

Ecosystems and Oceans Science Sciences des écosystèmes et des océans

Canadian Science Advisory Secretariat (CSAS)

Research Document 2021/061

National Capital Region

Evaluation of Existing Risk Assessment Methods for Granting Ballast Water Management Exemptions

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Foreword

This series documents the scientific basis for the evaluation of aquatic resources and ecosystems in Canada. As such, it addresses the issues of the day in the time frames required and the documents it contains are not intended as definitive statements on the subjects addressed but rather as progress reports on ongoing investigations.

Published by:

Fisheries and Oceans Canada Canadian Science Advisory Secretariat 200 Kent Street Ottawa ON K1A 0E6

http://www.dfo-mpo.gc.ca/csas-sccs/ csas-sccs@dfo-mpo.gc.ca



© Her Majesty the Queen in Right of Canada, 2021 ISSN 1919-5044 ISBN 978-0-660-40295-6 Cat. No. Fs70-5/2021-061E-PDF

Correct citation for this publication:

Ogilvie, D., Daigle, R., Chassé, J., and Bailey, S.A. 2021. Evaluation of Existing Risk Assessment Methods for Granting Ballast Water Management Exemptions. DFO Can. Sci. Advis. Sec. Res. Doc. 2021/061. vi + 29 p.

Aussi disponible en français :

Ogilvie, D., Daigle, R., Chassé, J., et Bailey, S.A. 2021. Évaluation des méthodes existantes d'évaluation des risques pour l'octroi de dérogations en matière de gestion des eaux de ballast. Secr. can. de consult. sci. du MPO. Doc. de rech. 2021/061. vi + 31 p.

TABLE OF CONTENTS

LIST OF TABLESIV
LIST OF FIGURESV
ABSTRACTVI
INTRODUCTION
JOINT HARMONIZED PROCEDURE
CANADIAN JOINT HARMONIZED PROCEDURE CASE STUDY4
Methods of the Joint Harmonized Procedure case study4
Results of the Joint Harmonized Procedure case study4
REVIEW OF THE JOINT HARMONIZED PROCEDURE5
SAME RISK AREA APPROACH
SUMMARY OF PREVIOUS STUDIES ON SAME RISK AREA
Study I6
Study II7
CANADIAN SAME RISK AREA CASE STUDY8
Methods of the Same Risk Area Case Study8
Results and Discussion of the Same Risk Area Case Study10
REVIEW OF THE SAME RISK AREA APPROACH11
CONCLUSION
ACKNOWLEGDEMENT
REFERENCES CITED13
TABLES
FIGURES
APPENDICES

LIST OF TABLES

Table 2. Average port connectivity across the three years (2009, 2011, and 2013) and trait combinations examined using the Same Risk Area method. The assessment of port connectivity was based on the release event with the largest number of individuals reaching a recipient port at a given dispersal time during the seven-day competence period. The port connectivity values are relative to the total number of individuals in a single release event (1,000 individuals).......17

LIST OF FIGURES

Figure 1. The Joint Harmonized Procedure decision tree used to determine the risk of ballast water transfers.	.19
Figure 2. Outcome from the Joint Harmonized Procedure decision tree for the Boston-Saint John shipping route.	.20
Figure 3. The 12 ports within the province of Québec examined in the Canadian Same Risk Area case study.	.21
Figure 4. Water circulation within the Gulf of St. Lawrence during the spring (April – June) in 2011.	.22
Figure 5. Water circulation within the Gulf of St. Lawrence during the summer (July – September) in 2011.	.23
Figure 6. Water circulation within the Gulf of St. Lawrence during the fall (October – December in 2011.	er) .24

ABSTRACT

The International Maritime Organization's (IMO) Ballast Water Management Convention permits nations to grant exemptions from specific ballast water management requirements to ships travelling or exclusively operating between specified ports. Furthermore, exemptions must be granted based on scientifically robust risk assessments that indicate a ship's ballast water activities have a low probability of damaging public health, environment, resources, or property of any nation.

Two existing risk assessment methods — i) Joint Harmonized Procedure and ii) Same Risk Area — that satisfy the requirements of the IMO's Guidelines for Risk Assessment were assessed by conducting a literature review and applying these methods to case studies in Canada.

The Joint Harmonized Procedure uses detailed port survey data and a decision tree to evaluate risk based on the salinity difference between source and recipient ports and the presence of species of concern. The Joint Harmonized Procedure was applied to a case study where ballast water was transported from Boston, MA, to Saint John, NB. The outcome of the risk assessment was high risk due to the occurrence of seven species of concern and the overlap in salinity between Boston and Saint John. Overall, conducting port surveys to identify harmful species that could be transported from the source to recipient port in ballast water is logical and straightforward, and the decision tree can be adapted to assess factors relevant for predicting survival associated with a given shipping route; e.g. evaluating temperature and salinity tolerances of species of concern against environmental conditions in the recipient port.

The Same Risk Area approach evaluates whether species of concern can disperse unassisted from the source to recipient ports, regardless of their transport in ballast water. To evaluate this method, the natural connectivity between 12 ports in the province of Québec was examined using a trait-based biophysical model, assessing various combinations of planktonic duration, swimming behavior, and spawning period. Port connectivity varied greatly between these ports across the trait combinations examined, with some ports having relatively higher connectivity, though most ports had lower or no connectivity. In summary, the Same Risk Area approach is flexible to assess specific species of concern or general character traits when species distribution data are or are not unavailable, respectively. However, port connectivity thresholds (high vs. low) are not well-defined, making it difficult to evaluate port connectivity relative to the likelihood of spreading harmful species to the recipient port via ballast water.

INTRODUCTION

The movement of ballast water through commercial shipping is one of the primary pathways for the introduction and spread of harmful aquatic species globally (Bailey et al. 2020). To mitigate the introduction and establishment of harmful species attributed to ballast water, the International Maritime Organization's (IMO) *International Convention for the Control and Management of Ships' Ballast Water and Sediments, 2004* (the Convention) establishes ballast water management standards and procedures for international shipping (IMO 2004; see Appendix 1 for a glossary of terms and definitions). As the Convention entered into force in 2017, parties are expected to transition from ballast water exchange requirements under Regulation D-1 — where ballast water taken at port is purged at sea and replaced with oceanic water — to the ballast water performance standard defined in Regulation D-2 (IMO 2004). The intent of Regulation D-2 is to mitigate the likelihood of establishment of harmful species by limiting the concentration of viable organisms in discharged ballast water. Most ships are expected to comply with Regulation D-2 by utilizing onboard ballast water management systems to treat their ballast water.

Nations may grant vessels exemptions from requirements to meet the ballast water performance standard under Regulation A-4 of the Convention, provided decisions are based on scientifically robust risk assessments and that movement of unmanaged ballast water has a low probability of impairing or damaging public health, environment, resources, or property of any nation (IMO 2017a). To date, two risk assessment methods — i) Joint Harmonized Procedure and ii) Same Risk Area — have been presented for consideration within the IMO community for granting exemptions under Regulation A-4 (IMO 2014; 2016a,b).

Canada, a signatory to the Convention, is currently undertaking regulatory updates to implement ballast water management requirements as per the Convention in Canadian waters. Canada's proposed ballast water regulations were published in the Canada Gazette in June 2019, including provisions for ballast water management exemptions under Regulation A-4 (Canada Gazette 2019). The objective of this Research Document was to evaluate the two existing risk assessment methods by conducting a literature review and applying the methods to case studies in Canada, in order to understand how these methods may be used within Transport Canada's regime for assessing exemption applications.

INTERNATIONAL MARITIME ORGANIZATION'S GUIDELINES FOR RISK ASSESSMENT

Regulation A-4 of the Convention states that a nation may grant exemptions from specific ballast water management requirements in waters under its jurisdiction when the following criteria are met:

- 1. Ships on a voyage or voyages between specified ports/locations or ships that operate exclusively between specified ports/locations;
- 2. Ships do not mix ballast water or sediments other than between such specified ports;
- 3. Exemptions are reviewed at least every five years; and,
- 4. Exemptions are granted based on the IMO's *Guidelines for Risk Assessment under Regulation A-4 of the BWM Convention (G7)* (IMO 2004).

The G7 Guidelines for risk assessment outline the procedure for granting ballast water management exemptions, including the types of risk assessment that may be used to evaluate

the risk of granting exemptions (IMO 2017a). The following paragraphs summarize the IMO G7 Guidelines for risk assessment.

A nation may grant an exemption under Regulation A-4 if a risk assessment indicates that unmanaged ballast water transferred between specific ports/locations has a low probability of impairing or damaging the environment, human health, property, or resources of the granting nation or other nations. These risk assessments must be scientifically defensible, distinguishing between ballast water transfers that are likely to have negative ecological or socio-economic impacts to nations, and transfers that are unlikely to have negative impacts. Suitable risk assessment methods include environmental matching, species' biogeographical, or species-specific risk assessments, and these may be used separately or in combination to determine overall risk.

Environmental matching risk assessments compare environmental conditions between donor and recipient ports or regions to determine the likelihood of survival and establishment of introduced species in the recipient port. Similar environmental conditions may indicate higher probability of establishment and no overlap in conditions may indicate lower establishment probability. Temperature and salinity are the most common conditions evaluated in environmental matching risk assessments, evaluating their mean, range (min/max), variability, or rate of change. Temperature and salinity measurements from both surface and bottom waters, and variability due to seasonality and tidal cycle should be considered in the assessment to capture the full range of conditions within a port. It is recommended to pair environmental matching risk assessment with a species-specific risk assessment that evaluates species of concern, as it is difficult to determine the risk of ballast water based on environmental matching alone.

Species' biogeographical risk assessments evaluate the ecological similarities between source and recipient ports or regions by comparing the presence or absence of cryptogenic, nonindigenous, and harmful species in each location; indigenous communities could be compared when spatial distribution data are unavailable for these species. The overlap of species indicates the potential for survival and establishment of species that may be transferred from the source to recipient port by unmanaged ballast water during the exemption period. The data required to complete this analysis include the spatial distribution of the abovementioned species in the source and recipient ports or regions, which can be obtained from field surveys, scientific literature, or species databases.

Species-specific risk assessments evaluate the potential arrival, survival, establishment, and impact of species of concern (i.e. target species) in a given recipient environment. Target species are species that could be introduced from the source to recipient port/region through ballast water and impair or damage the environment, human health, property or resources. Target species are defined for a specific port, State or biogeographic region.

The target species selection process typically begins by creating a list of species (cryptogenic, harmful, nonindigenous, and indigenous) that are present in the source port but absent in the recipient port. Target species are selected from this species list based on their history of invasion, evidence of causing harm, biogeographic distribution, and relationship with ballast water transport (see Gollasch et al. 2020 for a review of methods to select target species). Then, the target species are assessed to determine their probability of survival and establishment in the recipient port based on physiological tolerances (e.g. temperature and salinity) and ability to complete their life cycle in the recipient environment. Utilizing a robust target species selection method is critical for species-specific risk assessment, since the outcome of the assessment is sensitive to the selection of target species.

The IMO G7 Guidelines are general, giving nations flexibility to utilize diverse strategies to assess the level of risk attributed to transferring unmanaged ballast water between ports. The Joint Harmonized Procedure and Same Risk Area were developed in accordance with the IMO G7 Guidelines, and any modifications to these risk assessment methods should be consistent with these guidelines.

JOINT HARMONIZED PROCEDURE

The Joint Harmonized Procedure was developed by the Helsinki Commission (HELCOM) and the Oslo and Paris (OSPAR) Commission to help guide their contracting European nations with granting ballast water management exemptions under Regulation A-4. This risk assessment method was developed through input from multiple scientific experts (Gollasch et al. 2011; David et al. 2013), and assesses the risk of ballast water transfers using a combination of environmental matching and species-specific methods.

The Joint Harmonized Procedure uses a two-step approach to assess the risk of transferring ballast water from a source to recipient port (HELCOM and OSPAR 2020a). The first step involves conducting port surveys to detect target species at the ports and assessing the risk of transferring ballast water using a relatively simple decision tree.

Biological surveys are conducted for both source and recipient ports following the Joint Harmonized Procedure's port survey protocol (see Annex 6 in HELCOM and OSPAR 2020a for details), to create a robust list of species for each port. Their standardized port survey protocol includes guidelines on methods for sample collection (e.g. number of samples required, season/timing of surveys, taxonomic groups sampled, sampling gear type, and locations within the port to be sampled), sample processing and analysis. The taxonomic groups sampled include plankton (phytoplankton and zooplankton), fouling organisms, mobile epifauna, and benthic infauna, with the objective of sampling a sufficient number of organisms to identify most species at the port. Additionally, data are collected on the environmental conditions (e.g. temperature and salinity) at the port during sampling visits. Ports must be surveyed at least every five years, in alignment with the five-year review and renewal requirement of exemptions under Regulation A-4 (IMO 2004). The purpose of using a standardized port survey protocol is to create robust species lists that are comparable between surveyed ports, ensuring that the data used in the risk assessment are of sufficient quality to produce an adequate level of certainty in the results.

The species list for each surveyed port is compared against the regional list of target species to select species for assessment. HELCOM and OSPAR maintain a target species list for the Baltic and Northeast Atlantic regions to standardize and simplify the target species selection process (Appendix 2). Species are included on the regional target species list if they meet all of the following criteria:

- 1. Species introduced or spread via ballast water or species that have a life stage that is likely to be transported by ballast water (e.g. planktonic larvae or adult);
- 2. Species having distribution within a part but not the entire region; and,
- 3. Species with measurable negative impact on human health, environment, or economy.

The risk of transferring ballast water from the source to recipient port is then determined using the Joint Harmonized Procedure decision tree (Figure 1). The decision tree has two possible outcomes (high or low risk) based on two key risk criteria identified for transferring ballast water between ports in the semi-enclosed waterbodies of the Baltic and North Seas (HELCOM and

OSPAR 2020a). These risk criteria were salinity difference between ports and target species that are at the source port, but not at the recipient port.

The second step includes conducting a detailed risk assessment to evaluate other relevant factors that influence invasion risk on a case by case basis, such as the presence of target species in adjacent areas to the ports or the natural dispersal capacity of target species. For example, a high-risk outcome from the Joint Harmonized Procedure decision tree could be overruled if the target species are likely to disperse unassisted from the source to recipient port. The method used to conduct the final detailed risk assessment is at the discretion of the governing nation. Each exemption must be renewed every five years and is subject to an intermediate review to consider any newly available data that could influence the likelihood of introducing harmful species to the recipient port via ballast water.

CANADIAN JOINT HARMONIZED PROCEDURE CASE STUDY

Methods of the Joint Harmonized Procedure case study

The Joint Harmonized Procedure method was applied to assess the risk of ballast water transported from Boston, MA, to Saint John, NB. This case study was selected since a small fleet of ships operate within this region.

First, nonindigenous and cryptogenic species were identified in each port based on existing species distribution data from the <u>National Exotic Marine and Estuarine Species Information</u> <u>System (NEMESIS)</u> (Table 1). Since NEMESIS had limited species distribution data for Saint John, for illustrative purposes, it was assumed that there were no nonindigenous or cryptogenic species at this port. Note that the species list provided in Table 1 is not an exhaustive list of species for Boston or Saint John. A literature-based assessment was pursued because conducting port surveys were beyond the scope of this study. Future exemption applications would be expected to conduct port surveys according to the Joint Harmonized Procedure port survey protocol (or equivalent methodology).

Once port species lists were produced, target species were selected based on the Joint Harmonized Procedure target species criteria:

- 1. Species introduced or spread via ballast water or species that have a life stage that is likely to be transported by ballast water (e.g. planktonic larvae or adult);
- 2. Species having distribution within a part but not the entire region (in this case, Boston and Saint John); and,
- 3. Species with measurable negative impact on human health, environment, or economy.

Species meeting all three criteria were selected as target species based on relevant information obtained from <u>NEMESIS</u> and <u>DFO species-specific risk assessments</u>.

Finally, target species were run through the Joint Harmonized Procedure decision tree (Figure 1) to determine the outcome of the risk assessment. The salinity data for Saint John were collected from four locations within the port from May to October during 2019 and 2020 (ACAP 2020), while the salinity data for Boston were collected from a single location within the port from April 1983 to June 1984 (Shiaris 1989).

Results of the Joint Harmonized Procedure case study

Twenty-eight nonindigenous and cryptogenic species established in Boston Harbour were assessed, of which seven were selected as target species (*Agarophyton vermiculophyllum*, *Ascidiella aspersa*, *Carcinus maenas*, *Grateloupia turuturu*, *Hemigrapsus sanguineus*,

Membranipora membranacea, and *Mytilopsis leucophaeata*; Table 1). The outcome of the Joint Harmonized Procedure decision tree was high risk for the Boston to Saint John shipping route. This high-risk outcome was due to the overlap in environmental salinity between Boston (26 - 33%) and Saint John (0.14 - 36%), and the presence of target species at the source port (Boston) which were presumed absent at the recipient port (Saint John; Figure 2).

REVIEW OF THE JOINT HARMONIZED PROCEDURE

The Joint Harmonized Procedure uses a detailed, systematic port survey protocol to comprehensively sample a variety of taxonomic groups that can be transported in ballast water. However, a significant level of effort must be expended to thoroughly sample taxa across space (different habitats) and time (seasons). Additionally, it may be difficult to conduct biological surveys in remote locations and to maintain up-to-date data over time. Identifying sampled organisms to the species level can be a difficult task due to limited reference sequences within molecular libraries and availability of morphology-based taxonomic expertise. There is also the possibility that target species may not be detected by port surveys or may be detected after an exemption has been granted. Utilizing species accumulation curves may help to guide port surveys to ensure that sufficient effort has been taken to identify species in a port (Thompson and Withers 2003).

The outcome of the assessment is sensitive to the selection of target species. All cryptogenic, nonindigenous, and harmful species that are at the source port but not at the recipient port are potential target species. However, it is likely that the distribution and impacts of many of the organisms sampled at ports are poorly studied (e.g. invertebrates and algae), reducing the utility of the assessment. The Joint Harmonized Procedure is precautionary by recommending the inclusion of species with unknown impacts (Annex 2 in HELCOM and OSPAR 2020a), but this may overemphasize the importance of ballast water as an introduction vector. There can also be uncertainty when extrapolating species information (such as establishment potential) from other regions (Diez et al. 2011). This uncertainty can be reduced by extrapolating information from regions that are similar to the recipient environment (e.g. within the same biogeographic region; Diez et al. 2011).

The Joint Harmonized Procedure decision tree is a quick and simple method to determine the risk of ballast water transfers, and the high or low risk determination is straightforward and easy to interpret. The decision tree can also be modified to address specific invasion risks for a shipping route or biogeographic region. For example, the salinity tolerance of target species could be assessed against the salinity at the recipient port to account for potential survival of euryhaline species. Additionally, the temperature tolerance of target species could be examined to evaluate shipping routes where temperature could be a limiting factor of survival in the recipient port.

SAME RISK AREA APPROACH

The Same Risk Area approach is a species-specific risk assessment that was initially proposed by the Danish government in 2014 (Stuer-Lauridsen and Overgaard 2014), and further developed with contributions from Belgium and Singapore (IMO 2016a,b; IMO 2017b). A Same Risk Area is a highly connected geographic area where target species are likely to disperse unassisted throughout the area within a reasonable timeframe (e.g. within a single year), regardless of their movement in ships' ballast water. Therefore, ships operating exclusively within a Same Risk Area could be exempted from managing their ballast water due to the high natural connectivity within the geographic area. It is acknowledged that organisms may disperse using other anthropogenic or natural vectors or pathways (e.g. hull fouling), but the Same Risk Area approach only assesses the dispersal of planktonic organisms via water circulation.

The boundaries of the Same Risk Area are determined by utilizing a biophysical model that couples a particle tracking model with a hydrodynamic model to simulate the transport of planktonic individuals (at any stage of development) via water currents. The dispersal of individuals can be examined for specific species (species-specific approach; e.g. Hansen and Christensen 2018), functional groups of species (e.g. Daigle et al. 2016), or general character traits that are applicable to a variety of nonindigenous species (trait-based approach; e.g. Baetens et al. 2018). The delineation of a Same Risk Area should be based on the target species, functional group, or trait combination having the lowest unassisted dispersal capacity, following a precautionary approach (IMO 2016b; Stuer-Lauridsen et al. 2018). Therefore, a Same Risk Area assessment is typically based on benthic species with a planktonic dispersal stage (e.g. meroplankton), but any species that disperses via water circulation (e.g. holoplankton) can be assessed. See Stuer-Lauridsen et al. (2018) for a detailed review of the Same Risk Area approach.

The data required to conduct the Same Risk Area assessment include but are not limited to:

- 1. Biological traits of target species that influence their dispersal via water circulation (e.g. planktonic duration, physiological tolerances, spawning period, depth preference, and swimming speed and behaviour); and,
- 2. Hydrodynamics, environmental conditions (e.g. temperature and salinity), and substrate type (when available) throughout the region of interest (Stuer-Lauridsen et al. 2018).

An important factor to consider is the number of consecutive years of stepping-stone dispersal to be modelled, as this influences the boundaries of the Same Risk Area (IMO 2016b). Evaluating the natural dispersal of species over a long period of time may diminish the importance of the movement of ballast water as an introduction pathway, whereas using too short of a time period may overemphasize the importance of ballast water (IMO 2016c). There is higher uncertainty associated with modelling stepping-stone dispersal of species, due to model assumptions required to estimate the establishment success of larvae after settlement (Hansen and Christensen 2018). Previous studies using Same Risk Area have modelled either one or five years of dispersal (Baetens et al. 2018; Hansen and Christensen 2018).

SUMMARY OF PREVIOUS STUDIES ON SAME RISK AREA

A standardized protocol has not yet been developed for the Same Risk Area approach, as modelling methods may vary depending on the context of the exemption request (e.g. species-specific vs. trait-based approach). Therefore, previous Same Risk Area studies from Europe were summarized to examine different modelling approaches used.

Study I

Hansen and Christensen (2018) conducted a Same Risk Area assessment in Kattegat and Øresund that connects the North Sea and the Baltic Sea.

The delineation of the Same Risk Area was based on modelling the larval dispersal of target species identified in the region. Twenty-three target species were selected for assessment that met all of the following criteria:

- 1. Benthic species with a planktonic dispersal stage;
- 2. Distributed in part but not the entire region;

- 3. Tolerates salinities \geq 10‰ (the study area only includes marine ecosystems); and,
- 4. Species not considered a macroalgae or macrophyte, as they typically have either very low or high dispersal rates (e.g. floating seaweed rafts).

Only benthic sessile species with a planktonic duration of days to weeks were selected as target species since these species were expected to have the lowest dispersal capacity in the study area relative to holoplankton.

The dispersal of larvae for each species was estimated using an agent-based model for both a single year and five consecutive years (i.e. through stepping-stone dispersal). The biological traits used in the model include spawning period, planktonic duration, and planktonic depth preference. Additionally, habitat maps were produced for each species given their settlement depth, salinity tolerance, and preferred substrate type. These maps were used to determine each species' suitable spawning (larval release sites) and settlement areas.

A cluster analysis was used to delineate the hydrographic regions, with clusters representing collections of sub-regions. The connectivity within a hydrographic region was estimated as the percentage of individuals that began and ended the simulation in the same region, whereas inter-regional connectivity was estimated as the percentage of individuals that ended the simulation in another region. Species were also evaluated based on their spatial distribution and extent of suitable habitat within the study area.

Based on the high connectivity demonstrated by this study, Denmark and Sweden designated the first Same Risk Area in Øresund in 2020 (HELCOM and OSPAR 2020b). On the other hand, the authors determined that Kattegat had weak natural connectivity for various target species. The low natural connectivity outcome for one species was disregarded because they were widely distributed throughout the study area in low abundances, but not considered invasive. The low connectivity outcomes for the remaining species were likely due to intolerance of larvae to marine water, relatively short planktonic duration, or lack of suitable habitat within Kattegat. This study highlights the sensitivity of the assessment method to which target species are assessed. Species that are not potentially harmful or invasive should not be selected as target species, since these species are not of concern for exemption decisions.

Study II

Baetens et al. (2018) completed a pilot study on behalf of the governments of Belgium and Netherlands to determine the ecological implications of creating a Same Risk Area for the ports of Antwerp, Zeebrugge, Vlissingen, and Rotterdam.

The authors used a trait-based approach to model the natural connectivity between ports. Their particle tracking model focused on spawning period (winter, spring, summer, and fall) and swimming behaviour (tidal, counter tidal, and passive). Tidal swimming behaviour is exhibited by individuals that rise to surface when tides rise and sink to the bottom during ebb tides, while individuals with counter tidal behaviour have movement opposite to that of tidal behaviour, and individuals with passive behaviour drift with water currents. Initially, simulated individuals were released at different depths in the water column (bottom, middle, and surface). However, as release depth did not influence the extent of natural dispersal, all release depths were combined in the final reporting of model results.

Connectivity was measured as the amount of time it took individuals to travel from a source to recipient port, recording the mean, minimum, and maximum dispersal times. Individuals taking longer than 200 days to reach their destination were excluded from the analysis, as it was assumed that this value exceeds the typical planktonic duration of benthic species. This study assessed a single year (2011) of dispersal of individuals. The final connectivity between ports

was produced by retaining the longest minimum dispersal times across all combinations of seasons and swimming behaviours.

The model results for minimum dispersal time indicated strong bilateral connections between Zeebrugge, Vlissingen, and Scheldt (referred to as the Scheldt zone) for each swimming behaviour year-round, during 2011. The Scheldt zone had weak bilateral connectivity with Rotterdam depending on swimming behaviour, while Antwerp only had a unilateral connection with the Scheldt zone overall (Antwerp is upstream from Vlissingen). Rotterdam and Antwerp did not have a bilateral connection.

This study highlights the importance of using an informative port connectivity metric that estimates the total number of individuals that reach a recipient port. Organism dispersal time (i.e. the time required for individuals to reach a destination) may produce misleading results, since it does not indicate the total number of individuals that reached a recipient port. Furthermore, organism dispersal time does not account for differences in planktonic duration across benthic species (McEdward 1995). Larvae that reach a recipient port outside of their settlement period would not be able to settle and establish in the port.

CANADIAN SAME RISK AREA CASE STUDY

Methods of the Same Risk Area Case Study

The Same Risk Area method was applied to both the Boston-Saint John route and a shipping route along Québec's shoreline in the Estuary and Gulf of St. Lawrence, calling on the ports of Rimouski, Sept-Îles, Port-Menier, Havre-Saint-Pierre, Natashquan, Kegaska, La Romaine, Harrington Harbour, Tête-à-la-Baleine, La Tabatière, Saint-Augustin, and Blanc-Sablon (Figure 3). The shipping route in Québec was selected as a complex example that includes multiple ports within a limited area where the shipping industry has expressed interest in the possibility of exemptions from aspects of ballast water management. This case study was not conducted using the Joint Harmonized Procedure due to limited species distribution data for these 12 ports.

This Same Risk Area case study used an existing peer-reviewed biophysical model from Daigle et al. (2016), who used a trait-based modelling approach to estimate the dispersal of marine benthic invertebrates in St. George's Bay, NS, Canada. A trait-based modelling approach was pursued because limited species distribution data were available for the ports of interest and to assess a broad range of life history characteristics applicable to a large number of species. See Daigle et al. (2016) for a detailed review of the biophysical model.

The biophysical model simulated the transport of individuals via water circulation by combining the circulation model developed by Brickman and Drozdowski (2012) with the particle tracking model designed by Chassé and Miller (2010); the circulation model is a variant of the NEMO-OPA (Nucleus for European Modelling of the Ocean – Océan Parallélisé) ocean model. This model setup has been validated in numerous previous studies (e.g. Lavoie et al. 2016, Quinn et al. 2017, Brennan et al. 2019).

The circulation model had a horizontal spatial resolution of $1/24^{\circ}$ and a vertical resolution with 46 layers of variable thickness (6m near the surface, with increasing thickness with depth; Daigle et al. 2016). The domain of the model includes the Gulf of Maine, Scotian Shelf, and Gulf of St. Lawrence. Currents were averaged over two-hour intervals to capture the effect of tides on the dispersal of individuals. This case study used hydrographic data from three years (2009, 2011, and 2013) to account for interannual variability in water circulation (Figures 4 – 6).

This trait-based assessment focused on the dispersal of meroplankton, since they typically have lower dispersal capacity than holoplankton. Three vertical swimming behaviours were modelled:

- 1. Diel migration, where individuals rise to the surface at night and sink during the day (swimming direction changed at 0600 and 1800 hours);
- 2. No swimming behaviour; and,
- 3. Tidal migration, where individuals rise to the surface during high tide and sink during low tide (swimming direction changed during slack tide; Daigle et al. 2016).

It was assumed that individuals had a vertical swimming speed of 1 mm/sec, representing the typical long-term swimming speed of caridean or brachyuran larvae (Daigle et al. 2016). The depth preference of individuals was 0 - 100m depth to account for a variety of nonindigenous species with varying depth preferences.

Some modifications were made to the model to run the Same Risk Area assessment. Two spawning periods of spring (April – June) and summer (July – September) were modelled, to match the typical spawning periods of marine invertebrate species on the East Coast of Canada (Fish and Johnson 1937; Lacalli 1981). Four planktonic durations were examined in this study (one week, four weeks, eight weeks, and four months), representing species with short, average, and long planktonic stages (McEdward 1995). For each planktonic duration, it was assumed that individuals had a settlement period of seven days during the final week of the planktonic stage (i.e. the period when individuals are able to settle; McEdward 1995).

One thousand individuals were released from each source port every two weeks at 0100 hours for each trait combination (24 combinations of planktonic duration, spawning period, and swimming behaviour) and year (2009, 2011, and 2013) examined. Individuals were released near harbour limits at the boundary of the open ocean, since the inner portions of the harbours were not included in the model. The position of individuals was recorded every two hours for 200 days, but the focus was on tracking the number of individuals that reached a recipient port (one grid cell, ~8.12 km²) at a given dispersal time during the seven-day competence period. Since the model output only recorded the location of individuals at a given dispersal time, individuals were not removed from the simulation once they reached a recipient port. The cumulative number of individuals reaching a recipient port during the seven-day competence period was not calculated to avoid double-counting individuals. The original model output from Daigle et al. (2016) that recorded the position of individuals at a given dispersal time was retained due to resource and time constraints. It is acknowledged that recording the cumulative number of individuals that settle in a recipient port would improve the estimation of port connectivity.

The assessment of port connectivity was based on the release event with the largest number of individuals reaching a recipient port at a given dispersal time during the seven-day competence period. Thus, the port connectivity values are relative to the total number of individuals in a single release event (1,000 individuals). This case study only examined a single year of dispersal of individuals.

Five-way analysis of variance (ANOVA) was conducted to assess the effects of planktonic duration, spawning period, swimming behaviour, release site, and year on port connectivity. The Cohen's f effect size was calculated for each factor and interaction to estimate the importance of statistical significance (Cohen 1988). The focus of the statistical analyses was on factors and interactions that were ecologically significant based on Cohen's f values greater than 0.10 (small effect), 0.25 (medium effect), or 0.40 (large effect; Cohen 1988).

Results and Discussion of the Same Risk Area Case Study

There were no individuals that travelled from Boston to Saint John via water circulation for any of the trait combinations examined (results not shown). Based on these results, nonindigenous species are unlikely to disperse unassisted from Boston to Saint John within a single year. This supports the high-risk outcome from the Joint Harmonized Procedure Canadian case study (above).

The results for each port pair combination for the 12 ports of interest within the province of Québec are summarized in Table 2 as the average port connectivity (APC) across years (2009, 2011, and 2013) and trait combinations examined. The minimum and maximum port connectivity values for each port pair are provided in Appendix 3, and an example of the results for a single trait combination is provided in Appendix 4.

The two most eastern ports of Saint-Augustin and Blanc-Sablon donated individuals to several western ports, especially those from La Romaine to Sept-Îles (1.58 - 46.33 APC), but only received a modest number of individuals from a few ports (e.g. Rimouski, 4.76 APC and Kegaska, 9.29 APC; Table 2). This was likely due to westward-flowing currents along the northern Gulf of St. Lawrence shoreline (Figures 4 - 6), transporting individuals towards the mouth of the St. Lawrence River. To the west of Saint-Augustin and Blanc-Sablon, some individuals were exchanged between Harrington Harbour, Tête-à-la-Baleine, and La Tabatière (0.07 - 1.54 APC), but these ports donated very few individuals to other ports (0.00 - 0.08 APC).

The exchange of individuals was highly variable from La Romaine to Port-Menier (0.00 - 44.29 APC), with most of these ports having unidirectional connectivity (Table 2). The port pair with the greatest bidirectional connectivity out of all ports examined was Havre-Saint-Pierre and Natashquan (19.53 and 44.29 APC), followed by Havre-Saint-Pierre and La Romaine (25.94 and 3.25 APC).

The two most western ports of Rimouski and Sept-Îles donated a modest number of individuals to several ports, especially those from Port-Menier to La Romaine (0.33 - 9.13 APC; Table 2). Sept-Îles received a relatively large number of individuals from a few ports (0.00 - 46.33 APC), while Rimouski received few individuals overall (0.01 - 1.18 APC).

Overall, port connectivity was highly variable between the port pairs examined, with some ports having relatively higher connectivity, though most ports had lower or no connectivity (Table 2 and Appendix 3).

Results of statistical analyses

Based on the results of the Cohen's f effect size analyses, both planktonic duration and release site (and their interaction) had a small effect on port connectivity. Planktonic duration and release site each produced effect sizes of 0.17, while the interaction of these two factors produced a slightly larger effect size of 0.21 (Table 3). The relatively strong effect size of planktonic duration indicates the importance of examining the planktonic durations of target species when conducting a Same Risk Area assessment. On the other hand, spawning period, swimming behaviour, year, and their interactions had a negligible effect on port connectivity. However, these factors are still important to include in a Same Risk Area assessment, as other studies determined that they had substantial effects on the dispersal of individuals (Roughan et al. 2011; Daigle et al. 2016; Baetens et al. 2018).

Sources of uncertainty

The total number of settlement-competent individuals that reached a recipient port was underestimated in this case study, since the model output only recorded the number of individuals reaching a recipient port at a given dispersal time rather than the cumulative number of individuals that reached a recipient port during the seven-day settlement period. In future Same Risk Area assessments, port connectivity should be based on the cumulative number of individuals that settle in a recipient port across release events to improve the estimation of port connectivity.

Any model is a simplification of complex processes and will have limitations in the representation of biological factors that influence the dispersal of organisms. For example, individuals were released once every two weeks at 0100 hours, but the timing of spawning events are based on various environmental cues, such as light, temperature or tidal cycle (McEdward 1995). The swimming behaviours (tidal, diel, and passive) were applied to individuals for the entirety of each simulation, but the swimming behaviour of organisms can change throughout their planktonic developmental stage, such as when migrating to suitable habitats (McEdward 1995). It is acknowledged that organism mortality would reduce the likelihood of individuals reaching a recipient port (Cowen et al. 2000), but mortality was not considered in this case study to examine the maximum dispersal potential of individuals.

Finally, the location within the source port where organisms are released could influence the number of individuals reaching a recipient port. Although the spatial resolution of the biophysical model (1/24°) is suitable for modelling the dispersal of individuals over large areas such as the Gulf of St. Lawrence, this spatial resolution was often too coarse to capture fine-scale details within ports (e.g. Boston Harbour). Therefore, individuals were released on the boundary between the port and open ocean rather than within the port, potentially influencing port connectivity.

REVIEW OF THE SAME RISK AREA APPROACH

The Same Risk Area approach is flexible to evaluate the dispersal of specific species, functional groups of species, or general character traits. The dispersal of specific species or functional groups can be assessed when species distribution data are available for the ports or region of interest. The species-specific approach can evaluate the probability of arrival (via natural dispersal) and survival of these species in the recipient port, providing greater certainty for the species examined (Hansen and Christensen 2018). When conducting a species-specific assessment, it is important to identify if any target species are not capable of surviving the environmental conditions (temperature and salinity) of waters between the ports, as these species could be transported in exempted ballast water to locations that are not reachable by unassisted dispersal alone. It is also important to identify and select target species that can survive in the recipient port, as these species have a higher probability of establishment if introduced.

On the other hand, a trait-based assessment that examines a broad range of character traits does not require detailed species distribution data. However, trait-based models may not reflect the probability of survival of species in the recipient port, and they do not examine the specific dispersal capacity of any one species. Species distribution data may not be required to conduct a trait-based Same Risk Area assessment, but this data can provide valuable insights on which species are likely to be transported in ballast water if an exemption is granted. Without such data, it is uncertain whether the biophysical model accounts for the dispersal of the specific harmful species that are established at the source port.

Particle tracking modelling is a well-established field of research and is commonly used in the management of fisheries (e.g. Chassé and Miller 2010), species at risk (e.g. Brennan et al. 2019), and invasive species (e.g. Brickman 2014). However, a detailed protocol does not currently exist for the Same Risk Area approach. Furthermore, it would be difficult to develop a

standardized protocol applicable to all Same Risk Area-based exemption applications since the modelling methods may need to be modified depending on the availability of species distribution data (species-specific vs. trait-based approach), geographic scale (e.g. spatial resolution of the model), and biological traits and environmental conditions influencing organism dispersal within a region (Stuer-Lauridsen et al. 2018). Nonetheless, best practices must be used when conducting particle tracking modelling to ensure the results are of sufficient quality to inform exemption decisions, as the outcome of the assessment is sensitive to the target species (or biological traits) examined and the assumptions and parameters of the model. For example, depth preference and mortality of organisms influence the estimated number of individuals reaching a recipient port (Cowen et al. 2000; Brennan et al. 2019).

Finally, the port connectivity threshold to distinguish between high or low naturally connected ports is not well-defined, making it difficult to analyze the port connectivity results relative to the likelihood of spreading nonindigenous species via ballast water transfers. Furthermore, it would be difficult to set port connectivity thresholds due to high uncertainty in the relationship between propagule pressure and establishment (NRC 2011). In general, highly connected ports would have a large number of individuals dispersing from the source to recipient port across the target species or biological traits examined. It is also important to ensure that ports are highly connected in the same direction as ballast water transfers.

CONCLUSION

This study reviewed the Joint Harmonized Procedure and Same Risk Area methods that were developed to assess ballast water management exemption applications under Regulation A-4. The Joint Harmonized Procedure makes use of port surveys to identify the presence of harmful species that could be introduced to the recipient port via ballast water, while the Same Risk Area approach identifies geographic areas with high natural connectivity. Both of these risk assessments follow the IMO's Guidelines for risk assessment and are adaptable to assess specific invasion risks for various biogeographic regions and shipping routes associated with ballast water transfers.

ACKNOWLEGDEMENT

Claudio DiBacco and Devin Lyons provided information on invasive species distributions and species dispersal modelling on the East Coast of Canada, and Oscar Casas-Monroy provided advice on the use of R statistical software.

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TABLES

Table 1. List of species assessed as target species for the Boston-Saint John case study using the Joint Harmonized Procedure. Species must meet all three criteria to be selected as target species; the impacts of a species were assessed only if the other two criteria were met.

		Tar	_		
Species	Taxonomic Group	Present at Boston but not at Saint John	Transported in Ballast Water	Measurable Negative Impacts	Target Species
Botrylloides violaceus	Tunicate	Yes	No	Not assessed	No
Botryllus schlosseri	Tunicate	Yes	No	Not assessed	No
Caprella mutica	Skeleton shrimp	Yes	No	Not assessed	No
Chelura terebrans	Marine wood-boring amphipod	Yes	No	Not assessed	No
Ciona intestinalis	Tunicate	Yes	No	Not assessed	No
Cordylophora caspia	Hydroid	Yes	No	Not assessed	No
Diadumene lineata	Sea anemone	Yes	No	Not assessed	No
Didemnum vexillum	Tunicate	Yes	No	Not assessed	No
Diplosoma listerianum	Tunicate	Yes	No	Not assessed	No
Microdeutopus gryllotalpa	Amphipod	Yes	No	Not assessed	No
Myosotella myosotis	Snail	Yes	No	Not assessed	No
Ostrea edulis	Oyster	Yes	No	Not assessed	No
Praunus flexuosus	Opossum shrimp	Yes	No	Not assessed	No
Styela canopus	Tunicate	Yes	No	Not assessed	No
Styela clava	Tunicate	Yes	No	Not assessed	No
Teredo navalis	Saltwater clam	Yes	No	Not assessed	No
Tricellaria inopinata	Bryozoan	Yes	No	Not assessed	No
Bugulina simplex	Bryozoan	Yes	Unknown	No	No
laniropsis serricaudis	Isopod	Yes	Yes	No	No
Melanothamnus harveyi	Red alga	Yes	Yes	No	No
Palaemon macrodactylus	Shrimp	Yes	Yes	No	No
Agarophyton vermiculophyllum	Red alga	Yes	Yes	Yes	Yes
Ascidiella aspersa	Tunicate	Yes	Yes	Yes	Yes
Carcinus maenas	Crab	Yes	Yes	Yes	Yes
Grateloupia turuturu	Red alga	Yes	Yes	Yes	Yes
Hemigrapsus sanguineus	Crab	Yes	Yes	Yes	Yes
Membranipora membranacea	Bryozoan	Yes	Yes	Yes	Yes
Mytilopsis leucophaeata	False mussel	Yes	Yes	Yes	Yes

Table 2. Average port connectivity across the three years (2009, 2011, and 2013) and trait combinations examined using the Same Risk Area method. The assessment of port connectivity was based on the release event with the largest number of individuals reaching a recipient port at a given dispersal time during the seven-day competence period. The port connectivity values are relative to the total number of individuals in a single release event (1,000 individuals).

Recipient Port	Rimouski	Sept-Îles	Port- Menier	Havre- Saint- Pierre	Natashquan	Kegaska	La Romaine	Harrington Harbour	Tête-à-la- Baleine	La Tabatière	Saint- Augustin	Blanc- Sablon
Rimouski	NA	0.39	0.01	0.01	0.07	0.56	0.03	0.08	0.07	0.01	1.18	0.43
Sept-Îles	6.28	NA	0.00	0.03	0.06	29.39	0.01	0.04	0.07	0.01	9.00	46.33
Port-Menier	2.29	4.10	NA	5.47	4.93	3.47	7.46	0.04	0.04	0.00	2.46	3.36
Havre-Saint- Pierre	5.24	7.01	0.00	NA	44.29	4.17	3.25	0.01	0.01	0.00	3.78	5.03
Natashquan	5.33	9.13	0.00	19.53	NA	4.81	0.31	0.03	0.00	0.00	3.75	5.47
Kegaska	6.36	0.33	0.01	0.06	0.11	NA	0.06	0.04	0.00	0.01	24.58	1.58
La Romaine	2.92	3.72	0.03	25.94	12.29	3.46	NA	0.03	0.01	0.00	2.47	3.22
Harrington Harbour	0.83	1.22	1.43	1.53	1.47	1.06	1.64	NA	1.54	1.31	0.74	0.94
Tête-à-la- Baleine	0.06	0.04	0.33	0.14	0.10	0.06	0.14	0.07	NA	0.58	0.03	0.04
La Tabatière	1.58	2.40	9.28	4.43	4.28	2.17	6.11	1.43	0.26	NA	1.54	2.31
Saint- Augustin	4.76	0.13	0.00	0.01	0.01	0.21	0.00	0.00	0.03	0.00	NA	0.21
Blanc- Sablon	2.78	1.04	0.00	0.06	0.03	9.29	0.00	0.00	0.00	0.01	2.63	NA

Table 3. Results of the ANOVA tests examining the effects of year (Y), planktonic duration (P), reproductive period (R), swimming behaviour (B), and release site (S) on port connectivity. Effect size values were calculated as Cohen's f, where values larger than 0.10, 0.25, and 0.40 indicate small, medium, and large effects, respectively.

Factors and Interactions	df	F	р		Cohen's f
Y	2	0.65	0.520	-	0.01
Р	3	79.43	< 0.001	***	0.17
R	1	5.55	0.018	*	0.03
В	2	1.01	0.365	-	0.02
S	11	21.81	< 0.001	***	0.17
Y * P	6	1.07	0.381	-	0.03
Y * R	2	3.11	0.045	*	0.03
P * R	3	1.26	0.286	-	0.02
Y * B	4	0.13	0.972	-	0.01
P * B	6	1.92	0.073	-	0.04
R * B	2	0.66	0.514	-	0.01
Y * S	22	0.28	1.000	-	0.03
P * S	33	11.23	< 0.001	***	0.21
R * S	11	0.74	0.698	-	0.03
B * S	22	0.23	1.000	-	0.02
Y * P * R	6	2.14	0.045	*	0.04
Y * P * B	12	0.13	1.000	-	0.01
Y * R * B	4	0.20	0.941	-	0.01
P * R * B	6	0.34	0.913	-	0.02
Y * P * S	66	0.32	1.000	-	0.05
Y * R * S	22	0.30	0.999	-	0.03
P * R * S	33	0.56	0.980	-	0.05
Y * B * S	44	0.06	1.000	-	0.02
P * B * S	66	0.22	1.000	-	0.04
R * B * S	22	0.08	1.000	-	0.01
Y * P * R * B	12	0.14	1.000	-	0.01
Y * P * R * S	66	0.29	1.000	-	0.05
Y * P * B * S	132	0.05	1.000	-	0.03
Y * R * B * S	44	0.07	1.000	-	0.02
P * R * B * S	66	0.07	1.000	-	0.02
Y * P * R * B * S	132	0.06	1.000	-	0.03
Significant Values	p < 0.05 * p < 0.01 ** p < 0.001 ***				

FIGURES



Figure 1. The Joint Harmonized Procedure decision tree used to determine the risk of ballast water transfers.



Figure 2. Outcome from the Joint Harmonized Procedure decision tree for the Boston-Saint John shipping route.



Figure 3. The 12 ports within the province of Québec examined in the Canadian Same Risk Area case study.



Figure 4. Water circulation within the Gulf of St. Lawrence during the spring (April – June) in 2011.



Figure 5. Water circulation within the Gulf of St. Lawrence during the summer (July – September) in 2011.



Figure 6. Water circulation within the Gulf of St. Lawrence during the fall (October – December) in 2011.

APPENDICES

Appendix 1. Glossary of terms and definitions.

Term	Definition
Guidelines for Risk Assessment under Regulation A-4 of the BWM Convention (G7)	The IMO's G7 Guidelines for risk assessment outline the procedure for granting ballast water management exemptions under Regulation A-4 of the Convention (e.g. types of risk assessment that can be used to assess the risk of granting exemptions).
International Convention for the Control and Management of Ships' Ballast Water and Sediments, 2004 (the Convention)	International maritime treaty that establishes standards and procedures for the management of ships' ballast water and sediment.
International Maritime Organization (IMO)	Specialized agency of the United Nations that regulates shipping.
Joint Harmonized Procedure	The Joint Harmonized Procedure uses port survey data and a decision tree to evaluate risk based on differences in salinity between ports and the presence of target species at the source port that are not at the recipient port.
Recipient port	Port where ballast water is unloaded.
	Regulation A-4 of the Convention allows nations to grant ships exemptions from the ballast water performance standard in waters under their jurisdiction when the following criteria are met:
	 Ships on a voyage or voyages between specified ports/locations or ships that operate exclusively between specified ports/locations;
Regulation A-4	 Ships do not mix ballast water or sediments other than between such specified ports;
	3. Exemptions are reviewed at least every five years; and,
	4. Exemptions are granted based on the IMO's <i>Guidelines for Risk</i> Assessment under Regulation A-4 of the BWM Convention (G7).
Regulation D-2	Regulation D-2 of the Convention is a ballast water performance standard that sets limits on the concentration of viable organisms in discharged ballast water. Most ships are expected to comply with Regulation D-2 by utilizing onboard ballast water management systems to treat their ballast water.
Same Risk Area	The Same Risk Area approach evaluates whether target species are likely to disperse unassisted via water circulation to recipient ports, regardless of their transport in ballast water.
Source port	Port where ballast is loaded.
Target species	Species of concern that could be transported in ballast water or sediment and could potentially impair or damage the environment, human health, property or resources. Target species are defined for a port, location, region, or State.

Appendix 2. HELCOM and OSPAR's target species list for the Baltic Sea and Northeast Atlantic Ocean.

Species Name Acartia tonsa Alexandrium acatenella Alexandrium monilatum Alexandrium ostenfeldii Amphibalanus eburneus Anadara transversa Arcuatula senhousia Asterias amurensis Brachidontes pharaonis Callinectes sapidus Caprella mutica Caulerpa cylindracea Caulerpa taxifolia Cercopagis pengoi Chama pacifica Chionoecetes opilio Corbicula fluminea Coscinodiscus wailesii Crassostrea gigas Crepidula fornicata Didemnum vexillum Dikerogammarus villosus Dinophysis sacculus Dreissena bugensis Dreissena polymorpha Dreissena rostriformis bugensis Elminius modestus Ensis americanus Ensis directus Eriocheir sinensis Fibrocapsa japonica Ficopomatus enigmaticus Gammarus tigrinus

Species Name Gracilaria vermiculophylla Grateloupia turuturu Grateulopia doryphora Halophila stipulacea Hemigrapsus sanguineus Hemigrapsus takanoi Hemimysis anomala Hydroides dianthus Hydroides elegans Karenia mikimotoi Lophocladia lallemandii Marenzelleria neglecta Marenzelleria viridis Microcosmus squamiger Mnemiopsis leidyi Mytilopsis leucophaeata Mytilus galloprovincialis Neogobius melanostomus Palaemon elegans Palaemon macrodactylus Paralithodes camtschatica Pfiesteria piscicida Phaeocystis pouchetii Potamocorbula amurensis Pseudochattonella verruculosa Rangia cuneata Rapana venosa Rhithropanopeus harrisii Styela clava Stypopodium schimperi Undaria pinnatifida

Appendix 3. Minimum and maximum port connectivity across the three years (2009, 2011, and 2013) and trait combinations examined. The assessment of port connectivity was based on the release event with the largest number of individuals reaching a recipient port at a given dispersal time during the seven-day competence period. The port connectivity values are relative to the total number of individuals in a single release event (1,000 individuals).

Recipient Port	Rimouski	Sept-Îles	Port- Menier	Havre- Saint- Pierre	Natashquan	Kegaska	La Romaine	Harrington Harbour	Tête-à-la- Baleine	La Tabatière	Saint- Augustin	Blanc- Sablon
Rimouski	0 - 0	0-6	0 – 1	0 – 1	0-2	0 – 10	0 – 1	0-4	0 – 3	0 – 1	0 – 12	0-6
Sept-Îles	0 - 40	0 – 0	0 – 0	0 – 1	0 – 1	0 – 205	0 – 1	0 – 1	0 – 1	0 – 1	0 – 88	0 – 347
Port-Menier	0 – 11	0 – 27	0 - 0	0 – 22	0 – 26	0 – 22	0 – 34	0 – 1	0 – 1	0 - 0	0 – 11	0 – 18
Havre-Saint- Pierre	0 – 28	0 - 48	0-0	0 - 0	0 – 267	0 – 26	0 – 30	0 – 1	0 – 1	0-0	0-23	0 – 31
Natashquan	0-41	0 – 71	0 - 0	0 – 145	0 - 0	0 – 37	0 – 3	0 – 1	0 - 0	0 - 0	0-23	0 - 34
Kegaska	0 - 40	0-4	0 – 1	0-2	0-2	0 - 0	0 – 1	0 – 1	0 - 0	0 – 1	0 – 131	0 – 15
La Romaine	0 – 15	0 – 22	0-2	0 – 190	0 - 89	0 – 19	0 - 0	0 – 1	0 – 1	0 - 0	0 – 14	0 – 22
Harrington Harbour	0 – 7	0 – 7	0-9	0 – 11	0 – 16	0 – 5	0-9	0 - 0	0 – 13	0 – 8	0-4	0 – 7
Tête-à-la- Baleine	0 – 2	0 – 1	0 – 7	0 – 4	0 – 2	0 – 2	0 – 4	0-2	0 - 0	0-6	0 – 1	0 – 1
La Tabatière	0 – 10	0 – 20	0 – 58	0 – 23	0-23	0 – 16	0 – 36	0 – 13	0 - 8	0 - 0	0 – 14	0 – 22
Saint- Augustin	0 - 36	0-2	0-0	0 – 1	0 – 1	0-4	0-0	0 - 0	0 – 1	0-0	0 - 0	0 – 5
Blanc- Sablon	0 – 26	0 - 34	0 - 0	0-2	0 – 1	0 – 71	0 - 0	0 - 0	0 - 0	0 – 1	0 – 24	0 - 0

Appendix 4. Port connectivity for a one-week planktonic duration with diel swimming behaviour and spring spawning period across the three years (2009, 2011, and 2013) examined. The assessment of port connectivity was based on the release event with the largest number of individuals reaching a recipient port at a given dispersal time during the seven-day competence period. The port connectivity values are relative to the total number of individuals in a single release event (1,000 individuals).

Recipient Port	Rimouski	Sept-Îles	Port- Menier	Havre- Saint- Pierre	Natashquan	Kegaska	La Romaine	Harrington Harbour	Tête-à-la- Baleine	La Tabatière	Saint- Augustin	Blanc- Sablon
Rimouski	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 – 0
Sept-Îles	0 – 0	0 – 0	0 – 0	0 – 0	0 - 0	144 – 205	0 - 0	0 - 0	0 – 0	0 - 0	17 – 80	115 – 210
Port-Menier	0 - 0	0 – 1	0 – 0	0 – 12	0 – 7	0 - 0	0 – 30	0 - 0	0 - 0	0 - 0	0 - 0	0 – 0
Havre-Saint- Pierre	0 - 0	1 – 21	0 – 0	0 – 0	126 – 224	0-2	0 – 23	0 - 0	0 - 0	0 - 0	0 - 0	0 – 14
Natashquan	0 - 0	6 – 29	0 - 0	12 – 145	0 - 0	0-3	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 – 14
Kegaska	4 – 20	0-2	0 – 0	0 – 0	0 - 0	0 - 0	0 - 0	0 - 0	0 – 0	0 - 0	86 – 131	3 – 13
La Romaine	0 - 0	0 – 1	0 – 0	78 – 100	64 – 87	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 – 0
Harrington Harbour	0 – 0	0 – 0	0 – 0	0 - 0	0 - 0	0 – 0	0 - 0	0 - 0	0 – 0	0 - 0	0 - 0	0 - 0
Tête-à-la- Baleine	0 – 0	0 – 0	0 - 0	0 - 0	0 - 0	0 – 0	0 - 0	0 - 0	0 – 0	0 - 0	0 – 0	0 - 0
La Tabatière	0 - 0	0 - 0	0 – 5	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0	0 - 0
Saint- Augustin	4 – 5	0 - 0	0 - 0	0 - 0	0 - 0	0-0	0-0	0 - 0	0 - 0	0 - 0	0 - 0	0-0
Blanc- Sablon	0 – 0	0 – 21	0-0	0-0	0 - 0	10 – 52	0 - 0	0 - 0	0 – 0	0 - 0	2-8	0 - 0