



## ASSESSMENT OF THE RISK POSED TO WILD ATLANTIC SALMON POPULATION ABUNDANCE AND GENETIC CHARACTER BY DIRECT GENETIC INTERACTION WITH ESCAPES FROM EAST COAST ATLANTIC SALMON AQUACULTURE



Figure 1. An aerial image of a finfish aquaculture facility in Atlantic Canada  
(Photo: Émilie Simard, DFO)

### Context:

Fisheries and Oceans Canada (DFO) conducts environmental risk assessments to support science-based decision making related to aquaculture activities. The Aquaculture Science Environmental Risk Assessment Initiative was implemented to assess the risks of aquaculture activities to wild fish and the environment. The risks associated with environmental stressors validated in the Pathways of Effects for finfish and shellfish aquaculture (DFO, 2010) are assessed as per the Aquaculture Science Environmental Risk Assessment Framework ensuring a systematic, consistent and transparent process.

DFO's Aquaculture Directorate has requested science advice on the risks to wild Atlantic Salmon (*Salmo salar*) population abundance and genetic character resulting from direct genetic interactions with escaped farmed Atlantic Salmon. This request supports DFO's role in the sustainable management of fisheries and aquaculture and the protection of fish and fish habitat.

This Science Advisory Report summarizes the June 6-9, 2023 National Peer Review Meeting on the Assessment of the risk posed to wild Atlantic Salmon population abundance and genetic character by direct genetic interaction with escapes from East Coast Atlantic Salmon aquaculture. Additional

publications from this meeting will be posted on the [Fisheries and Oceans Canada \(DFO\) Science Advisory Schedule](#) as they become available.

## SUMMARY

- Direct genetic interactions, which arise from the interbreeding between wild and escaped farmed Atlantic Salmon and their offspring, pose a threat to the genetic integrity and abundance (fitness) of wild Atlantic Salmon populations.
- The risks posed to wild Atlantic Salmon population abundance and genetic character in Atlantic Canada by direct genetic interaction with escapes from Atlantic Salmon aquaculture were assessed in three main steps: a likelihood assessment, a consequence assessment, and a risk estimation.
- The risks were assessed for wild salmon populations in the six designatable units (DUs) in Atlantic Canada in proximity to Atlantic Salmon net pen aquaculture. These populations were assessed in 2010 by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC) for recommended listing as Endangered or Threatened under Canada's *Species at Risk Act*. The Inner Bay of Fundy DU has been listed as Endangered since 2003.
- The risk assessment used multiple peer-reviewed analytical approaches and both domestic and international data sources. These included the use of available demographic and dispersal modeling, reports of escape events by industry, detections of escapees from in-river monitoring or opportunistic sampling, and results of genetic screening for interbreeding.
- The likelihood assessment was carried out in three steps: the likelihoods of release (escape), exposure (freshwater entry), and interbreeding. The results were then combined to determine an overall likelihood. Each step assumed that 2011 to 2021 management practices were maintained and production levels used in the models followed either transfer records or maximum allowable production levels, recognizing the maximum allowable production levels were not achieved and wild population sizes were likely overestimated.
- The consequence assessment determined the potential impacts to wild Atlantic Salmon population abundance and genetic character, depending on the number of escaped Atlantic Salmon estimated to have entered rivers and interbred with wild Atlantic Salmon.
- The risk to abundance across modeled escape rates was **low** for Nova Scotia Southern Upland East, Inner Bay of Fundy, and South Newfoundland East, **low to high** for Nova Scotia Southern Upland West and South Newfoundland West, and **medium to high** for Outer Bay of Fundy DUs.
- The risk to genetic character across modeled escape rates was **low** for Nova Scotia Southern Upland East and South Newfoundland East, **medium** for Inner Bay of Fundy, **medium to high** for Nova Scotia Southern Upland West, and **high** for Outer Bay of Fundy and South Newfoundland West DUs.
- Among the model variables, the level of risk related to direct genetic interactions increased by proximity to, and intensity of, aquaculture operations, and by declining wild population size and worsening conservation status; risk decreased by farming sterile fish.
- Based on peer-reviewed literature and available data, certainty at each step of the likelihood and consequence assessments ranged from **high certainty** to **reasonable certainty**.

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- Results and conclusions of this analysis were generally consistent with observations from other jurisdictions spanning the North Atlantic.
- To assess what level of mitigation may be required to reduce risk, simulations estimated the effects of reducing escapees for the level of production assumed here. In general, where risk was assessed to be **high**, simulations estimated that a reduction of 50% or greater of escapees was required to reduce the risk to **low**.
- The conclusions of this risk assessment should be regularly reviewed and revised as new and relevant information becomes available, such as changes to industry practices, production levels, escape rates, or sizes of wild salmon populations.
- Further research studies and monitoring are needed to improve model accuracy and validate the model assumptions and outputs.
- An overview of potential mitigation measures led to a conclusion that eliminating all human errors and equipment failures associated with Atlantic Salmon net pen escapes is not realistic. Therefore, no single measure will necessarily eliminate risk, but cumulative effects of multiple measures will contribute to an effective reduction in escapes and risk.
- Technologies such as fully closed containment or fully sterile populations would eliminate direct genetic interactions between escaped and wild Atlantic Salmon but the utility of these approaches has not been widely demonstrated and assessed.
- Demonstration of efficacy of implemented mitigation measures will require that experts evaluate results from comprehensive monitoring programs.

## INTRODUCTION

Atlantic Salmon, *Salmo salar*, are an anadromous salmonid, distributed throughout the North Atlantic that exhibit highly variable life histories (Garcia de Leaniz et al., 2007), including different reproductive and migratory patterns, even within populations. Differences in the genetic structure and diversity of wild Atlantic Salmon populations occur at a variety of spatial scales including across the Atlantic Ocean (e.g., King et al., 2001; Lehnert et al., 2019; Bradbury et al., 2022), among regions and rivers (e.g., Moore et al., 2014; Bradbury et al., 2018; Jeffery et al., 2018) and within large river systems (e.g., Primmer et al., 2006; Aykanat et al., 2015) across their native range. These differences arise from the strong natal homing behaviour of the species and high degree of local adaptation to their natal rivers across a wide range of latitudes and temperatures.

Since 1985, the number of wild adult Atlantic salmon returning to many rivers across the North Atlantic has significantly decreased and stocks have declined or collapsed (Dadswell et al., 2022). Fisheries and Oceans Canada's (DFO) *Wild Atlantic Salmon Conservation Policy*, considers Atlantic Salmon "wild" if they have spent their entire life cycle in the wild and originate from parents who were also produced by natural spawning and continuously lived in the wild (DFO, 2018). Many Atlantic Canadian salmon populations are currently at critically low levels and considered as "threatened" or "endangered" by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC), or listed under Canada's *Species at Risk Act* (SARA). During this time period, Atlantic Salmon aquaculture has expanded throughout Atlantic Canada. Atlantic Salmon aquaculture escapees, and their effects on wild salmon population abundance and genetic character, are among a range of factors identified as contributors to this decline (Glover et al., 2017). Aquaculture has been recognized as a threat to wild Atlantic Salmon populations in all regions where they are produced (Glover et al., 2017; Bradbury et al., 2020b; Glover et al., 2020; Gilbey, 2021).

Genetic interactions between wild and farmed salmon may involve interbreeding (i.e., direct genetic interactions) or be ecological in nature (i.e., indirect genetic interactions). Direct genetic interactions, which refers to the interbreeding that occurs between wild and escaped farmed Atlantic Salmon and their offspring, have been repeatedly shown to genetically alter wild populations, impacting local adaptation, and potentially causing population decline. In some instances, where examined, farm escapees can account for a large proportion of Atlantic Salmon in rivers (e.g., Karlsson et al., 2016; Wringe et al., 2018; McGinnity et al., 2003; Castellani et al., 2018) but variability has been observed in levels of farm-wild interbreeding among regions and rivers within regions (e.g., Glover et al., 2013; Karlsson et al., 2016; Glover et al., 2019; Diserud et al., 2022). This suggests that the impacts on abundance and/or genetic character are river or population-dependent and that not all interactions may result in such impacts (Castellani et al., 2018). Nonetheless, factors such as proximity to and intensity of aquaculture, and wild population size, are found to predict escapee abundance and interaction between wild and escapee salmon, which supports the ability to predict impacts using models (Heino et al., 2015; Mahlum et al., 2020; Diserud et al., 2022).

These direct interactions are cause for concern regarding the health and sustainability of wild Atlantic Salmon populations, especially for those with small population sizes. Indirect genetic interactions, which refer to the ecological interactions that occur between farm and wild salmon without interbreeding (e.g., disease, parasites, predation, competition), are also important and can have similar impacts to wild populations as direct genetic interactions. However, this assessment considers only direct genetic interactions and an integrated understanding of both direct and indirect genetic interactions will require further study (Bradbury et al., 2020a).

In the three Atlantic provinces where Atlantic Salmon are farmed in Canadian coastal waters (Newfoundland and Labrador (NL), Nova Scotia (NS), and New Brunswick (NB)), the province is the lead regulator for aquaculture activities. However, the sustainable management of fisheries and aquaculture, and the protection of fish and fish habitat, fall within the mandate of DFO. DFO provides input, in the form of advice, to the provinces on new or expanded aquaculture sites, and shares responsibility with the provinces for issuing permits for introductions and transfers (I&T) of fish into marine farm cages.

To support this role, DFO's Aquaculture Directorate requested peer-reviewed science advice on the risks posed by escaped farmed Atlantic Salmon to the abundance and genetic character of wild Atlantic Salmon through direct genetic interactions.

This risk assessment was conducted under the DFO Aquaculture Science Environmental Risk Assessment Initiative, implemented as a structured approach to provide risk-based science advice to support sustainable aquaculture in Canada. Risk assessments conducted under this initiative follow the Aquaculture Science Environmental Risk Assessment Framework, which is adapted from international and national risk assessment frameworks (GESAMP, 2008; ISO, 2009; Mandrak et al., 2012). Details about the initiative and the framework are available on the DFO Aquaculture Science Environmental Risk Assessment Initiative [webpage](#). Risk assessments conducted under the initiative do not include socio-economic considerations.

This Science Advisory Report summarizes the consensus advice on the risk posed to wild Atlantic Salmon population abundance and genetic character by direct genetic interaction with escapees from east coast Atlantic Salmon marine aquaculture sites. The advice also includes a characterization of sources of uncertainty and an assessment of potential mitigation options aimed at reducing risk.

The information and current scientific knowledge about direct genetic interactions between farmed and wild Atlantic Salmon and the risk assessment were presented in the following documents:

- Assessment of the risk posed to wild Atlantic Salmon population abundance and genetic character by direct genetic interaction with escapes from East Coast Atlantic Salmon aquaculture (Coulson et al., in press).
- Mitigation options for reducing the risk of direct genetic interactions between farm escapes and wild Atlantic Salmon populations in Atlantic Canada (Coulson et al., in press).

## **ANALYSIS**

### **Units of Assessment**

The risks posed to wild Atlantic Salmon population abundance and genetic character in Atlantic Canada by direct genetic interactions with escapees from Atlantic Salmon aquaculture were assessed for wild salmon populations in the six biologically defined designatable units (DUs) in Atlantic Canada in proximity to Atlantic Salmon marine net pen aquaculture (Figure 2). COSEWIC defines DUs on the basis of two criteria: that they be discrete, and that they represent evolutionarily significant units of the species. Two of these DUs are along the south coast of Newfoundland and Labrador (NL) and the other four are within the Maritimes region in Nova Scotia (NS) and New Brunswick (NB). COSEWIC assessed these populations in 2010 for recommended listing as Endangered or Threatened under Canada's *Species at Risk Act*. The Inner Bay of Fundy DU has been listed as Endangered since 2003.

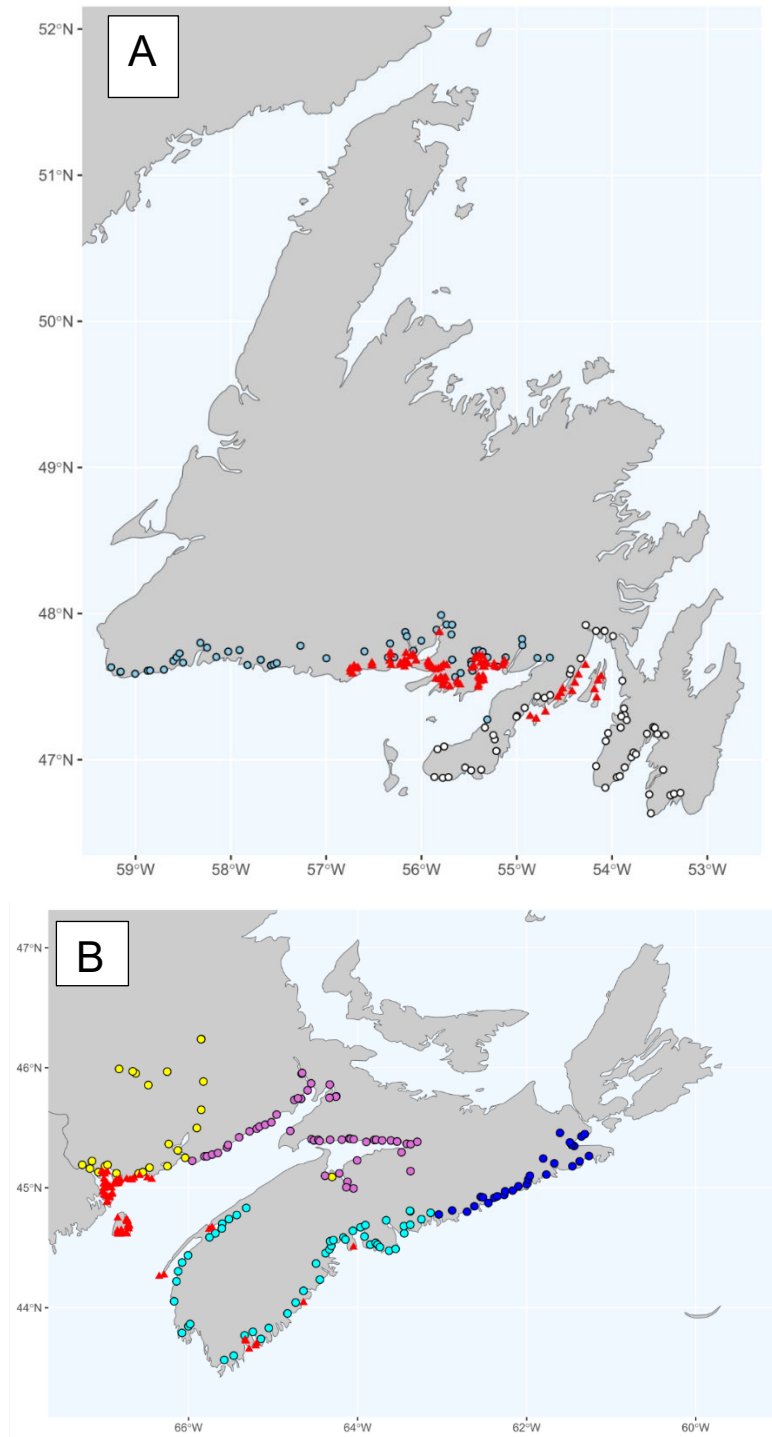


Figure 2. Maps of A) the island of Newfoundland and B) the Maritime Provinces of Atlantic Canada showing locations of approved sites for Atlantic Salmon farms (red) and location of Atlantic Salmon river mouths across the six designatable units (DUs) considered in the risk assessment (NL: DU 4A = white, DU 4B = light blue, NS: DU 14A = dark blue, DU 14B = cyan, NS/NB: DU 15 = purple, and NB: DU 16 = yellow).

## Data Sources

The risk assessment used multiple peer-reviewed analytical approaches as well as both domestic and international data sources. These approaches included available demographic and dispersal models, reports of escape events by the industry, detections of escapees from in-river monitoring or opportunistic sampling, and results of genetic screening for interbreeding between farm escapees and wild Atlantic Salmon.

The modeling used two published approaches that have previously been used to assess direct genetic interactions between farmed and wild Atlantic Salmon. The first was an Individual-Based Salmon Eco-Genetic Model (IBSEM) (Castellani et al., 2015), which estimates changes in abundance and genetic character in response to varying levels of farm escapees entering wild salmon rivers. This model has consistently predicted impacts to both salmon abundance and genetic character when the proportion of farm escapees in a river is equal to or greater than 10% of the total number of salmon in the river (Castellani et al., 2015, 2018; Sylvester et al., 2019; Bradbury et al., 2020b). Norway (Taranger et al., 2015; Glover et al., 2020) and Iceland (MFRI, 2020) routinely use this threshold as part of their risk assessments and mitigation measures.

The second was a dispersal model (Bradbury et al., 2020b) that incorporates information on local levels of aquaculture production, rates of escape, escapee survival, behaviour and dispersal, environment, and size of wild salmon populations to predict the proportion of escapees (relative to the wild population size) within each river. The dispersal model has been shown to be consistent with detections of escapees and observed levels of hybridization (Bradbury et al., 2020b). This model was run for each region (NL or Maritimes) separately, using the best available data, and results were summarized for each DU. Given the uncertainty in the actual rate of escapes, the assessment used four different values for escape rate throughout (0.1, 0.2, 0.4, and 0.8 escapees/tonne of production). These values are consistent with estimates from reported escape events across salmon producing jurisdictions, including rates calculated for Canada based on industry reports, and information available on underreporting of escape events (Skilbrei et al., 2015). It should be noted that currently farmed salmon in DU 4A (South Newfoundland East) are triploid and therefore sterile. However, triploidy induced sterility is not 100%, but results suggest that triploidy success is high and 98% or greater should routinely be achievable on commercial scales (Benfey, 2016; Stien et al., 2019; Glover et al., 2020; DFO, 2022). Therefore, we used 98% triploidy induction success, and as a result the model only uses 2% of the production in this area for estimating the number of escapees that may contribute to direct genetic interactions (i.e., are reproductively viable). The assessments are therefore only based on the escapees derived from 2% of production.

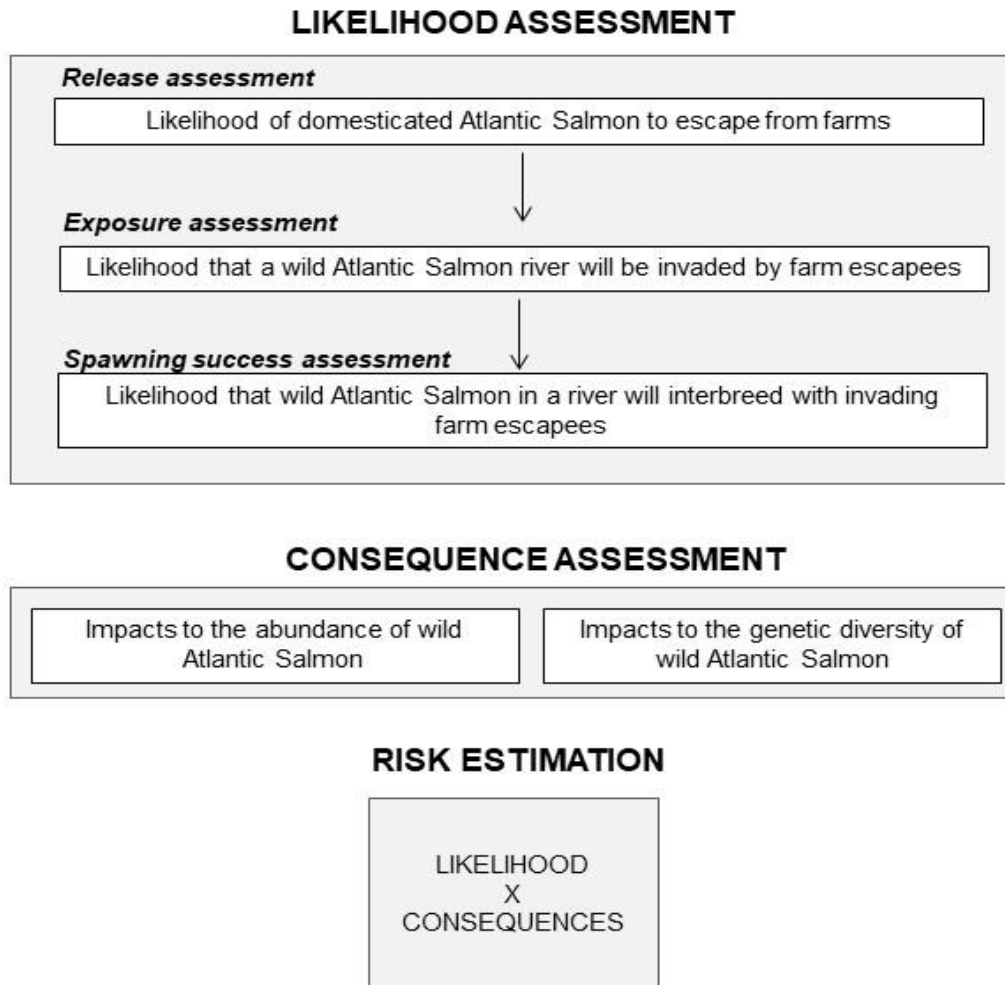
## Risk Assessment

For this assessment, the risks posed to wild Atlantic Salmon population abundance and genetic character in Atlantic Canada by direct genetic interaction with escapees from Atlantic Salmon marine net pen aquaculture were evaluated in three steps: a likelihood assessment, a consequence assessment, and a risk estimation (Figure 3).

The likelihood assessment was carried out in three sub-steps: the likelihoods of release (escape), exposure (freshwater river entry), and interbreeding. The results were then combined to determine an overall likelihood. Given that each step in the likelihood is dependent on the previous step occurring, the lowest likelihood category of the three individual steps defines the overall likelihood. Each step was based on escape data and information available from 2011 to 2021, and production levels used in the models followed either transfer records where available (NS and NB) or maximum allowable production levels (NL), recognizing the maximum allowable

production levels were not achieved. Wild population sizes were likely overestimated given direct comparison with census data and stock assessments and ongoing evidence of continued declines for several DUs.

Uncertainties are reported for each step of the likelihood and consequence assessments. Uncertainty includes both natural variability, which is a function of the system that is not reducible with additional measurements, and a lack of knowledge that may be reduced with additional data or expert opinion (Vose, 2008). This risk assessment does not combine uncertainties in the overall likelihood and consequence assessments to emphasize the uncertainty associated with each step. Likelihoods and uncertainty rankings are summarized for each step in Table 1. The criteria associated with the uncertainty rankings are outlined in Appendix I.



*Figure 3. Conceptual model used to assess the risks of direct genetic interactions between escaped farmed and wild Atlantic Salmon in Atlantic Canada.*

**Likelihood Assessment**

**Release assessment**

The release assessment determined the likelihood that Atlantic Salmon escape from marine net pens in the region (NL or Maritimes) in a given year. This step focused on how often escapes



occur on an annual basis, and not the numbers of escapes, which the risk assessment considers elsewhere. From 2011 to 2021, 29 Atlantic Salmon escape events were reported to the North Atlantic Salmon Conservation Organization (NASCO) ([NASCO Annual Reports](#)) for marine Atlantic Salmon farms in Atlantic Canada. However, only 10 of these were confirmed escapes reporting estimated numbers of suspected escapees. Previous analyses by Morris et al. (2008) and Keyser et al. (2018) summarized the occurrence of escapees in rivers throughout Atlantic Canada as far back as the 1980s and showed evidence of escape events, through the presence of escapees in rivers, in at least one river in all years considered for either NL or Maritimes region. Furthermore, river monitoring at the Magaguadavic River (NB) showed evidence of escape events in every year for which data were available. In NL, a combination of river monitoring at the Garnish River (NL) along with genetic screening in multiple rivers in southern NL showed evidence of escape events in each year when the data were combined. Based on reported escape events as well as evidence of escapees in rivers and genetic screening, the analysis concluded that the likelihood of release in both NL and the Maritimes is extremely likely. This conclusion was made with high certainty (Table 1).

### **Exposure assessment**

Given that farmed Atlantic Salmon will escape marine net pens in the region in a given year, the exposure assessment focused on the likelihood that farm escapees will invade rivers with wild Atlantic Salmon within a given DU. This step of the assessment generally relied on observations reported in Morris et al. (2008) and Keyser et al. (2018), and specifically on the use of the dispersal model (Jóhannsson et al., 2017; Bradbury et al., 2020b) to predict the number of escapees entering each river within a DU. The model considers parameters and calculations for farm-specific production values, escape rate, dispersal distance, estimates of river-specific wild salmon population size and other key parameters. To account for uncertainty in the rate of escape from farms, four separate escape rates (0.1, 0.2, 0.4, and 0.8 escapees/tonne of production) were used throughout the risk assessment. Likelihood estimates ranged from extremely unlikely to very likely depending on the DU and the escape rate used. These conclusions were made with reasonable certainty (Table 1).

### **Spawning success assessment**

This likelihood step considered data on genetic hybridization and introgression from eight years of annual juvenile genetic screening surveys in NL as well as published scientific literature for the Maritimes and other jurisdictions. Although this step assumes that farmed salmon are already in the river, it does not consider their reproductive success but rather the likelihood they will spawn with wild Atlantic Salmon. Modeling (IBSEM and dispersal models) addressed decreased reproductive fitness of farm escapees as part of the consequence assessment. Numerous studies provide evidence of hybridization/introgression between escaped farmed and wild Atlantic Salmon, including in Canada (e.g., DFO, 2018; Keyser et al., 2018; Sylvester et al., 2018; Wringe et al., 2018; Sylvester et al., 2019; Bradbury et al., 2020b; Bradbury et al., 2022; Holborn et al., 2022), Ireland (Clifford et al., 1997, 1998), Norway (e.g., Glover et al., 2012; Glover et al., 2013; Karlsson et al., 2016; Diserud et al., 2022), and Scotland (e.g., Gilbey, 2021). Although the reproductive success of any single escapee in a river is impossible to predict, the frequent detection of offspring of escaped farmed Atlantic Salmon when no escape events have been reported suggests appreciable survival and reproductive capacity of escapees, and that the presence of even small numbers of escapees places rivers at risk of direct genetic impacts (Wringe et al., 2018). Barring any physical barrier that may disproportionately affect farmed salmon, as well as any biological barrier to reproduction, such as induced sterility of farmed Atlantic Salmon, there is no evidence to suggest that escaped farmed Atlantic Salmon could not spawn with wild Atlantic Salmon. Despite the generally inferior

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reproductive success of escaped farmed salmon relative to their wild conspecifics (reviewed in Glover et al., 2017), multiple studies provide evidence for hybridization between escaped farmed salmon and their counterparts in all areas where marine salmon farming and wild Atlantic Salmon populations coexist (Clifford et al., 1998; Glover et al., 2012; Karlsson et al., 2016; Glover et al., 2017; Wringe et al., 2018; Gilbey, 2021) and the linkages between single escape events and interbreeding (e.g., Wringe et al., 2018). Consequently, the analysis concludes the likelihood of successful spawning between farm escapees already present within a river and wild Atlantic Salmon in Atlantic Canada is very likely and with reasonable certainty (Table 1).

*Table 1. Summary of the likelihood rankings (see footnote for definitions) for the likelihood assessment for each Atlantic Salmon DU. Release and spawning success assessments were considered across the whole geographic range, whereas the exposure step was assessed with the dispersal model for each DU separately. The level of uncertainty is reported for each step of the likelihood (Appendix I provides criteria associated with levels of uncertainty).*

Likelihood Step	Unit of Assessment (DU)					
	DU 4A	DU 4B	DU 14A	DU 14B	DU 15	DU 16
	South Newfoundland East*	South Newfoundland West	Nova Scotia Southern Upland East	Nova Scotia Southern Upland West	Inner Bay of Fundy	Outer Bay of Fundy
Release Assessment	Extremely Likely <b>(High Certainty)</b>					
Exposure Assessment	Very unlikely – Likely	Likely – Very likely	Extremely unlikely	Moderately likely – Likely	Very unlikely	Likely
	<b>(Reasonable Certainty)</b>					
Spawning success assessment	Very likely <b>(Reasonable Certainty)</b>					
<b>Overall likelihood</b>	Very unlikely - Likely	Likely – Very Likely	Extremely unlikely	Moderately likely - Likely	Very unlikely	Likely

*Note: Likelihood categories are associated with definitions (and range of values) as follows: Extremely likely – Event will occur/is expected to occur (>95%); Very likely – Event will occur in most instances (>75% - 95%); Likely – Event will usually occur (>50% - 75%); Moderately likely – Event could occur occasionally (>25% - 50%); Very unlikely – Event could occur rarely (>5% - 25%); Extremely unlikely (0 – 5%).*

*\*Currently farmed salmon in DU 4A are triploid. However, assuming 98% efficacy of triploidy induction, the model only uses 2% of the production for estimating the number of escapees that may contribute to direct genetic interactions (i.e., are reproductively viable). The assessments are therefore based only on the escapees derived from 2% of production.*

## Consequence Assessment

The consequence assessment determined the potential impacts to wild Atlantic Salmon population abundance and genetic character, depending on the predicted number of escaped Atlantic Salmon estimated to have entered rivers and potentially interbred with wild Atlantic Salmon. While impacts may occur at any level of farm escapees in river, previous analyses have shown that the IBSEM model consistently predicts that when farm escapees exceed roughly 10% of the total salmon in a given river, impacts to both abundance and genetic character will occur (Castellani et al., 2015, 2018; Sylvester et al., 2019; Bradbury et al., 2020b). The variability in model runs and differences between rivers, at present, makes it difficult to associate a particular magnitude of impact with a given proportion of farmed fish invasion for a given river. However, simulations using a variety of model parameters for farmed and wild Atlantic Salmon generally show consistent impacts at or above the 10% threshold (Castellani et al., 2015; B. Wringe, DFO, unpublished data). Additionally, the magnitude of the predicted modelled impacts are positively correlated so that the greater the proportion of invaders, the greater, on average, the magnitude of impacts to wild salmon abundance and genetic character. Therefore, for the purpose of the consequence assessments we use the amount by which the proportion of escapees exceeds 10% threshold as a proxy for the relative magnitude of impact.

### Consequence to abundance

To estimate the consequence to abundance, the model used predicted numbers of both wild Atlantic Salmon population size across all rivers within the DU, as well as the total number of predicted farm escapees in rivers within the DU (from the dispersal modeling). This analysis resulted in a DU-level proportion of farmed Atlantic Salmon and given the positive relationship between the proportion of farmed salmon and impact to abundance, the higher this proportion the higher the consequence category. Consequence rankings for abundance varied from negligible to extreme depending upon the DU considered and the escape rate used, with reasonable certainty (Table 2). This assessment considers only the direct consequences of interbreeding between farmed and wild Atlantic Salmon and does not consider ecological effects.

### Consequence to genetic character

To assess impacts to genetic character, the analysis considered individual rivers within a DU as the unit of diversity. Using the dispersal model, the analysis determined the number of rivers within a DU that exceeded 10% farm escapees. As more rivers within the DU are potentially impacted, this represents a greater proportion of the total diversity within the DU. Consequence rankings for genetic character varied from negligible to extreme depending on the DU considered and the escape rate used, with reasonable certainty in all rankings (Table 2).

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Table 2. Summary of the consequence to abundance (before the /) and genetic character (after the /) for each Atlantic Salmon designatable unit (DU). Values report the estimated population size of wild Atlantic Salmon across all rivers within a DU as well as the number of Atlantic Salmon rivers considered for each DU. Consequence assessments are summarized for each of the four escape rates (0.1, 0.2, 0.4, and 0.8 escapees per tonne of production).

			Consequence ranking for abundance / genetic character			
			Escape rate			
DU	Estimate of wild salmon population size across all rivers in the DU	Number of wild salmon rivers included in the assessment	0.1	0.2	0.4	0.8
DU 4A	26,488	54	Negligible / Negligible	Negligible / Negligible	Negligible / Negligible	Negligible / Minor
DU 4B	12,450	52	Negligible / Severe	Minor / Extreme	Moderate / Extreme	Major / Extreme
DU 14A	1,669	35	Negligible / Negligible	Negligible / Negligible	Negligible / Negligible	Negligible / Negligible
DU 14B	3,413	44	Negligible / Minor	Negligible / Moderate	Minor / Severe	Moderate / Severe
DU 15	1,309	55	Negligible / Minor	Negligible / Minor	Negligible / Moderate	Negligible / Moderate
DU 16	1,704	24	Minor / Extreme	Moderate / Extreme	Severe / Extreme	Extreme / Extreme

**Risk estimation**

The estimated risks to abundance and genetic diversity for the six Atlantic Salmon DUs considered here build on the results of the likelihood and consequence assessments. Risk matrices were based on the Department’s [Framework for Aquaculture Risk Management \(FARM\)](#) and the risk-approach on the movement of live fish under Section 56 of the Fishery (General) Regulations, modified to reflect the status of the individual DUs (Appendix II). Risk was categorized as Low, Medium, or High risk with the risk tolerance across matrices reflecting the status of the DU under consideration (Not at Risk, Threatened/Special Concern, or Endangered). Assessment of six DUs, each for abundance and genetic character, resulted in 12 risk matrices for each of four assumed escape rates. Table 3 summarizes risk assessment outcomes.

The risk to abundance across modeled escape rates was **low** for Nova Scotia Southern Upland East, Inner Bay of Fundy, and South Newfoundland East, **low to high** for Nova Scotia Southern Upland West and South Newfoundland West, and **medium to high** for Outer Bay of Fundy DUs.

The risk to genetic character across modeled escape rates was **low** for Nova Scotia Southern Upland East and South Newfoundland East, **medium** for Inner Bay of Fundy, **medium to high** for Nova Scotia Southern Upland West, and **high** for Outer Bay of Fundy and South Newfoundland West DUs.

Among the model variables, the level of risk related to direct genetic interactions increased by proximity to, and intensity of, aquaculture operations, and by declining wild population size and worsening conservation status; risk decreased by farming sterile fish, a strategy currently used in Placentia Bay, NL (DU 4A).

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Table 3. Summary of the risk estimates for abundance and genetic character of the six Atlantic Salmon designatable units (DU) considered as part of this assessment, shown for each of the four escape rates used. COSEWIC Status is based on the 2010 Atlantic Salmon assessment.

DU	COSEWIC Status	Risk – abundance	Risk – genetic character
South Newfoundland East (DU 4A)	Threatened (as part of South NL 2010 COSEWIC)	0.8 – LOW 0.4 – LOW 0.2 – LOW 0.1 – LOW	0.8 – LOW 0.4 – LOW 0.2 – LOW 0.1 – LOW
South Newfoundland West (DU 4B)	Threatened (as part of South NL 2010 COSEWIC)	0.8 – HIGH 0.4 – MEDIUM 0.2 – LOW 0.1 – LOW	0.8 – HIGH 0.4 – HIGH 0.2 – HIGH 0.1 – HIGH
Nova Scotia Southern Upland East (DU 14A)	Endangered (as part of SU 2010 COSEWIC)	0.8 – LOW 0.4 – LOW 0.2 – LOW 0.1 – LOW	0.8 – LOW 0.4 – LOW 0.2 – LOW 0.1 – LOW
Nova Scotia Southern Upland West (DU 14B)	Endangered (as part of SU 2010 COSEWIC)	0.8 – HIGH 0.4 – MEDIUM 0.2 – LOW 0.1 – LOW	0.8 – HIGH 0.4 – HIGH 0.2 – HIGH 0.1 – MEDIUM
Inner Bay of Fundy (DU 15)	Endangered (listed under SARA – 2003)	0.8 – LOW 0.4 – LOW 0.2 – LOW 0.1 – LOW	0.8 – MEDIUM 0.4 – MEDIUM 0.2 – MEDIUM 0.1 – MEDIUM
Outer Bay of Fundy (DU 16)	Endangered	0.8 – HIGH 0.4 – HIGH 0.2 – HIGH 0.1 – MEDIUM	0.8 – HIGH 0.4 – HIGH 0.2 – HIGH 0.1 – HIGH

To assess the level of mitigation required to reduce risk, simulations estimated the effects of reducing escapees for the level of production assumed here. The results from Table 3 resulted in exclusion of two DUs from this simulation because they were consistently **low** risk (DU 4A and DU 14A). For the four remaining DUs, in general, where risk was assessed to be **medium - high**, simulations estimated that to reduce the risk to **low** required a 50% or greater reduction of escapees (Table 4).

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Table 4. Summary of the risk to abundance and genetic character for the four Atlantic Salmon designatable units (DU) with MEDIUM-HIGH risk under scenarios simulating reductions in the number of escapees. The 'Full' model refers to the risk assessment results in Table 3 compared to reductions of 25%, 50%, 75% and 95% for two levels of escape rate (0.2 and 0.4 escapees/tonne production). Risk is reported for both abundance (left of the /) and diversity (right of the /) for each scenario per DU. SU=status update, COSEWIC= Committee on the Status of Endangered Wildlife in Canada

DU	COSEWIC Status	Risk – Abundance / Genetic character			
		0.2 escapees / tonne production		0.4 escapees / tonne production	
Nova Scotia Southern Uplands West	Endangered	Full	LOW / HIGH	Full	MEDIUM / HIGH
		25% reduction of escapees	LOW / HIGH	25% reduction of escapees	LOW / HIGH
		50% reduction of escapees	LOW / MEDIUM	50% reduction of escapees	LOW / HIGH
		75% reduction of escapees	LOW / LOW	75% reduction of escapees	LOW / MEDIUM
		95% reduction of escapees	LOW / LOW	95% reduction of escapees	LOW / LOW
Inner Bay of Fundy	Endangered	Full	LOW / MEDIUM	Full	LOW / MEDIUM
		25% reduction of escapees	LOW / MEDIUM	25% reduction of escapees	LOW / MEDIUM
		50% reduction of escapees	LOW / MEDIUM	50% reduction of escapees	LOW / MEDIUM

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<i>DU</i>	<i>COSEWIC Status</i>	<i>Risk – Abundance / Genetic character</i>			
		<i>0.2 escapees / tonne production</i>		<i>0.4 escapees / tonne production</i>	
		<i>75% reduction of escapees</i>	<i>LOW / LOW</i>	<i>75% reduction of escapees</i>	<i>LOW / MEDIUM</i>
		<i>95% reduction of escapees</i>	<i>LOW / LOW</i>	<i>95% reduction of escapees</i>	<i>LOW / LOW</i>
<i>Outer Bay of Fundy</i>	<i>Endangered</i>	<i>Full</i>	<i>HIGH / HIGH</i>	<i>Full</i>	<i>HIGH / HIGH</i>
		<i>25% reduction of escapees</i>	<i>HIGH / HIGH</i>	<i>25% reduction of escapees</i>	<i>HIGH / HIGH</i>
		<i>50% reduction of escapees</i>	<i>MEDIUM / HIGH</i>	<i>50% reduction of escapees</i>	<i>HIGH / HIGH</i>
		<i>75% reduction of escapees</i>	<i>LOW / HIGH</i>	<i>75% reduction of escapees</i>	<i>MEDIUM / HIGH</i>
		<i>95% reduction of escapees</i>	<i>LOW / LOW</i>	<i>95% reduction of escapees</i>	<i>LOW / HIGH (*LOW at 98%)</i>
<i>South Newfoundland West</i>	<i>Threatened</i>	<i>Full</i>	<i>LOW / HIGH</i>	<i>Full</i>	<i>MEDIUM / HIGH</i>
		<i>25% reduction of escapees</i>	<i>LOW / HIGH</i>	<i>25% reduction of escapees</i>	<i>MEDIUM / HIGH</i>
		<i>50% reduction of escapees</i>	<i>LOW / HIGH</i>	<i>50% reduction of escapees</i>	<i>LOW / HIGH</i>
		<i>75% reduction of escapees</i>	<i>LOW / MEDIUM</i>	<i>75% reduction of escapees</i>	<i>LOW / HIGH</i>
		<i>95% reduction of escapees</i>	<i>LOW / LOW</i>	<i>95% reduction of escapees</i>	<i>LOW / LOW</i>

## Mitigation Options

Mitigating potential direct genetic interactions mutually benefits both farm producers and wild Atlantic Salmon. The review of mitigation options for reducing the risk of direct genetic interactions between farm escapees and wild Atlantic Salmon populations targeted different parts of the pathway leading to genetic interactions (release, exposure, spawning). While other mitigation measures certainly exist, this review considered improvements in containment, licence conditions, marine recapture, freshwater recapture, genetic traceability, consideration of siting, introductions and transfers of farmed salmon to marine cages, and sterilization of farmed salmon.

The review indicated that eliminating all human errors and equipment failures associated with Atlantic Salmon net pen escapes is not realistic and that currently no single measure will necessarily fully eliminate risk. However, cumulative effects of multiple measures can contribute to an effective reduction in escapees and risk. Furthermore, given the range of risk assessment outcomes for the six DUs considered, it is indicated that different locations across Atlantic Canada may not warrant the same mitigation approach or approaches. When deciding on which measures to implement, the goals of escape management should be considered for the individual farm or area. Demonstration of the efficacy of implemented mitigation measures will require that experts evaluate results from comprehensive monitoring programs.

Technologies such as fully closed containment or fully sterile populations would eliminate direct genetic interactions between escaped and wild Atlantic Salmon. However, the utility and feasibility of these approaches has not been widely demonstrated or assessed.

## Sources of Uncertainty

Total uncertainty includes both variability, which is a function of the system that additional measurements cannot reduce, and lack of knowledge that may be reduced with additional data or expert opinion (Vose, 2008).

Based on peer-reviewed literature and available data, certainty at each step of the likelihood and consequence assessments ranged from **high certainty** to **reasonable certainty**.

Main sources of uncertainty include: the accuracy of reported escape events in reflecting actual escapes, the actual number of escapees per unit of production, escapee dispersal and other key parameters used in the dispersal model (summarized in Table 5), the likelihood of successful spawning for an individual escapee, the stochasticity of the magnitude of impacts across independent IBSEM model runs for a given level of escapees, and estimates of wild Atlantic Salmon population sizes.

A sensitivity analysis by Bradbury et al. (2020b) included several key dispersal model parameters and formed the basis for model parameter estimates in the current risk assessment. This analysis took estimates of model parameters from the best available sources in the literature. Although the analysis took wild Atlantic Salmon population size into account, uncertainty remains both in the estimates of the population size as well as the vulnerability of individual wild salmon populations given that multiple characteristics of a population (e.g., female fecundity, male to female sex ratios) could affect the level of impact of direct genetic interactions from farm escapees.



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*Table 5. Overview of the main sources of uncertainty in the risk assessment, considerations used to account for this uncertainty, and the overall likely impact on the risk estimates.*

<b>Source of uncertainty</b>	<b>Step in the risk assessment</b>	<b>Considerations to account for uncertainty</b>	<b>Overall likely impact to risk estimate</b>
Accuracy of reported escape events	Release assessment	Combined multiple, independent but complimentary sources of information	None because of the combination rules, the exposure assessment determines the overall likelihood
Escape rate	Exposure assessment	Sensitivity analysis conducted using four escape rates in the risk assessment	None unless actual escape rates are outside the values used in the assessment
Proportion of early vs. late escapes	Exposure assessment	Sensitivity analysis in Bradbury et al. (2020b); assumed 50:50 early vs. late escapes in the risk assessment	Risk may increase as proportion of late escapees increases
Dispersal distance	Exposure assessment	Estimates from literature and tagging in NL suggest ~200 km	Risk for rivers (and the DU) will vary depending on proximity and population size
Proportion of escapees that are sexually mature	Exposure assessment	Sensitivity analysis in Bradbury et al. (2020b); values used in risk assessment based on tagging and counting fence data in NL	Risk may increase as proportion of sexually mature escapees increases
Likelihood of spawning for a farm escapee is difficult to predict	Spawning assessment	Experimental and observational studies suggest that when considered as an aggregate, spawning by farm escapees will occur	None because of the combination rules, the exposure assessment determines the overall likelihood
Estimates of wild Atlantic Salmon population size	Exposure assessment	Estimates based on habitat and conservation egg requirements, adjusted for regional declines in wild Atlantic Salmon	Risk may increase because these estimates may still represent an overestimate of the actual population sizes of the DUs
Variability in the degree of impacts across independent model runs (IBSEM)	Consequence assessments	Region-specific model parameterization and the identification of a consistent threshold for impacts (i.e., 10%)	Could result in an increased risk given the uncertainty in the relationship between consequence categories and thresholds and variation among populations due to differences in population characteristics

## CONCLUSION

The results of the risk assessment revealed a range of risk outcomes depending on the specific DU considered and the escape rate used. The risk to abundance across modeled escape rates was **low** for Nova Scotia Southern Upland East, Inner Bay of Fundy, and South Newfoundland East, **low** to **high** for Nova Scotia Southern Upland West and South Newfoundland West, and **medium** to **high** for Outer Bay of Fundy DUs. The risk to genetic character across modeled escape rates was **low** for Nova Scotia Southern Upland East and South Newfoundland East, **medium** for Inner Bay of Fundy, **medium** to **high** for Nova Scotia Southern Upland West, and **high** for Outer Bay of Fundy and South Newfoundland West DUs.

Given the limited local data available and reliance upon the use of models and their assumptions and parameters, experts should regularly review and revise the conclusions of this risk assessment as new and relevant information becomes available. Such information might include changes to industry practices, production levels, escape rates, or sizes of wild salmon populations. In addition, improving the model accuracy and validation of model assumptions and outputs will require further research studies and monitoring. Despite the uncertainties associated with this risk assessment, the results and conclusions of this analysis were generally consistent with observations from other jurisdictions spanning the North Atlantic.

## OTHER CONSIDERATIONS

- Indirect genetic effects and ecological effects (e.g., disease, parasites, predation, and competition) are also important threats to wild Atlantic Salmon and an integrated understanding of both direct and indirect genetic interactions requires further study. Furthermore, other important human-related and environmental impacts should be considered in addition to direct genetic impacts on the overall impact to wild Atlantic Salmon populations (see Cote et al., 2015).
- Freshwater hatcheries were outside the scope of this risk assessment and any escapees from freshwater facilities would be in addition to the risks modeled and assessed in the current risk assessment.
- This analysis summarized consequence to abundance at the DU level, which may obscure specific, river-level impacts and variability among rivers, depending on the proportion and wild population size of impacted rivers. The associated risk assessment research document includes an appendix of the river-level proportion of escapees.
- Further studies and examples where other data sources such as counting fences can validate the model predictions of the number of escapees in rivers, will help to assess the accuracy and assumptions of the model.

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**SOURCES OF INFORMATION**

This Science Advisory Report results from the June 6-9, 2023 National Peer Review on Assessment of the risk posed to wild Atlantic Salmon population abundance and genetic character by direct genetic interaction with escapes from East Coast Atlantic Salmon aquaculture. Additional publications from this meeting will be posted on the [Fisheries and Oceans Canada \(DFO\) Science Advisory Schedule](#) as they become available.

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**APPENDICES****Appendix I***Table A1. Categories and definitions used to describe the level of uncertainty associated with scientific data and information.*

<b>Categories</b>	<b>Definition</b>
High uncertainty	<ul style="list-style-type: none"> <li>● No or insufficient data</li> <li>● Available data are of poor quality</li> <li>● Very high intrinsic variability</li> <li>● There is no consensus in the scientific literature</li> </ul>
Reasonable uncertainty	<ul style="list-style-type: none"> <li>● Limited, incomplete, or only surrogate data are available</li> <li>● Available data can only be reported with significant caveats</li> <li>● Moderate to high intrinsic variability</li> <li>● Scientific literature and/or models come to different conclusions</li> </ul>
Reasonable certainty	<ul style="list-style-type: none"> <li>● Available data are abundant, but not comprehensive</li> <li>● Available data are robust</li> <li>● Low intrinsic variability</li> <li>● Scientific literature and/or models mostly agree</li> </ul>
High certainty	<ul style="list-style-type: none"> <li>● Available data are abundant and comprehensive</li> <li>● Available data are robust, peer-reviewed and published</li> <li>● Very low intrinsic variability</li> <li>● Scientific literature and/or models agree</li> </ul>



Appendix II

Endangered

Likelihood	Negligible	Minor	Moderate	Major	Severe	Extreme
Extremely likely	Low	Medium	High			
Very likely						
Likely						
Moderately likely						
Very unlikely						
Extremely unlikely						

Threatened/Special Concern

Likelihood	Negligible	Minor	Moderate	Major	Severe	Extreme
Extremely likely	Low	Medium		High		
Very likely						
Likely						
Moderately likely						
Very unlikely						
Extremely unlikely						

Not at Risk

Likelihood	Negligible	Minor	Moderate	Major	Severe	Extreme
Extremely likely	Low	Medium			High	
Very likely						
Likely						
Moderately likely						
Very unlikely						
Extremely unlikely						

Figure A1. Risk matrices from Section 56 Fisheries (General) Regulations for combining the results of the assessment of likelihood and consequences to Atlantic Salmon abundance and genetic diversity. Risk matrices and associated tolerances are presented separately for DUs assessed by the Committee On the Status of Endangered Wildlife in Canada (COSEWIC) as Endangered, Threatened or Special Concern, and Not at Risk. Green, yellow and red represent the areas of low, medium and high risk, respectively within each of the risk matrices.

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