved in freshwater fisheries management with stakeholders and in-season decision-making. It also included employees in the MOE Conservation Science Section who were identified as working closely with fisheries managers and stakeholder groups. A few employees from the DFO Science Branch were identified for their expertise in genomic applications to fish conservation. The stakeholder group includes representatives of recreational and subsistence fisheries, BC Hydro (the province-owned electricity utility that has a major water and land footprint in BC), academia, First Nations communities, ENGOs, and environmental consultants who are hired by stakeholders and play a role in management processes. The affiliations of respondents are provided in Table 2. We recognize that the term stakeholder does not comprehensively describe the diversity and nuances of all individuals involved shown in Table 2. For example, First Nations communities are grouped as stakeholders (those with vested interests in managing freshwater fish and recreational and subsistence fisheries), but it is important to note that under BC legislation they are in truth ‘rights-holders’ given the special legal status of indigenous rights and territorial claims. Each stakeholder has distinct interests, values, identities, and perspectives. This group is, however, distinct from government employees occupying similar roles in that they are all involved in the management of BC rainbow trout but external to government (see Young et al., 2016a; Young et al., 2016b; Nguyen et al., 2018; Young et al., 2018) so stakeholders is an imperfect term that we employ with this important caveat. While the focus of this research is recreational rainbow trout fisheries, it is important to recognize that the term ‘fisheries management’ may be limiting in this research-context as several of the respondents manage fish (and not anglers) while others manage both fish and wildlife populations. Therefore, the responses in this article are most specific to fisheries management but are described throughout under the broader term ‘fish and wildlife management’. Among the respondents, 56 were male and 9 were female. Government employee respondents covered each of the 9 different resource management regions in BC (Region 1: Vancouver Island, Region 2: Lower Mainland, Region 3: Thompson-Nicola, Region 4: Kootenay, Region 5: Cariboo, Region 6: Skeena, Region 7A: Omineca, Region 7B: Peace, Region 8: Okanagan). Some respondents elected to remain anonymous while others released their identities. Interviews lasted between 18 min and 2 h, depending on the level of detail provided by the respondent.

3. Results

3.1. Familiarity with genomics research (understanding of genomics)

As mentioned previously, a lack of familiarity with genomics

Table 3
Mean responses to twelve Likert-style opinion statements about genomics research (0 = strongly disagree, 1 = disagree, 2 = neither agree nor disagree, 3 = agree, 4 = strongly agree).

	Government employees		Stakeholders		Significance
	Mean	SD	Mean	SD	
1. Genomics research provides reliable information about rainbow trout populations	3.07	0.62	3.21	0.68	0.422
2. Genomics research about rainbow trout would help me make better decisions	2.83	0.71	2.88	0.98	0.488
3. Genomics research is worth the monetary cost	2.57	0.84	3.04	0.76	0.043*
4. Genomics research provides us with information we wouldn't otherwise have from other sources or studies	3.30	0.53	3.35	0.88	0.319
5. Genomics should play a more central role in rainbow trout management than it currently does	2.57	0.69	2.71	0.81	0.305
6. The benefits of genomics research for trout management are over-stated	1.76	0.83	1.48	0.80	0.188
7. Genomics data should be freely available to anyone who wants it	3.26	0.68	3.16	0.97	1
8. I have ethical concerns about genomics research on trout	1.03	0.98	0.71	0.86	0.169
9. I am worried about incorporating genomic technologies into rainbow trout populations	–	–	1.16	0.99	–
10. I am worried that stakeholders will think that genomics research on rainbow trout means incorporating genomic technologies (transgenics/genetic modification) into rainbow trout populations	1.70	1.17	1.38	1.19	0.494
11. I am worried that stakeholders will think genomics research on rainbow trout may eventually lead to incorporating genomic technologies (transgenics/genetic modification) into rainbow trout populations	2.10	1.14	1.50	1.20	0.245
12. I am worried about genomics research on rainbow trout populations	–	–	0.82	0.81	–
N	33		32		

$N = 65$; $^{*}p < 0.05$, based on Wilcoxon rank-sum test for ordinal data (Mann-Whitney two-sample significance test).

research among potential users is a major barrier to uptake. Consistent with this, only 26% of respondents in our study stated that they are familiar with genomics research, while 42% were vaguely familiar and 32% were unfamiliar. Of those that were vaguely familiar, very few understood the difference between genetics and genomics so overall, the vast majority (~74%) were not familiar with genomics nor understood the difference between genomics and genetics.

Table 3 presents findings from the twelve Likert-style opinion statements about genomics research that were read to or shared with respondents during interviews. The results are presented below linked to these twelve statements.

3.2. Benefits of conservation genomics research

Despite low overall familiarity with genomics, government employee and stakeholder respondents overwhelmingly saw genomics research as a valuable endeavor ($N = 60$), providing both reliable and novel information and knowledge about rainbow trout populations (Table 3, #1 & #4) that generally would help improve their conservation decision-making (Table 3, #2) (see Table 4-1 for illustrative quotations). Positive responses included descriptions of genomic science as "robust", "accurate", "enormously-detailed", "fast-paced", and the "future for molecular-based research".

Respondents recognized the value of genomics research for: understanding disease outbreaks or prevalence to diseases, identifying and helping prevent hybridization, and identifying introgression of domestic and wild genotypes (risks associated with wild and hatchery fish interactions). However, the benefits respondents most-often identified and discussed were: identifying threats and threatened populations, identifying genetically distinct unique populations, and understanding genomic diversity and linking it to phenotypic diversity.

With respect to BC freshwater fisheries, respondents consistently mentioned the threats of high pH (alkalinity) and water temperatures. Thus, respondents were able to identify the value in genomics research exploring resilience, adaptation, and sensitivity (i.e. tolerance and limitation thresholds in strains, stocks, or individual fish to temperature, pH, oxygen) (see Table 4-1.1).

Identifying fish that might be better locally adapted to drought conditions or water quality changes was seen as a significant benefit, especially given – as many respondents indicated – that these are expected to be increasing threats down the road, threatening intraspecific (within-species) biodiversity. Other mentioned threats which could be addressed by genomics research include the role of hatchery stock in the fitness of wild stock, the impact of invasive species on fitness, and impacts to habitat quality.

Respondents recognized the benefits of genomics research in identifying the source of genetic uniqueness, distinctness, and relatedness (i.e. defining populations) (see Table 4-1.2). These benefits may extend to identifying completely isolated populations or genetically distinct populations. There was strong agreement this knowledge would help in conserving unique or distinct populations and stocks of rainbow trout by identifying which stocks to protect and which stocks management could be more or less risk adverse with. To this goal, several respondents acknowledged genomics would help in providing data on historical fish-stocking (i.e. on the lineage and population history [trends, decline, expansion] of domesticated strains in BC and their possible origins) for which records were poorly kept, if at all; identifying the distribution (*where* and *when*) of feral (historically-domesticated) versus wild fish populations; and how that information might correspond with, for example, indigenous and local knowledge.

Moreover, government employees identified the value of genomics research to efficiently assess populations through population or stock monitoring, especially in mixed-composition fisheries and *when* and *where* stock identification is difficult or impossible to do visually (see Table 4-1.3).

There was common support that genomics research could benefit fish and wildlife management by characterizing meaningful genetic diversity. Respondents provided numerous examples where genomics could help in understanding the levels of biodiversity within fish which might have implications for the way in which fish are managed. For example, the benefits of genomics research were referenced with respect to triggering or differentiating: stream- versus shore-spawning fish; resident (e.g. rainbow trout or kokanee) versus anadromous (e.g. steelhead or sockeye) fish; run-timing (i.e. migration composition, strength, and competition); life-history stages and characteristics; ecotypes (i.e. distinct form of a species occupying a particular habitat); local adaptations; fidelity (see Table 4-1.4).

The ability to get detailed genomic information to then compare to phenotypic variation and attributes – being able to link genotype and phenotype (i.e. the genetic basis of physical characteristics and traits) – was seen as highly informative to understand within-species and population-type diversity so that conservation efforts could be managed to protect and maintain sufficient genetic diversity and to enhance the resilience of populations (see Table 4-1.5).

3.3. Tension between conservation genomics and conservation practice

While, in general, genomics research was viewed favorably, the

Table 4

Illustrative quotations from government employee and stakeholder respondents about the benefits, the uncertainty and relevance, and barriers to implementation of conservation genomics.

1. Benefits of conservation genomics research

I think it's a fundamental tool now in a manager's toolbox. Like, I've seen it in the last 5 years working here, we've used it to inform management decisions. Maybe not even inform management decisions in some cases but used as a tool to help us understand more about the population in a way that helps guide further monitoring work or helped us determine a certain question around what the underlying biology of the population is. (Interview #27; male; First Nations fishery affiliation).

1.1 Identifying threats and threatened populations

In the summer of 2015, the drought year, stream levels receded. Temperatures increased. And all of a sudden, we were faced with making decisions on which streams to close to protect fish. And there's a lack of information about temperature thresholds. So, I guess if we had some information like this strain will be ok up to 22 (°C), while this one suffers at 18 (°C) it might help us manage stream-flows, seasonal openings, and closures. (Interview #28; male; FLNRORD affiliation).

I think looking at some of these different things, we're going to have to find Rainbow Trout strains that are more tolerant to pH or temperature and if we don't, people are putting Bass and Perch in these lakes. So, what we'll see is that if we can't keep Rainbow Trout alive in some of our lakes – I mean this area is known for Rainbow Trout, this is a mecca in North America for Rainbow Trout – but if we can't sustain those populations people will move other fish in; non-native fish that we have to then deal with. (Interview #18; male; FLNRORD affiliation).

1.2 Identifying genetically distinct unique populations

We're really able to understand the genetic architecture and how particular phenotypes arise and whether they're worthy or not of special consideration when it comes to management. So, for example, the genes that produce summer-run fish opposed to winter-run fish. Knowing exactly where that is, understanding the likelihood of those re-evolving quickly or slowly has important practical consequences. I mean even the way we split up conservation units, plays directly into and elevates the importance of say conserving a particular population; closing a certain fishery right down to direct economic impacts to a particular stakeholder group. So, it helps to clarify what's important and what's not. (Interview #19; male; FLNRORD affiliation).

1.3 Assessing and monitoring populations

I think it's a super helpful tool to identify related groups of fish, for example. Any kind of plant or animal actually. But once you know that you have some discrete conservation unit – and genomics can help to inform that – you can do a better job of conservation if you have a notion of what the geographic focus is and also then the relative abundance of that particular unit might be and whether it's of concern or not. (Interview #24; male; FLNRORD affiliation).

1.4 Characterizing meaningful genetic diversity

Shore-spawning and stream-spawning kokanee: you know, are the shore-spawners just stream-spawners that are too lazy to go into the stream? But actually, they seem to have different genomes. The DNA is different. So, that corroborates phenotypic observations of behaviour. (Interview #24; male; FLNRORD affiliation).

The relationship between Steelhead and Rainbow Trout – that's not something we clearly know. It appears like they can switch between Rainbow Trout and Steelhead even though there are differences genetically. But I don't think we fully know that yet. So, some of those questions are huge because for example, the Thompson River-Steelhead, we're down to < 200 fish. And it's a very unique world class fishery that we can't even open anymore. And so, there's some thought that we still have this genetic bank of Rainbow Trout that at some point can turn into Steelhead. So, understanding some of those relationships I think is pretty important for sure. (Interview #18; male; FLNRORD affiliation).

1.5 Understanding genomic diversity and linking it to phenotypic diversity

We used genomics to actually look at the structure of early-time spawners and average-time spawners in tributaries and they're basically all one big population. So, it's a benefit to us. It's helped us effectively manage what our mitigation responses are to potential impacts. (Interview #61; male; BC Hydro affiliation).

2. Tension between conservation genomics and conservation practice

2.1 Questioning the relevance of genomics to management and conservation

I think we already know a lot of that, in terms of climate change, impacts of fishing and land use. It's just actually making and implementing the decisions to address those types of conservation concerns, is the challenge. (Interview #5; male; FLNRORD affiliation).

Are we going to be deriving information which is going to allow us to be more specific than the general knowledge out there? And I would probably imagine that no – we probably already know what we need to know in order to manage 99% of what we would do in the Steelhead realm, for instance. And again, it's unclear to me as we drill right down to that level of individual program management how any level of additional information is going to help inform that. I might be wrong there but I'm not sure that we see a bunch of specific management outcomes proliferate from this work. (Interview #33; male; FLNRORD affiliation).

Table 4 (*continued*)

On the conservation side, my experience is that it is generally not a data deficiency issue. It's usually pretty clear what's causing the conservation concern and its more just the difficulty of implementation. There's not – I don't think – a data shortage in genomics that's going to help the conservation part. I could be wrong. (Interview #20; male; FFSBC affiliation).

2.2 Discrete and limited conservation and management levers

We mostly think about fishing regulations as the thing that we control but when it comes to things like temperature tolerance or sensitivity, we're talking about water use, we're talking about forestry, we're talking about other things. So, if I think a bit more globally, I could imagine maybe ways in which genomics information gets incorporated or could be incorporated into population management at a level that's beyond our fish section here. (Interview #32; male; FLNRORD affiliation).

3. Barriers to implementation of conservation genomics

3.1 Communication disconnects between researchers and knowledge users

I've heard of the genome project. I don't know much about it. We haven't had much involvement, right? So, I think there's a little bit of a disconnect – there always is – between research and how that research can be applied for management. We're management, there's research – and there's a bit of a gap in between. And so, I think maybe within the Ministry we should be better at pursuing some of that research. But I think there must be a mechanism for management and research to meet in the middle. We often work with universities and describe the management goals we hope the research will inform and often what we get back is great information, but it's not applicable to management. So, how is this research going to actually help us with decisions? And that seems to be the disconnect sometimes, because researchers love to do research and then they get off on a tangent and that's great. It's interesting information. But from my perspective, it's how can we can use that information to make more informed management decisions? (Interview #18; male; FLNRORD affiliation).

I have seen the downsides of some research here in BC in that the process takes so long, and we aren't actually given the tools or the application in the end. It gets published in some journal and we're not even told about it. And then all of a sudden you come across this piece of published research. Oh, that's my colleagues and this isn't even something that was sent out to us. To be honest these models are so complicated and amazing and they're really neat but then giving us (the managers) the tools, there's a real gap in the middle. I'm kind of waiting, waiting, waiting. So that would be the downside is just that gap between these really, really complex models and then giving us something to manage by. Or maybe even convincing us to use it. (Interview #25; female; FLNRORD affiliation).

3.2 Practitioner misunderstanding and confusion leading to potential misuse and misapplication

There's a lot of unfamiliarity with the techniques and a lot of times people may not understand it. I mean, I think it can be intimidating to a lot of people because they don't have the background in the science behind the tool. So, a lot of times it's a tool that seems like it has a lot of black magic behind it. So, people are maybe intimidated by it or don't trust it. I've definitely seen too, where there's less uptake on the use of the tool because people don't really understand what it can be used for and the science behind it. So, that's definitely a downside. It's just a suspicion that it's not being used to its full potential. (Interview #27; male; First Nations fishery affiliation).

I'm optimistic around some of the new technologies but I'm very limited – I have a limited understanding of it. Because they [fish populations] somehow seem different or better, realistically, I'm totally unclear how much better or different they might be. (Interview #33; male; FLNRORD affiliation).

3.3 Misunderstanding genomics research as genetic modification

I would say that I agree with both of the statements based on the feedback we get on our work with triploid rainbow trout and kokanee. There is a small but vocal minority of our angler stakeholders that equate what we're doing (pressure shocking eggs to render them subsequently sterile) with inserting genes and making transgenic fish (which we don't do and have no interest in). So, based on that, I think that some stakeholders could be confused by the term genomics and interpret is as something else. (Interview #1; male; FFSBC affiliation).

I'd have to 'neither agree nor disagree' to these questions. On one hand I've had anglers who I thought were quite knowledgeable express concern over these same issues. On the other hand, most knowledgeable anglers who I talk to are aware and understand. This is quite clearly an education issue which needs some resources dedicated to it. (Interview #50; male; FFSBC affiliation).

We get the question all the time – not just about triploid fish – are these genetically modified? People are very leery about genetically choosing a specific fish. And that's a really big concern for the public. So that's something that could be a negative perception of doing any – not that we're modifying – but even just selecting for certain genetics, that scares people, I think. There are probably some dangers involved with that. (Interview #18; male; FLNRORD affiliation).

(*continued on next page*)

Table 4 (*continued*)

3.4 Differences in data and results interpretations

I guess one generalized comment is that some researchers are able to find with some incredible accuracy and precision interesting things around lineage and diversity and similarities or differences in populations and population structure. Whereas others are able to not infer almost anything at all given large datasets and it's unclear to me how we can have such resolution on one hand and such opacity on the other given the same technique used for two different populations. So, in some cases I'm not even in a position to really critically review or understand. I mean, it's kind of looking at a binary code, a series of 1s and 0s. I'm certainly not in a place to be as critical as I think I'd like to be. (Interview #33; male; FLNRORD affiliation).

3.5 Uncertainty over whether differences or variation have any meaningful or demonstrable value, or ecological relevance

Someone did some kokanee work for us on the west-arm of Kootenay Lake analyzing Single Nucleotide Polymorphisms (SNPs), and they determined that shoal-spawning kokanee were different than tributary-spawning kokanee in the west-arm. So, I guess the downside of it is, what does that actually mean, right? Where's the phenotypic difference – is it the pH? O_2? is it they can live in lower O_2? So, we can get the difference, but we don't know what it means. So, I think that's one of the downsides of it, is you can find the difference but actually linking it to something is maybe difficult. (Interview #62; male; BC Hydro affiliation).

3.6 Cost

Well that comes down to the cost change on a sliding scale – how much you do and what kinds of SNPs you develop right? So, it can come down. But in general, we are confined to these funding pots that we use and so you're talking about sometimes taking up a large portion of a typical project fund to put into that. So, I think it is worth it in very specified situations definitely, but the costs have to come down for it to be used as a general tool. So, if the costs come down then yeah it could end up becoming a standard practice for us for a lot of different projects. If it's making up the majority of the expense, then you really want to make sure it's providing you some target information you're specifically after. (Interview #20; male; FFSBC affiliation).

3.7 Potential to misspend limited resources

As facetiously described: Why bother cutting back on forestry and buffers around streams when you can just introduce fish that are more adaptable to increased turbidity and temperatures? (Interview #31; male; FLNRORD affiliation).

3.8 Temporal mismatches between the supply of genomics and the demands of conservation practitioners

And then of course, operationalizing the results of finding a stock of rainbow trout that are tolerant to low or lower oxygen or high pH or whatever it is that we're seeking – making it an operational reality just seems so far off right now. It truly is an academic undertaking and climate change, environmental change, is happening at a much faster pace than perhaps our research is getting done. (Interview #51; male; FFSBC affiliation).

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exact role of genomics in rainbow trout management was less clear (Table 3, #5). Some respondents noted that use of genomics research in decision-making depends on management objectives and the ability to use genomics in support. Others noted that species other than rainbow trout (i.e. those with greater conservation concerns) would benefit more from genomics research. A substantial number ($N = 25$) of respondents questioned the relevance of genomics to fish and wildlife management. Most of these questions centred around *whether* or *how* genomics research could influence management outcomes and change the way that management levers could be pulled (see Table 4-2.1). These opinions mostly align with the description from Shafer et al. (2015) of the disconnect between conservation genomics research and conservation practice as being associated with political rather than knowledge limitations.

Others noted an important limitation -specifically, there are only a discrete number of levers most fish and wildlife managers have at their disposal (see Table 4-2.2). In other words, the use of genomics knowledge to inform management decisions may be limited by organizational structure and processes that implicate other facets of decision-making beyond those traditionally associated with fish and wildlife management.

3.4. Barriers to implementation of conservation genomics

A substantial number of respondents ($N = 44$) provided feedback on what they perceive to be downsides, risks, or barriers of genomics research, while seven respondents explicitly stated they do not see any. Among those with concerns, key issues included: that enormous amounts of information make it too difficult to integrate; overwhelming researchers and users searching for a signal in ample noise; focusing on economically important resources; contributing to increased handling of already sensitive or endangered organisms; and diverting interest and attention from more basic and broad biological questions which may be more relevant for conservation. Other barriers described in more detail include: communication disconnects between researchers and knowledge users; practitioner misunderstanding and confusion; differences in data and results interpretations; linking genomics to something meaningful; cost; potential to misspend resources; and the applied-genomics process being too slow for conservation and management.

There was general agreement that the benefits of genomics research for trout management are not over-stated (Table 3, #6). However, this result was not unanimous, suggesting communication disconnects between researchers and knowledge users. The implementation space between genomics research scientists and knowledge users was described as disconnected on account of poor engagement and communication (see Table 4-3.1). Upon completion of some partnered genomics projects, government employees indicated with concern, that they were never informed about and actually given genomics applications and management recommendations (see Table 4-3.1).

A considerable number of responses described genomics as overly-technical and complex – especially for when engaging directly with stakeholders. There was some worry that knowledge users may take genomics findings at face-value, over-estimating the potential of the science to solve problems and answer questions. If true, respondents recognized that this may potentially open doors for the science to be misused or misapplied (e.g. putting more pressure on fish stocks, misuse of the designatable conservation unit concept). These responses further explained a potential loss of engagement with any knowledge user not interested in the technical details. Genomics was even analogized as a "bit of a black art" (see Table 4-3.2).

Government employees and stakeholders described a (rare) concern that some knowledge users, including the general public, may misunderstand genomics as genetic modification (Table 3, #9–11) (i.e. transgenics, genetic modifications); misunderstandings or assumptions that some respondents suggested could be addressed by clear communication (see Table 4-3.3). Ethical concern over applying genomic technologies to fish, however, was generally not the prevailing opinion held by the government and stakeholder respondents interviewed in this article (Table 3, #8, 9, & 12).

The confusion and complexity of genomics science may be compounded by differences in the interpretation of data and results according to some government employees and stakeholders. Several respondents claim that differing results and conclusions between genomics research scientists may alienate or mislead potential knowledge users who have no way themselves of validating the accuracy and precision of results (see Table 4-3.4). Thus, genomics research and its scientists may cultivate skepticism and may be perceived as arrogant or audacious by knowledge users.

Respondents also expressed concerns about the implications of detecting the presence or absence of genomic differences or variation and what this means in practice (i.e. the ability to translate genomics results to conservation and management decisions, polices, and practices). There was uncertainty as to whether differences or variation that genomics research scientists find have any meaningful or demonstrable value, or ecological relevance (see Table 4-3.5).

In the absence of meaningful differences or variation respondents expressed uncertainty and questioned whether that is a product of failed or false detection (perhaps due to poor study design), or whether conclusions are indeed biologically significant. There were also concerns that genomics results could potentially either confuse, over-sell,

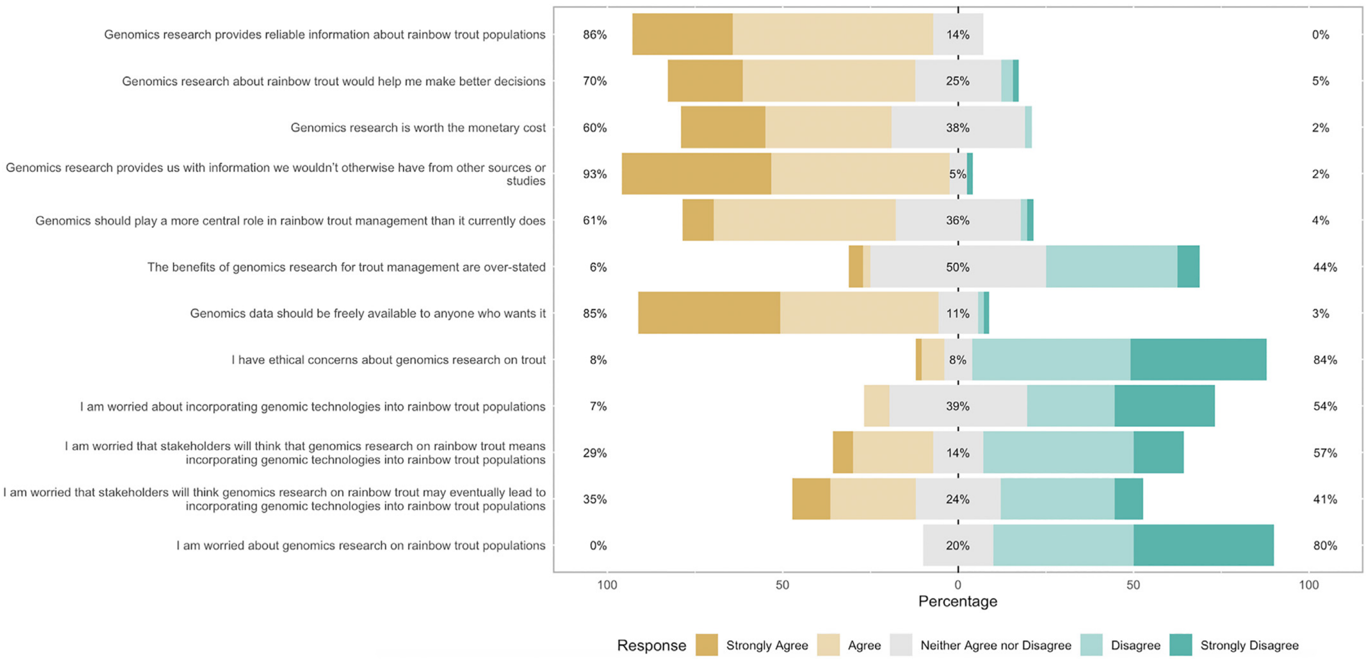

Fig. 1. Likert-bar plot of the responses to twelve Likert-style opinion statement about genomics research pooled by respondents ($N = 33$ government employees, $N = 32$ stakeholders).

or under-sell the environmental factors that regulate gene expression (i.e. a lack of genomic understanding of the genetic basis of phenotypic variation). It was suggested by respondents that genomics research scientists should communicate genomics results in an objective way that is accessible to knowledge users; clearly focusing on and communicating the limitations, possibilities, and advantages of genomics science (i.e. what it can and cannot do).

There was general agreement that genomics research is worth the monetary cost (Table 3, #3) but like #5 & #6 (Table 3) these results were not unanimous, suggesting practitioners may not be educated on the costs or benefits of genomics. This is the only opinion statement on which government employees and stakeholders significantly differed in their responses. Stakeholders tended to agree with the statement more than government employees; although the statistical significance or clarity (Dushoff et al., 2019) is marginal when measured along a continuum of statistical significance. Given that this was the only statistical difference, and it was only marginally clear at best, we present findings of the responses to opinion statements in Fig. 1 pooled for stakeholders and government employees. Some responses supported the idea that genomics research is an expensive and time-consuming pursuit, especially for large geographical ranges or regions such as rainbow trout in BC, where comprehensive spatial coverage for sample-collection is required (see Table 4-3.6).

There was a strong consensus that genomics data should be freely available to those who want it (Table 3, #7). However, a respondent expressed concern that freely available genomic data would influence angler preferences while another acknowledged the 'double-edged sword' between sharing data and protecting data for publication.

There may be a risk that investments of (limited) resources in genomics science may be poorly spent if investments elsewhere may yield higher beneficial returns for conservation, identified some respondents. Particularly, spending on genomics could limit funding to other forms of (e.g. small-scale, rudimentary) research or to clear conservation concerns whereby investments could instead be made into preserving and protecting those populations by, for example, habitat restoration; habitat enhancement; monitoring of fish and fisheries; and enforcement. If money spent on genomics could be better spent on direct conservation measures or practices, genomics could undermine or undervalue these measures or practices and instead promote or unintentionally-facilitate "worst practices", noted some respondents (see Table 4-3.7).

Several respondents made statements based on their own experiences, that the applied-genomics process of collecting and reporting back data for monitoring and management purposes takes too long (i.e. is too slow to inform management dealing with environmental changes that are happening at faster paces) (see Table 4-3.8).

4. Discussion

The potential for research-implementation "gaps" or "spaces" (Roux et al., 2006; Arlettaz et al., 2010; Cook et al., 2013; Toomey et al., 2017) between conservation science and evidence-based management in conservation practice have been well documented. If conservation practitioners aspire to make conservation and management decisions informed by the best-available science (Dicks et al., 2014a; Dicks et al., 2014b), and conservation scientists aspire to produce conservation and management-relevant science (Liu et al., 2008; Cook et al., 2013), implementation and integration spaces between these two complementary goals suggest real (or perceived) barriers. We explored the role of conservation practitioners in the "conservation genomics gap" (Shafer et al., 2015; Garner et al., 2016; Taylor et al., 2017) by consulting directly with potential genomics knowledge users using a specific case of a recreational and subsistence freshwater fishery. Overall, respondents were largely unfamiliar with genomics yet highly receptive to embracing genomics as a science to inform conservation and management decisions, policies, and practices; similar to results found in New Zealand (Taylor et al., 2017). By revealing preferences, demands, experiences, knowledge of, and viewpoints of conservation practitioners we highlight some of the barriers that they perceive to conservation genomics knowledge transfer (i.e. knowledge mobilization and exchange) into conservation practice. The interviews also revealed opportunities (potential solutions) to overcome barriers in the translation of genomics research into conservation practice in our case study.

There was rather low familiarity of genomics (i.e. the complete genome-wide high-throughput sampling and sequencing of nucleic acids of organisms) science held by conservation practitioners, representing an opportunity to increase genomics education and outreach targeting conservation practitioners. Like practitioner respondents in Taylor et al. (2017), in our case, practitioners were also aware of their lack of knowledge in genomics (and genetics) and were keen to receive more information, presenting an opportunity for genomics researchers to communicate the relevance of their science. However, many of the benefits identified by the smaller proportion of respondents familiar with genomics were management-specific. Conservation practitioners were therefore able to recognize – despite in cases, low familiarity with the science – precise conservation-relevant benefits. This should be encouraging for genomics scientists for two reasons. First, the majority of identified benefits are prevalent issues in conservation practice and can be disseminated to contexts beyond our specific case. Second, conservation practitioners have a good understanding of what specific knowledge they need and want to inform conservation and management. If genomics researchers hope to produce salient science that will be translated into practice, they need to focus on these benefits and address management-relevant questions (Fazey et al., 2005), and appreciate the practical demands of conservation practitioners. For example, respondents were very focused on resilience, interested in the capacity of genomics to inform the sensitivity and adaptation potential of the populations they manage – both wild and hatchery (stocked) fish populations – to environmental threats particularly linked to climate change. Respondents were also very interested in genetic distinctness and uniqueness to inform management by the delineation of discrete populations (e.g. management or conservation units - Bradbury et al., 2013; Flanagan et al., 2018); linking genomic diversity to phenotypic diversity; prevalence and susceptibility to disease; fitness consequences from introgression between domestic and wild genotypes; monitoring populations; assessing gene flow; detecting local adaptation; and species hybridization – real-world issues prevalent across conservation and management, which could potentially be informed by genomics (Allendorf et al., 2010; McMahon et al., 2014; Grueber, 2015; Shafer et al., 2015; Garner et al., 2016; Waples et al., 2019). For rainbow trout specifically, interest from practitioners in the heritable basis of ecologically relevant traits should be encouraging as salmonids are among the key model species for applying conservation genomics.

Our findings also help in identifying and understanding the barriers and challenges that exist in the implementation of conservation science. It is important to recognize from the perspective of a researcher, a substantial number of conservation challenges may be limited by political or social will, and not by scientific knowledge. All of the ‘knowledge to action’ barriers mentioned by respondents, especially a lack of genomics expertise, are characterized by a communication disconnect between researchers and practitioners, implying an obvious need for clearer communication, echoing calls for better communication between genomics researchers and practitioners (Shafer et al., 2015; Garner et al., 2016). Effective communication is imperative to bridge the gap between research and conservation (Cook et al., 2013). The perceived lack of genomics expertise in Canada is also worrying given it too is a country with an active conservation genomics community (see Taylor et al., 2017). In our experience, we believe a) external genomic scientists are not proactively engaging with practitioners, *and* b) external genomic scientists have very few main contacts at FLNRORD, MOE, or nongovernmental stakeholder groups.

Our study reveals that like conservation genetics (Taylor et al., 2017), conservation genomics is particularly susceptible to misunderstanding and potential of mis-application due to a lack of technical expertise. This is likely not exclusive of genetics or genomics, with similar findings attributed to biotelemetry science (e.g. Nguyen et al., 2017b). To many practitioners, the difference between genomics, traditional genetic approaches, and genetic modifications (i.e. transgenics) may be ambiguous which could potentially widen both the “conservation genomics gap” and the broader “conservation genetics gap”. This result is congruent with results found by Taylor et al. (2017). In relation to salmonid management and in particular for *O. mykiss* the difference between genetics and genomics is no small issue as for example, rainbow trout and steelhead trout, different forms of the species, are ecologically very different and are managed as such. Genetics is more likely to result in “false negatives”, for example, in interpreting the genetic basis for ecologically relevant traits (see Piccolo, 2016). Different interpretations of genomics data and how these relate to meaningful conservation-outcomes prompts skepticism – relating to potential linguistic and epistemic uncertainty (see Regan et al., 2002). Major barriers that were also mentioned included the expensive start-up and large-scale data-management costs of genomics (see Chow-White and Green Jr., 2013; Shafer et al., 2015) and a lack of funds to pursue this research (see Taylor et al., 2017). Another perceived barrier is the return on investment (i.e. cumulative benefits) and the time taken to produce conservation genomics results. In the case of cost, it is well-understood that conservation practitioners are limited in funding and human-resource power and reducing both of these costs to practitioners would likely improve science-implementation. In the case of time, applications from a science like genomics may be delivered too slowly to address management concerns that are happening at a faster rate on-the-ground and in-the-water – indicating potential mismatches in demand and supply in conservation science (Nguyen et al., 2017b; Taylor et al., 2017; Nguyen et al., 2018). In contrast to biotelemetry science (Young et al., 2018), there was not a clear desire or signal for genomics to play a greater role in rainbow trout management perhaps due to the uncertainty of how and where genomics can translate into conservation applications. In general, it was not clear to practitioners what the costs of genomics research are, and to most, what the precise benefits are, and what management applications or recommendations it would produce. If the limitations to the science itself, limitations to interpretations or understanding of the science, and explanations of *how* and *where* the science could inform conservation and management go unaddressed (i.e. not communicated clearly), this can potentially alienate and erode the trust of conservation practitioners who feel they have no potential way of validating the accuracy and precision of the scientific claims that are made. A perceived lack of transparency in science communication might suggest an important role for science translators and knowledge-brokers to decrease conservation practitioner credulity. Access to research data was also recognized as a potential barrier which may suggest strong competing interests between research for academic publication and management-relevancy which may widen the “conservation genomics gap”.

In contrast to Taylor et al. (2017) very few respondents had collaborated with external conservation genomics researchers and when they had, their experiences were mixed. The collaborations generally started out positive with clear communication and robust science. However, the final management applications (tools), and recommendations were often provided in a form that was not useable for management. Practitioners in collaborations thus perceived genomics as too focused on fundamental science goals rather in generating mission-oriented findings relevant to end users. Clearly, when practitioners find the results of their collaborative genomics research in academic journal articles and only after it has been published, there are communication or incentive issues to producing and sharing genomics research.

As we have revealed here, there is positive evidence that genomics has considerable potential to help in directing priorities and informing decisions, policies, and practices in conservation and management. Like other fields of conservation science, it is important to recognize that genomics represents exploratory frontier-research (Shafer et al., 2015; Shafer et al., 2016) for which the benefits of research are most likely to be realized in the future, especially as threats to biodiversity increase or become increasingly complex to manage. It should also be recognized that genomics knowledge may be unique in that it may help inform the conservation and management of species by providing valuable information and knowledge on the processes and functions at the genetic-, and ecosystem-levels which underpin species-level biodiversity (McMahon et al., 2014; Grueber, 2015). Ultimately, genomics should be recognized and utilized as one conservation knowledge-source among many (i.e. one tool in the conservation practitioner's toolbox).

We conclude with a set of guidelines informed by this research which we feel will improve knowledge mobilization and exchange in the implementation of conservation genomics into conservation practice emphasized by clearer communication between genomics researchers and conservation practitioners. These are potential solutions to overcome barriers to the use of conservation genomics by practitioners focused on improving conservation genomics expertise among practitioners. Overcoming these barriers could lead to better integration of genomics into conservation in a meaningful way that truly benefit fish and wildlife populations and their stewards and users.

4.1. Guidelines for improving the implementation of conservation genomics research into conservation practice

1. Conservation science research institutions (and their funding agencies) in collaboration with conservation practitioners should instate a knowledge and sharing interface or platform (Roux et al., 2006) to facilitate increased communication, information flow, and personal agency-academic and cross-cultural relationships and collaborations (Pullin and Knight, 2003; Gibbons et al., 2008; Shafer et al., 2015; Garner et al., 2016) between conservation research scientists and conservation practitioners around conservation projects, if one does not exist. Potential interfaces include a “national conservation genetics hub”, sabbaticals for researchers and practitioners to exchange information and ideas, and networking events where conservation genomics scientists visit government and stakeholder offices and are introduced to staff (see Taylor et al., 2017).

   Conservation practitioners should engage with conservation research scientists to communicate clearly what sorts of data or information could be applicable in affecting a management lever (i.e. informing a conservation or management decision, policy, or practice). For example, focusing on genetic uniqueness and distinctness to inform discrete conservation units or for differentiating resident and anadromous fish, ecotypes, spatial separation at spawning. We recommend genomics scientists target practitioners: working with threatened species, interested in mapping genetically distinct populations, or interested in linking genomic variation to ecological traits.
2. Conservation genomics scientists, perhaps aided by ‘science-advisors’ (i.e. knowledge-brokers, science-translators) need to improve science-communication about conservation genomics by helping enhance practitioner knowledge and familiarity of genomics concepts. Specifically, education campaigns should clearly focus on objectively communicating the limitations, possibilities, and advantages of conservation genomics in lay language. This could include for example, one day workshops, three-minute videos covering genomics concepts using Canadian case studies, or an online self-guided conservation genomics course (e.g. Taylor et al., 2017). In the case of workshops or other researcher-practitioner interfaces, it is necessary that many practitioners are identified and engaged, not just a few representatives of practitioner groups. For conservation genomics, communication should also focus on the advantages and contributions of genomics versus traditional genetics (i.e. that it can address a broader range of questions, Shafer et al., 2015) and the differences between genomics research and genetic modification (i.e. transgenics). Again, our results show that practitioners are keen to engage with researchers and improve their genomics knowledge. They are, in our case, generally willing to use new conservation genomics insights to improve management (see Piccolo, 2016).
3. Conservation research scientists should promote to practitioners that genomic costs are decreasing and should provide realistic cost estimates when possible. Conservation genomics scientists should also promote their ability to attract external funding and when possible look to secure alternative (additional) funding to aid collaborators (i.e. practitioners) in collecting data (Shafer et al., 2016). In certain cases, it should be communicated transparently that conservation genomics research may not be a worthwhile use of resources (Flanagan et al., 2018). More on-the-ground examples disseminated to conservation practitioners will build momentum for navigating the conservation implementation space and ‘bridging the gap’ (Shafer et al., 2015; Garner et al., 2016).
4. Conservation research scientists should promote that research on economically important fish or wildlife populations produces benefits that spill-over to other species and organisms of lesser economic-importance. Examples should be provided and communicated when and where possible (e.g. genomics research on rainbow trout provides the genetic basis and infrastructure to learn about other salmonids and freshwater fish).
5. Conservation research scientists should aspire to share their data openly (if a project is in the public interest) unless there are ethical concerns for not doing so (e.g. potential of resource exploitation, risk of potential harm). Academic journals and funding agencies in turn, should mandate conservation research articles to publish or deposit the associated data openly for further use in conservation science and practice. Collaborative agreements between researchers and practitioners should clearly describe how and when management applications and recommendations will be provided to practitioners.
6. Conservation research scientists should engage more practitioners rather than the targets (e.g. fish and wildlife practitioners). For example, genomics information could be relevant to and incorporated into management levels beyond what is traditionally targeted (e.g. to forestry, water use, land use planning).
7. Conservation science funding agencies and schemes need to provide creative incentives for academic researchers to engage fully in conservation. Performance indicators that measure rigour of conservation impact are needed to move away from “publish or perish” models in conservation science. Admittedly, this is an issue that is much broader than conservation genomics.

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Declaration of competing interest

We declare no conflict of interest.

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Appendix A. Supplementary data

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References

Allendorf, F.W., Hohenlohe, P.A., Luikart, G., 2010. Genomics and the future of conservation genetics. Nat Rev Genet 11, 697–709. https://doi.org/10.1038/nrg2844.

Arlettaz, R., Schaub, M., Fournier, J., Reichlin, T.S., Sierro, A., Watson, J.E.M., Braunisch, V., 2010. From publications to public actions: when conservation biologists bridge the gap between research and implementation. BioScience 60, 835–842. https://doi.org/10.1525/bio.2010.60.10.10.

Axinn, W., Pearce, L., 2006. Mixed Method Data Collection Strategies. Cambridge University Press, New York.

Aykanat, T., Johnston, S.E., Orell, P., Niemela, E., Erkinaro, J., Primmer, C.R., 2015. Low but significant genetic differentiation underlies biologically meaningful phenotypic divergence in a large Atlantic salmon population. Mol. Ecol. 24, 5158–5174. https://doi.org/10.1111/mec.13383.

Bailey, M., Sumaila, U.R., 2012. Freshwater Angling and the B.C. Economy. Report prepared for the Freshwater Fisheries Society of B.C.54.

Barson, N.J., et al., 2015. Sex-dependent dominance at a single locus maintains variation in age at maturity in salmon. Nature 528, 405–408. https://doi.org/10.1038/nature16062.

Bradbury, I.R., et al., 2013. Genomic islands of divergence and their consequences for the resolution of spatial structure in an exploited marine fish. Evol. Appl. 6, 450–461. https://doi.org/10.1111/eva.12026.

Bryer, J., Speerschneider, K., 2016. Package "Likert". Available from. http://cran.pau.edu.tr/web/packages/likert/likert/pdf.

Check, E., 2002. Environmental impact tops list of fears about transgenic animals. Nature 418, 805. https://doi.org/10.1038/418805a.

Chow-White, P.A., Green Jr., S.E., 2013. Data mining differences in the age of big data: communication and the social shaping of genome technologies from 1998 to 2007. Int. J. Commun. 556–583.

Cook, C.N., Mascia, M.B., Schwartz, M.W., Possingham, H.P., Fuller, R.A., 2013. Achieving conservation science that bridges the knowledge-action boundary. Conserv. Biol. 27, 669–678. https://doi.org/10.1111/cobi.12050.

Cvitanovic, C., Hobday, A.J., van Kerkhoff, L., Wilson, S.K., Dobbs, K., Marshall, N.A., 2015. Improving knowledge exchange among scientists and decision-makers to facilitate the adaptive governance of marine resources: a review of knowledge and research needs. Ocean & Coastal Management 112, 25–35. https://doi.org/10.1016/j.ocecoaman.2015.05.002.

Dicks, L.V., Hodge, I., Randall, N.P., Scharlemann, J.P.W., Siriwardena, G.M., Smith, H.G., Smith, R.K., Sutherland, W.J., 2014a. A transparent process for "evidence-informed" policy making. Conserv. Lett. 7, 119–125. https://doi.org/10.1111/conl.12046.

Dicks, L.V., Walsh, J.C., Sutherland, W.J., 2014b. Organising evidence for environmental management decisions: a '4S' hierarchy. Trends Ecol. Evol. 29, 607–613. https://doi.org/10.1016/j.tree.2014.09.004.

Dushoff, J., Kain, M.P., Bolker, B.M., O'Hara, R.B., 2019. I can see clearly now: reinterpreting statistical significance. In: Methods in Ecology and Evolution, https://doi.org/10.1111/2041-210x.13159.

Fazey, I., Fischer, J., Lindenmayer, D.B., 2005. What do conservation biologists publish? Biol. Conserv. 124, 63–73. https://doi.org/10.1016/j.biocon.2005.01.013.

Fazey, I., et al., 2012. Knowledge exchange: a review and research agenda for environmental management. Environ. Conserv. 40, 19–36. https://doi.org/10.1017/s037689291200029x.

Flanagan, S.P., Forester, B.R., Latch, E.K., Aitken, S.N., Hoban, S., 2018. Guidelines for planning genomic assessment and monitoring of locally adaptive variation to inform species conservation. Evol. Appl. 11, 1035–1052. https://doi.org/10.1111/eva.12569.

Freshwater Fisheries Society of BC, 2013. 2013 Freshwater Sport Fishing Economic Impact Report.

Garner, B.A., et al., 2016. Genomics in conservation: case studies and bridging the gap between data and application. Trends Ecol. Evol. 31, 81–83. https://doi.org/10.1016/j.tree.2015.10.009.

Gibbons, P., et al., 2008. Some practical suggestions for improving engagement between researchers and policy-makers in natural resource management. Ecological Management & Restoration 9, 182–186. https://doi.org/10.1111/j.1442-8903.2008.00416.x.

Grueber, C.E., 2015. Comparative genomics for biodiversity conservation. Comput Struct Biotechnol J 13, 370–375. https://doi.org/10.1016/j.csbj.2015.05.003.

Hoban, S., et al., 2013. Conservation Genetic Resources for Effective Species Survival (ConGRESS): bridging the divide between conservation research and practice. J. Nat. Conserv. 21, 433–437. https://doi.org/10.1016/j.jnc.2013.07.005.

Liu, Y., Gupta, H., Springer, E., Wagener, T., 2008. Linking science with environmental decision making: experiences from an integrated modeling approach to supporting sustainable water resources management. Environ. Model Softw. 23, 846–858. https://doi.org/10.1016/j.envsoft.2007.10.007.

McMahon, B.J., Teeling, E.C., Höglund, J., 2014. How and why should we implement genomics into conservation? Evol. Appl. 7, 999–1007. https://doi.org/10.1111/eva.12193.

Nguyen, V.M., Young, N., Cooke, S.J., 2017a. A roadmap for knowledge exchange and mobilization research in conservation and natural resource management. Can. J. Fish. Aquat. Sci. 31, 789–798. https://doi.org/10.1111/cobi.12857.

Nguyen, V.M., Young, N., Cooke, S.J., 2017b. Applying a knowledge-action framework for navigating barriers to incorporating telemetry science into fisheries management and conservation: a qualitative study. Conserv. Biol. https://doi.org/10.1139/cjfas-2017-0303.

Nguyen, V.M., Young, N., Corriveau, M., Hinch, S.G., Cooke, S.J., 2018. What is "usable" knowledge? Perceived barriers for integrating new knowledge into management of an iconic Canadian fishery. Can. J. Fish. Aquat. Sci. 1–12. https://doi.org/10.1139/cjfas-2017-0305.

Pearse, D.E., 2016. Saving the spandrels? Adaptive genomic variation in conservation and fisheries management. J. Fish Biol. 89, 2697–2716. https://doi.org/10.1111/jfb.13168.

Piccolo, J.J., 2016. Conservation genomics: coming to a salmonid near you. J. Fish Biol. 89, 2735–2740. https://doi.org/10.1111/jfb.13172.

Pullin, A.S., Knight, T.M., 2003. Support for decision making in conservation practice: an evidence-based approach. J. Nat. Conserv. 11, 83–90. https://doi.org/10.1078/1617-1381-00040.

QSR International Pty Ltd, 2018. NVivo Qualitative Data Analysis Software, Version 12.

R Core Team, 2018. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria. https://www.R-project.org/.

Regan, H.M., Colyvan, M., Burgman, M.A., 2002. A taxonomy and treatment of uncertainty for ecology and conservation biology. Ecol. Appl. 12, 618–628. https://doi.org/10.1890/1051-0761(2002)012[0618:Atatou]2.0.Co;2.

Roux, D.J., Rogers, K.H., Biggs, H.C., Ashton, P.J., Sergeant, A., 2006. Bridging the science-management divide: moving from unidirectional knowledge transfer to knowledge interfacing and sharing. Ecol. Soc. 11 (4). http://www.ecologyandsociety.org/vol11/iss1/art4/.

Salter, B., Salter, C., 2017. Controlling new knowledge: genomic science, governance and the politics of bioinformatics. Soc. Stud. Sci. 47, 263–287. https://doi.org/10.1177/0306312716681210.

Shafer, A.B., et al., 2015. Genomics and the challenging translation into conservation practice. Trends Ecol. Evol. 30, 78–87. https://doi.org/10.1016/j.tree.2014.11.009.

Shafer, A.B.A., et al., 2016. Reply to Garner et al. Trends Ecol. Evol. 31, 83–84. https://doi.org/10.1016/j.tree.2015.11.010.

Soomai, S.S., 2017. The science-policy interface in fisheries management: insights about the influence of organizational structure and culture on information pathways. Mar. Policy 81, 53–63. https://doi.org/10.1016/j.marpol.2017.03.016.

Taylor, H.R., Dussex, N., van Heezik, Y., 2017. Bridging the conservation genetics gap by identifying barriers to implementation for conservation practitioners. Global Ecology and Conservation 10, 231–242. https://doi.org/10.1016/j.gecco.2017.04.001.

Thomas, D.R., 2006. A general inductive approach for analyzing qualitative evaluation data. Am. J. Eval. 27, 237–246. https://doi.org/10.1177/1098214005283748.

Toomey, A.H., Knight, A.T., Barlow, J., 2017. Navigating the space between research and implementation in conservation. Conserv. Lett. 10, 619–625. https://doi.org/10.1111/conl.12315.

Waples, R.S., Naish, K.A., Primmer, C.R., 2019. Conservation and Management of Salmon in the Age of Genomics. Annu. Rev. Anim. Biosci. https://doi.org/10.1146/annurev-animal-021419-083617.

Wiens, J.A., 2008. Uncertainty and the relevance of ecology. Bulletin of the British Ecological Society 39, 47–48.

Young, N., Gingras, I., Nguyen, V.M., Cooke, S.J., Hinch, S.G., 2013. Mobilizing new science into management practice: the challenge of biotelemetry for fisheries management, a case study of Canada's Fraser River. Journal of International Wildlife Law & Policy 16, 331–351. https://doi.org/10.1080/13880292.2013.805074.

Young, N., Corriveau, M., Nguyen, V.M., Cooke, S.J., Hinch, S.G., 2016a. How do potential knowledge users evaluate new claims about a contested resource? Problems of power and politics in knowledge exchange and mobilization. J. Environ. Manag. 184, 380–388. https://doi.org/10.1016/j.jenvman.2016.10.006.

Young, N., Nguyen, V.M., Corriveau, M., Cooke, S.J., Hinch, S.G., 2016b. Knowledge users' perspectives and advice on how to improve knowledge exchange and mobilization in the case of a co-managed fishery. Environ. Sci. Pol. 66, 170–178. https://doi.org/10.1016/j.envsci.2016.09.002.

Young, N., Corriveau, M., Nguyen, V.M., Cooke, S.J., Hinch, S.G., 2018. Embracing disruptive new science? Biotelemetry meets co-management in Canada's Fraser River. Fisheries 43, 51–60. https://doi.org/10.1002/fsh.10015.