Assessing Atlantic Salmon populations in the Belliveau, Meteghan, and Salmon Rivers, Nova Scotia Canada

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Disclaimer

Intended Use and Technical Limitations of the Assessing Atlantic Salmon populations in the Belliveau, Meteghan, and Salmon Rivers, Nova Scotia Canada. The sole purpose of this report is to: assess what is the current state of Atlantic salmon in the Belliveau, Meteghan, and Salmon Rivers, Nova Scotia. The information contained herein does not necessarily represent the opinion of UNBSJ and/or CRI.

Abstract

Economic development and ecological sustainability can often be at odds with one another. Atlantic salmon are a culturally and economically important species in Atlantic Canada, however they have undergone a significant decline over the last few decades, with many populations considered endangered. Understanding the current population status of Atlantic salmon is important to help inform on the suitability of proposed economic development involving salmon and salmon habitat. The purpose of this project was to assess river populations of wild Atlantic salmon in three Digby County rivers: the Meteghan, Salmon, and Belliveau rivers in Nova Scotia. No Atlantic salmon were observed across 9 electrofishing sites spanning the three rivers. Additionally, eDNA samples were analyzed to bolster detection. While there were a few positive eDNA detections, that these were deemed contamination, rather than true detections. The results of this study show that there are no self-sustaining, reproductive Atlantic salmon populations in any of the studied rivers.

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Introduction

To assess population abundance of freshwater fish species, in particular salmonids, electrofishing is a commonly used monitoring method in wadeable rivers. The general principle is that a power source (*e.g.,* generator, battery) will generate a high-voltage current between a submerged anode and cathode. When a fish encounters a large enough potential gradient, it will induce galvanotaxis in the fish (*i.e.,* uncontrolled muscular convulsion) making it swim towards the anode, allowing an easy capture of individuals to be sampled. Electrofishing can be used in a range of sampling techniques to estimate local population abundance such as multi-pass successive removal or single-pass Catch Per Unit Effort (CPUE) (Matson et al., 2018). Multi-pass and single-pass removal sampling typically only requires a single site visit to provide a metric of population abundance. Multi-pass techniques often involve using fence/barrier/block nets and are more labour intensive than single-pass sampling but can provide accurate estimates of population abundance (Carle and Strub, 1978; Seber and Whale, 1970; Zippin, 1958). Single-pass methods are often seen as more flexible than multi-pass methods as they are typically less resource intensive. However, in order to provide a population abundance estimate, they need to be calibrated with sampling techniques producing population estimates (Dauphin et al., 2009; Dauphin et al., 2019, Robinson 2024). When estimating population abundance at the river- or basin-scale, a combination of multi-pass and single-pass sampling methods are often used as single-pass methods allow for a broader spatial coverage, while the multi-pass depletion methods allow more accurate population abundance estimates and can be used to calibrate the single-pass sampling methods (Hanks et al., 2018; Myvold and Kennedy, 2017; Robinson 2024).

Additional sampling approaches, such as environmental DNA (eDNA), are valuable in monitoring threatened fishes (Mauvisseau et al., 2020). Monitoring

populations at risk through physical capture of the species can be extremely difficult when the population is in extreme low abundance, resulting in inaccurate abundance estimates (Gu & Swihart, 2004), and may negatively impact status assessments and management decisions of imperiled taxa. While effective physical capture and eDNA sampling both require extensive prior knowledge of fish life history and location (e.g., migration and local distribution) in the monitored ecosystem, eDNA methods allow greater sensitivity for rare target species (Jerde et al., 2011; Laramie et al., 2015).

This project was conducted as a result of the successful contract with Perennia Food & Agriculture Corporation to estimate river populations of wild Atlantic salmon in three Digby County rivers: the Meteghan, Salmon, and Belliveau rivers in Nova Scotia. The objectives of the project were to: 1) produce credible juvenile Atlantic salmon (i.e., fry and parr) population estimates (where present), that is reflective of the current state-of-the-science; and 2) in the absence of physical sampling, identify presence/absence of Atlantic salmon. Using a combined sampling protocol such as this, is quickly becoming the gold standard of population assessment of extremely low and/or suspected extirpated rivers and is recommended by Fisheries and Oceans Canada (DFO). If juvenile salmon are found, the collection and population assessment methodologies employed will provide a robust assessment that is recognized by DFO and North Atlantic Salmon Conservation Organization (NASCO).

Methods

Site Selection

A total of 15 sites were surveyed September 2025, across the Meteghan, Salmon, and Belliveau rivers in Digby County, Nova Scotia. There were four sites on the Meteghan River (two sites above and two sites below the Bangor Sawmill), eight sites on the Salmon River (which include the three previously established DFO electrofishing sites, 2 CMAR sampling sites, and 3 additional sites), and three sites on the Belliveau River (which includes one previously established DFO electrofishing site and two additional sites. Sites consisted of either rifle or run habitats. Riffle type habitats are characterized by shallow, fast moving water with a broken flow over the substrate, while run habitats, often found at the end of pools, have fast flow but more uniform with no broken water surface, often slightly deeper.

Electrofishing Surveys

Backpack electrofishing surveys were conducted to estimate Atlantic salmon fry and parr abundance. Closed site electrofishing took place at six different sites across the three rivers, with one closed electrofishing site on Belliveau River, two on the Meteghan River, and three on the Salmon River. When sampling closed sites or multiple pass sites, a 25 meter-long block or barrier nets was installed perpendicular to the river banks at the lower and upper boundaries of the site in order to ‘close’ the site for the duration of the sampling and prevent fish movement from or to the site. Typically, nets are made of nylon with a 7 mm mesh size, allowing the water to flow but no fish of interest to swim through them. In order, to maintain the fish population as close as possible to its state prior the installation of the nets, the lower net was installed first to minimize the number

of fish escaping the site during net installation, as disturbed fish tend to primarily follow the current (personal observation). Rocks from the riverbed were used to anchor the net bottom, while wooden stakes were used the elevate the net top out of the water and seal the site. The size of the site was characterized by two length measurements (one on each side) and two width measurements (upstream, downstream), forming a sampling area.

The general methodology was to electrofish each square meter of the site to sample all fish present. Following the first pass through the site, all fish were brought to the processing area where fish were placed in live wells waiting to be processed. In compliance with DFO permitting, all fish species are collected and recorded. Fish were kept outside of the sampling area until all the passes were completed. The second pass started no less than 10 minutes after the precedent one ended to let the remaining fish settle back in their habitat. Three to six passes were conducted at each site with the objective of observing a depletion (i.e., less and less fish captured after each pass). However, given that no salmon were detected in any of the passes at any site, a third pass was not conducted as it was deemed no salmon to be present. Electrofishing surveys were conducted by a four-person crew, which includes a certified operator, two crew members using a ~1.5 m collection lip seine downstream of the electrofisher operator, and one dip netter. Sampling passes were conducted from the downstream to upstream end of the site to mimic how open sites are sampled (see below). Power was standardized across sites and voltage was systematically adjusted to ensure an ~80-watt output, using a SmithRoot LR24 backpack electrofisher, set to 30Hz, 12% duty cycle, and pulsed DC.

The remaining nine electrofishing sites were surveyed using the single-pass method (open sites) method. The protocol is similar to the multi-pass site protocol, except

no barrier nets were installed and only one pass was conducted. The lower operational requirements in comparison to the closed site method allowed for a larger number of sites to be sampled throughout the catchments over the assessment period. The single-pass method does require calibration or pairing with variance data from the multi-pass removal sites in order to estimate population abundance.

Data collected at the sampling site consisted of the sampling effort, number of passes, fish captures per pass (including species), standard morphometric data for salmon only (including but not limited to sex, length, and weight), site area, and GPS location.

Density Estimates

Juvenile salmon density estimates would have been calculated using the methodologies developed by John Robinson (see Robinson 2024), in collaboration with Parks Canada, DFO, and the University of New Brunswick. Population estimate methodology is recognized by DFO and NASCO.

In general, for any given year t and river k, the total abundance of an Atlantic salmon at life stage l in site i is drawn from a Poisson distribution:

Equation 1. $$N^{tot}_{t,k,i,l} \left| \lambda^{N}_{t,k,i,l} \sim \text{Poisson}(\lambda^{N}_{t,k,i,l}) \right.$$

where $\lambda_{t,k,i,l}$ is the product of the density $d_{t,k,i,l}$ (in fish of lifestage l per m^2) multiplied by the area $A_{t,k,i}$, of the sites (in m^2) and $\lambda_{t,k,i,l} = d_{t,k,i,l} \times A_{t,k,i}$.

eDNA Sampling

For additional confirmation of the presence/absence of Atlantic salmon in the Meteghan, Salmon, and Belliveau rivers, 15 eDNA samples were collected. Water samples were collected in duplicate from one site on the Belliveau River, two sites on the

Meteghan River, and three sites on the Salmon River. In addition, a field blank sample was collected from each of the river to test for contamination in the sampling procedure.

Field sampling followed the protocol established by Dr. Scott Pavey, Director of the CRI Genomics Laboratory at the University of New Brunswick Saint John. Forceps, cellulose nitrate membrane filters (Whatman—47 mm diameter/0.45 µl), and a filter funnel were packaged in a sterile laboratory prior to field sampling. At each site, we pumped 1 L of water through a filter using a GeoPump 2 Peristaltic Pump while wearing disposable gloves. Upon completion of filtration, samples were placed in vials and topped with ethanol. Samples were stored in an ice-filled cooler and moved within 24 hrs to a −20°C freezer. Three field blanks (one from each river) were collected to test for contamination. This requires filtering 1 L of deionized water using the same techniques and equipment outlined above. Samples were taken to the University of New Brunswick Saint John campus and stored at −20°C until DNA analysis. Samples underwent quantitative PCR (qPCR) analysis for the detection of any salmon DNA.

Results

Electrofishing Surveys

Electrofishing surveys took place in the Belliveau, Meteghan, and Salmon rivers between September 16th – 21st, 2024. A total of nine sites were surveyed, with six sites being closed sites (one in the Belliveau River, two in the Meteghan River, and three in the Salmon River), with an additional two open sites in the Belliveau River, two open sites in the Meteghan River, and five open sites in the Salmon River (Table 1). Across the 9 electrosfishing sites, a total area of 7456.27 m^2 was surveyed (794.96 m^2, 1102.54 m^2, 5558.77 m^2 in the Belliveau, Meteghan, and Salmon rivers respectively) (Table 1). The smallest site sampled was in the Belliveau River, measuring 173.68 m^2, while the largest site sampled was in the Salmon River, measuring 3200.00 m^2 (Table 1). Shocking time (i.e., the amount of time that current was being transmitted through the water to catch fish) ranged from 422 sec/site to a max of 2680 sec/site, with a total shock time of 17198 sec or 4.78 hours (Table 2).

No Atlantic salmon were captured (or observed) at any of the nine sites (Table 2). In total, 792 fish across nine different species were sampled. American eel was the most abundant species encountered, having been found at all sampling sites, with a total 657 eels captured (Table 2). The largest site, in terms of both area and shock time, had 296 American eels captured. A total of 65 juvenile gaspereau (the collective term for alewife and blueback herring) at one site (SR7) on the Salmon River (Table 2). All other species were found in very low abundance.

eDNA

Environmental DNA samples were collected from three rivers in September 2024. CRI Genomics Lab conducted qPCR analysis for Atlantic Salmon (*Salmo salar*) on the 15 samples (Table 3). Each field sample was run using four qPCR replicates. When the quantity of DNA is near the level of detection, variability in the replicates can occur. For any sample that had zero replicates amplify DNA of the target species, this doesn't necessarily mean that the species was not present only that any signal was below our detection threshold. There are many factors that can affect an eDNA signal: sunlight, temperature, number individuals present, organic material (especially leaves).

There were three types of negative controls (field, extraction, and quantitative polymerase chain reaction) used throughout the process to detect if contamination occurred at any step. Atlantic Salmon DNA was found in one field control (BR control: 3/4 replicates) (Table 3). It is extraordinarily rare for our lab to see any positive field controls that have positive qPCR results. Because the field control contamination was somewhat strong, the positives in BR should not be considered true positives. It also casts a shadow of doubt on the other positive results, since the same field crew did the sampling. I acknowledge that there may not have been rigorous decontamination of the waders used for the project that there should have been, and that waders have previously been used for Atlantic Salmon work. This is a perfect vector for eDNA contamination. The safest course of action would be to repeat the sampling, paying close attention to possible contamination sources. Ideally, waders that have never touched an Atlantic Salmon would be used, though decontamination may be possible. Felt sole boots are not recommended for eDNA sampling.

No DNA was found in any of the extraction or qPCR controls, which means that no contamination occurred, and positive detections are a result of Atlantic Salmon DNA being present at these sites. An internal positive control was also used on all the samples to test whether PCR inhibition was present and preventing target species DNA from amplifying. This control found no inhibition present.

Conclusions

Multiple methods of investigation were used to assess Atlantic salmon populations in the Belliveau, Meteghan, and Salmon rivers, Nova Scotia. Traditional electrofishing surveys found no Atlantic salmon in any of the rivers. While there were a few positive eDNA detections, it was the opinion of Dr. Scott Pavey, the director of the CRI Genomics Lab, that these were likely due to contamination, rather than true detections. Assessing these two lines of evidence in concert, it is highly probable that there are no Atlantic salmon remaining in these three rivers. If those positive eDNA results where in fact true Atlantic salmon detections, it would suggest that there may be a few remnant Atlantic salmon in the Belliveau and Salmon rivers. However, the results of this study show that in either case there are no self-sustaining, reproductive Atlantic salmon populations in any of the studied rivers.

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Table 1: Electrofishing site locations and dimensions.

				Electrofishing Site Dimensions				
River	Site ID	Latitude	Longitude	RR Length (m)	RL Length (m)	Upstream Width (m)	Downstream Width (m)	Size (m^2)
Belliveau	BR1	44.3742068	-66.0759552	54	49.4	4.7	3.7	217.14
Belliveau	BR1	44.3742068	-66.0759552	54	49.4	4.7	3.7	217.14
Belliveau	BR2	44.3734	-66.04858	43.7	40	3.6	4.7	173.68
Belliveau	BR3	44.3520938	-66.0267665	46.5	47	3.5	4.5	187.00
Meteghan	MR1	44.2156148	-66.1086912	29.5	29.5	5.8	7	188.80
Meteghan	MR2	44.2177097	-66.0989277	19	19	12.4	13.4	245.10
Meteghan	MR3	44.22118	-66.07069	20.2	20.2	13.6	12.8	266.64
Meteghan	MR4	44.2192281	-66.0759552	15	15	13.3	13.5	201.00
Meteghan	MR4	44.2192281	-66.0759552	15	15	13.3	13.5	201.00
Salmon	SR1	44.05792102	-66.1384146	14	14	15.5	14.5	210.00
Salmon	SR1	44.05792102	-66.1384146	14	14	15.5	14.5	210.00
Salmon	SR2	44.0590018	-66.0976493	875	875	8.2	6.4	3200.00
Salmon	SR3	44.0982142	-66.0711266	52	48	6.7	8.5	380.00
Salmon	SR4	44.1278012	-66.0647476	34.4	34.2	6.2	5.3	197.23
Salmon	SR4	44.1278012	-66.0647476	34.4	34.2	6.2	5.3	197.23
Salmon	SR5	44.15892	-66.02977	50	50	3.9	4.5	210.00
Salmon	SR5	44.15892	-66.02977	50	50	3.9	4.5	210.00
Salmon	SR6	44.0617426	-66.1436592	12.6	13.3	15.7	15.2	200.08
Salmon	SR7	44.17495	-66.01136	50.2	50.9	7.7	4.1	298.25
Salmon	SR8	44.1516884	-66.0594938	24	24	9.9	10.6	246.00

Table 2: Summary of fish species caught at each site.

River	Site ID	Size (m^2)	Month	Day	Year	Pass #	Site (Open/Closed)	Effort (s)	Water Temp (ºC)	Atlantic salmon	American eel	Brook trout	Brown trout	White Sucker	Smallmouth bass	Chub spp.	Banded killifish	Brown bullhead	Alewife	Chain pickerel	Cyprinids	Other
Belliveau	BR1	217.14	9	20	24	1	Closed	791	16	0	27	1	0	0	0	0	0	0	0	0	0	0
Belliveau	BR1	217.14	9	20	24	2	Closed	510	16	0	16	2	0	0	0	0	0	0	0	0	0	0
Belliveau	BR2	173.68	9	20	24	1	Open	802	17	0	51	0	0	0	0	0	0	0	0	0	0	0
Belliveau	BR3	187.00	9	21	24	1	Open	700	17	0	14	0	1	0	0	0	0	0	0	3	0	0
Meteghan	MR1	188.80	9	19	24	1	Closed	422	19	0	3	0	0	0	0	0	0	0	0	0	0	0
Meteghan	MR2	245.10	9	21	24	1	Open	525	17.5	0	6	0	0	0	0	0	0	0	0	0	0	0
Meteghan	MR3	266.64	9	21	24	1	Open	560	17	0	3	0	0	0	3	0	0	0	0	0	0	0
Meteghan	MR4	201.00	9	19	24	1	Closed	621	19	0	5	0	0	0	0	0	0	0	0	0	0	0
Meteghan	MR4	201.00	9	19	24	2	Closed	629	19	0	4	0	0	0	2	0	0	0	0	0	0	0
Salmon	SR1	210.00	9	16	24	1	Closed	869	20	0	27	0	0	0	5	0	0	0	0	0	0	0
Salmon	SR1	210.00	9	16	24	2	Closed	975	20	0	24	0	0	0	5	0	0	0	0	0	0	0
Salmon	SR2	3200.00	9	20	24	1	Open	2680	17	0	296	4	0	2	4	0	0	1	2	0	0	0
Salmon	SR3	380.00	9	18	24	1	Open	901	20	0	24	7	0	0	0	0	0	0	0	0	0	0
Salmon	SR4	197.23	9	17	24	1	Closed	636	20	0	13	0	0	0	4	0	0	1	0	0	0	0
Salmon	SR4	197.23	9	17	24	2	Closed	526	20	0	6	0	0	0	0	0	0	0	0	0	0	0
Salmon	SR5	210.00	9	18	24	1	Closed	1096	19	0	36	0	0	0	0	0	0	7	0	0	0	0
Salmon	SR5	210.00	9	18	24	2	Closed	831	19	0	12	0	0	1	0	0	2	4	0	0	0	0
Salmon	SR6	200.08	9	16	24	1	Open	996	21	0	44	0	0	1	0	0	3	0	0	0	0	0
Salmon	SR7	298.25	9	17	24	1	Open	1171	20	0	15	1	0	1	0	0	0	1	65	0	0	0
Salmon	SR8	246.00	9	18	24	1	Open	957	21	0	31	1	0	1	0	0	0	0	0	0	0	0

Table 3: Atlantic Salmon results from samples collected in September 2024.
Each sample is reported as the number of qPCR replicates that amplified each species' DNA.

Sample Site	Atlantic Salmon
BR 1A	1/4
BR 1B	0/4
BR Control	3/4
MR 1A	0/4
MR 1B	0/4
MR 2A	0/4
MR 2B	0/4
MR Control	0/4
SR 1A	0/4
SR 1B	1/4
SR 4A	2/4
SR 4B	1/4
SR 5A	2/4
SR 5B	0/4
SR Control	0/4