Bio-physical models for the management of micropathogens in Scottish aquaculture: a preliminary view to farming further offshore

Meadhbh Moriarty*, David Tulett, Berit Rabe, Alexander G. Murray

Marine Scotland Science, Marine Laboratory, 375 Victoria Road, Aberdeen AB11 9DB, Scotland, UK

ABSTRACT: Transmission of pathogens increases with population density associated with larger populations within farms and higher number of farms within an area. These pathogens can also spill over (or back) into wild populations. Owing to transmission between and from farms, many diseases are best managed at an area level. Current area management practice in Scotland was developed 20 yr ago, but as aquaculture evolves, farm size and environmental exposure will change. To assess if potential aquaculture management changes require spatial disease management changes, 3 scenarios for particle spread to help inform on pathogen transmission are evaluated: (1) current farm distribution, (2) medium-term development (farms in exposed coastal areas), and (3) long-term development (offshore farms). Climatological output from a hydrodynamic model is used to drive movements of passive particles representing infectious pathogens released from these farms. The potential distribution of particles allows assessment on possible transmission of infection, around farm locations, subject to various modelling assumptions and limitations. Dispersal distances increased with time in all scenarios. For medium-term development, the average dispersal distance (3.0 ± 1.3 km) was marginally larger than dispersal from existing sites (2.7 ± 1.6 km) after 12 h, whereas for the longer-term development, this was 4.8 ± 2.9 km. These results indicate that short- to medium-term aquaculture expansion is consistent with existing disease management areas, at least from these models. However, offshore aquaculture may result in transmission distances for pathogens that exceed existing limits, and therefore will likely require re-assessment of management areas, subject to consideration of all relevant epidemiological factors.

KEY WORDS: Marine pathogens · Disease mitigation · Bio-physical modelling · Spatial management · Disease management area · Atlantic salmon · Coupled hydrodynamic–particle-tracking models

1. INTRODUCTION

Aquaculture is an increasingly important source of protein production, with a rise of 527 % in global aquaculture production from 1990 to 2018 (FAO 2020). With over half (~52 %) of the fish available for human consumption currently originating from aquaculture production, and an expected increase in demand on aquaculture to provide almost 60 % of the fish available for human consumption by 2030 (FAO 2020), the global aquaculture industry will play a growing role in food security (Pradeepkiran 2019). The annual global salmon production has expanded to 2.25 million t and the Scottish aquaculture industry currently contributes about 7 % to this global production, equating to 203 881 t of Atlantic salmon *Salmo salar* in 2019, with a farm gate value of £1.07 billion (Munro 2020). Salmon production occurs in areas with few year-round employment options, thus it is a vital industry for the Scottish economy.

There are industry aspirations to expand Scottish aquaculture, doubling production value by 2030 (Burnett 2017), although this is considered optimistic (HIE 2017). At the same time as working toward increasing production value, the Scottish salmon industry is striving towards more sustainable and environmentally responsible production, through the code of good practice for Scottish finfish aquaculture (CoGP 2015), combined with regulation. Sustainable salmon production is hampered by a number of issues, which need to be addressed with management decisions incorporating the best scientific inference. Important issues which the salmon aquaculture industry must contend with, include, but are not limited to, risks to wild fish such as the potential for introgression from escaped fish, and transmission of diseases and parasites within and between farms (Murray et al. 2010, Taranger et al. 2015).

A range of pathogens can cause significant mortalities of farmed salmon (Murray et al. 2016), accounting for about a third of all losses (Soares et al. 2011). Since pathogens are transported by the movement of water, more robust pathogens can be transported over larger distances; many pathogens are best managed for groups of farms at the area level (Murray & Gubbins 2016). With this in mind, disease management areas (DMAs) were first established in Scotland in 2000. They are based on fixed separation distances around active farms; originally envisaged to be based on tidal excursions, they are in fact based on smaller distances. Specifically, the radius for the separation distance around an active farm used to define a DMA on mainland Scotland is 7.258 km, while on the Shetland Islands, a radius of 3.629 km is used (Scottish Executive 2000). These fixed separation distances are consistent with distances of epidemiological risk for infectious salmon anaemia (ISA), that can include both water source transmission effects, such as the speed and dilution in seawater currents (Vike et al. 2014), as well as other epidemiological factors (Scottish Executive 2000). They are updated regularly to include all active farms.

The industry aspirations to expand will inevitably lead to new aquaculture sites being required and increased biomass allowance being requested for sites. As the aquaculture industry expands, the number of potential pathogen hosts on farms will increase. Increases in biomass and temperatures on farms explain up to 85% of the variance in mortality (Moriarty et al. 2020). Higher biomasses are particularly common towards the end of the production cycle, which has been shown to be a factor in the transmission of pathogens (Salama & Murray 2011). Thus, working to decrease the environmental stresses and pathogen load on fish is increasingly important in order to support sustainable growth of the industry.

Particle-tracking simulation studies provide a cost-effective method for developing a theoretical understanding of the movement of parasites (to identify potential risk of infection or dispersion in the marine environment; Kough et al. 2015) and animals (to identify potential migratory patterns; Hinckley et al. 1996, Li et al. 2014, Chang et al. 2016). Hydrodynamic model outputs are used to run simulations of virtual particles that can represent inert particles such as plastics or parasites, or active particles such as fish or other animals. The use of coupled hydrodynamic–particle-tracking simulations, also known as bio-physical models, for parasites such as salmon lice has increased in recent years (e.g. Asplin et al. 2004, 2011, Murray & Gillibrand 2006, Gillibrand & Willis 2007, Amundrud & Murray 2009, Adams et al. 2012, Salama et al. 2013, 2018, Johnsen et al. 2014, Rabe et al. 2020). These models are widely used to calculate dispersion distance and the area of influence of salmon lice from single farms to map high-concentration areas in larger fjord or loch systems and to identify the exposure connectivity between fish farms (e.g. Adams et al. 2015, 2016, Samsing et al. 2015, 2017, Salama et al. 2016, Kragesteen et al. 2018). In Scotland, to date, bio-physical models have not been used in the management of pathogens other than sea lice.

Sea lice *Lepeophtheirus salmonis* (Krøyer, 1837) are the most significant single pathogen of salmon, both in terms of economic damage to farmed salmon (equivalent to 9% of revenues, Abolofia et al. 2017) and impact on wild salmonids (Taranger et al. 2015). However, the longer survival in the water and more complex behaviour of sea lice relative to other microbial pathogens (Adams et al. 2016, Salama et al. 2018), such as harmful viral or bacterial microorganisms, referred to collectively herein as micropathogens, means that different management strategies are required for sea lice relative to those for micropathogens. Therefore, while the bio-physical models used for sea lice are relevant and help inform the model used here, sea lice as a pathogen is not considered further in this paper.

Micropathogens like infectious salmon anaemia virus (ISAV) which causes the serious notifiable disease ISA are currently contained and eradicated using DMAs. Major disruptive epidemics of ISA have occurred in Scotland in 1998–99 and 2008–09 (Murray et al. 2010). The recommendations include advice

on acceptable stocking strategies so that all sites in a DMA are fallowed in a systematic manner to reduce risk (Scottish Executive 2000). However, systematic culling has never been required, except for confirmed sites. DMAs were specifically developed for the eradication of ISA (Murray et al. 2006), but the same approach would also be used for control of infectious haematopoietic necrosis virus (IHNV), which leads to infectious haematopoietic necrosis (IHN), although this exotic disease has not occurred in Scotland to date. In farmed trout, viral haemorrhagic septicaemia (VHS), caused by viral haemorrhagic septicaemia virus (VHSV), is managed in a similar way, and for marine farmed trout, a DMA approach would be used: although VHS has occurred only in non-salmonids and freshwater trout farms to date in the UK (Stone et al. 2008), it has occurred in wrasse held as lice cleaner fish on salmon farms (Munro et al. 2015). Populations affected by these notifiable diseases are subject to culling (in the case of VHS in cleaner fish, these were culled but the salmon were allowed to remain, as these were VHSV-negative), and other farms within the DMA are placed under movement restrictions until the last farm has been depopulated either through culling or normal harvest if the site is not itself infected. These viruses all decay relatively rapidly in the environment (Oidtmann et al. 2018), and so after 24 h are likely to be reduced to low prevalence; this limits the time over which transmission can occur.

The existing methodology for implementing discrete DMAs (Scottish Executive 2000) adequately describes the pathogen transmission from nearshore farms. In conjunction with statutory movement restrictions and compulsory eradication, this methodology has successfully contained and eradicated outbreaks of ISA in the past (Murray et al. 2010). Here, the efficacy of bio-physical modelling in supporting and informing potential changes required to the current DMA framework for an expanding industry is assessed. We first examine the inference from bio-physical modelling of passive particles which represent the likely trajectories of pathogens from existing farms. We assess if this differs in inference from the current spatial management tools for disease mitigation in Scotland which have proven effective to date. We then assess whether there is a difference in the inference from bio-physical modelling of passive particles and the current methodology for hypothesised developments in more exposed areas than are traditionally used by the industry. The assessments allow us to provide recommendations for future development of evaluating particle spread through bio-physical modelling in relation to DMAs, should the industry seek to change its current practices and farm in more exposed nearshore locations or further offshore.

2. METHODS

2.1. Study area

Our study area covers all Scottish marine waters and beyond, as indicated by the hydrodynamic model mesh in the inset in Fig. 1. Salmon farm locations (n = 215) are situated on the west coast and the islands, and, for ease of analysis, have been divided into 5 regions: Shetland, Orkney, Western Isles (Eilean Siar), Northwest and Southwest (Fig. 1). The duration of the study was from 1 January to 31 December inclusive. Passive particles from active salmon farms were released for the full simulation period.
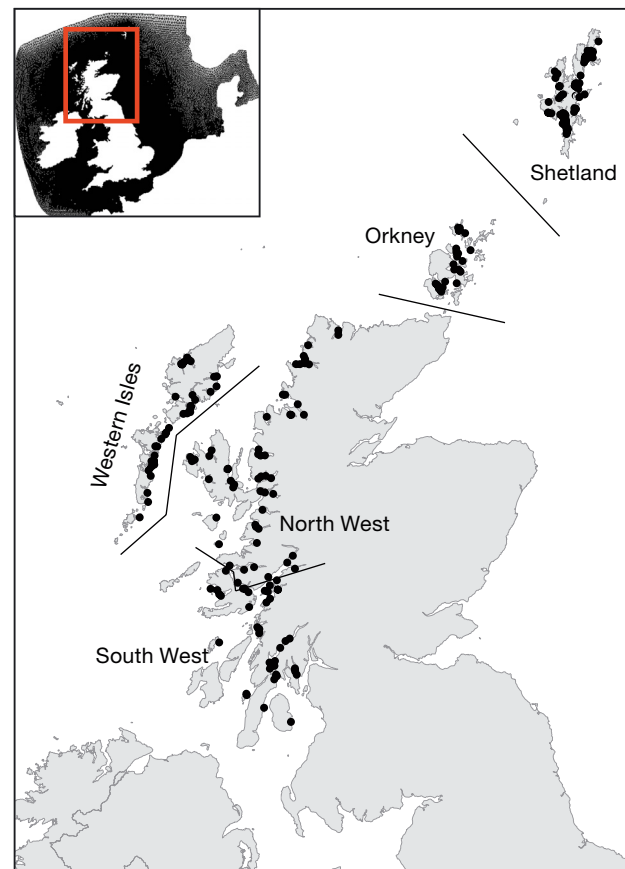

Fig. 1. Locations of 215 active marine salmon farms in Scotland in 2018, divided between 5 regions for Shetland, Orkney, Western Isles (Eilean Siar), Northwest and Southwest. Inset: extent of the Scottish Shelf Model and its mesh

2.2. Bio-physical model

The output from a hydrodynamic model (described in Section 2.2.1) was used to drive a particle-tracking application (described in Section 2.2.2). The particle-tracking application simulates the likely trajectories and densities of pathogens during their viable phase from all active salmon farms in Scottish waters. This allows for an assessment of potential connectivity rates between salmon farms.

2.2.1. Hydrodynamic model

The Scottish Shelf Model (SSM) is a validated unstructured-grid, 3-dimensional, Finite-Volume Community Ocean Model (FVCOM) implementation (Chen et al. 2003) and was developed by Marine Scotland Science and used in this study. The SSM consists of a wider-domain coarser-resolution model covering the whole of the British Isles, including the Scottish continental shelf (inset in our Fig. 1) (Wolf et al. 2016a) as well as a number of high-resolution sub-models in some areas within that domain (Price et al. 2016a,b,c,d, Wolf et al. 2016b, O'Hara Murray & Gallego 2017). The horizontal resolution varies between 15 m in the sub-models to about 10 km at the open boundary, and the vertical resolution includes 10 or 20 vertical layers in the sub-models or wider domain (Wolf et al. 2016a,b). The SSM model runs (version 2.01) for a single climatological year, representing averaged present-day climatic conditions for 1990–2014, with a 1993 tidal component, have been used (De Dominicis et al. 2018). As this is an average climatological year, it means that specific extreme storm events were not included and inter-annual variability cannot be estimated. An integrated hydrodynamic output file, which uses the combination of the finer resolution of sub-models and coarser resolution of the wider model, forced the particle-tracking model (details about the model integration can be found in Wolf et al. 2016b and Rabe et al. 2020).

2.2.2. Particle-tracking model

To predict the pathogen densities and trajectories, output from the SSM was used to drive a particle-tracking application that simulated a range of passive movements of particles from active salmon farms. The particle-tracking application is adapted from the Lagrangian particle-tracking model, FVCOM I-State Configuration Model or FISCM (Liu et al. 2015), which was developed for the FVCOM framework. This code tracks released virtual 'super individuals' (Scheffer et al. 1995). Super individuals are used to represent many particles of a virus like ISAV, which are forced by the SSM integrated model outputs of current speed and direction. Using a smaller number of super individuals with parameters that allow random movements (e.g. horizontal diffusivity) allows for a less computationally expensive model, that still captures the variance in the general movement of individuals rather than trying to model every single individual in a population separately. Particles were released from each location of interest at a rate of 5 h^{-1} for the full climatological year.

The particles were tracked on a 10 min interval, using hourly hydrodynamic model outputs, and the particle locations saved to a file every 3 h. Hourly hydrodynamic model outputs were interpolated using the 4th-order Runge-Kutta method to match the 10 min particle-tracking time step. We have assumed that pathogens remain near the surface at all times, by confining horizontal velocities between the surface and 1 m depth. Here, the pathogen particles are passive (no directed swimming) and were subject to advection by currents and diffusion, with a horizontal diffusivity of 10 m^2 s^{-1} as described and implemented in other similar studies (i.e. Okubo 1971, Wolf et al. 2016b, Rabe et al. 2020). The SSM integrated model has at least a 1 km resolution around the Scottish coast, while the typical resolution within highly resolved sea lochs is around 50–100 m. Thus, a horizontal diffusivity of 10 m^2 s^{-1} still allows for the more highly resolved areas to be compared to the areas where the model has lower resolution but further sensitivity analyses with regard to the diffusivity term is required. Horizontal diffusivity is simulated simply by moving the particle in the horizontal, but not in the vertical. Thus, pathogen particles move with the currents generated from the hydrodynamic model plus diffusion. When particles reach solid boundaries representing coastline, they do not cross the boundary. The FISCM settling option was implemented here, where after the pelagic duration of 12, 24 or 48 h, the particles cease to be viable and are no longer tracked. These viability timescales were chosen to reflect likely maximum active time for the viruses commonly seen in Scotland, given the average water temperatures (Oidtmann et al. 2018). Here we are interested in understanding relative infection pressure to evaluate potential risk of infection between farms, thus no farm-based abundance, reproduction or mortality rate was applied.

2.3. Particle origin

To achieve our aim, which is to assess the value of using bio-physical modelling to describe the maximum particle spread to inform the DMA framework for an expanding industry, it is necessary to carry out 3 scenarios. First we examine the current farms, comparing the inference from the bio-physical model to the DMAs. We then hypothesise on potential developments in more exposed areas than traditionally used by the industry, and compare the inference from the bio-physical model to the DMAs in 2 further scenarios. These further scenarios assume that in the short to medium term, businesses will continue to utilise existing infrastructure, while in the longer term, we may see a move to farm in more exposed areas. New technologies are likely to emerge, which may change the types of cages and thus the transmission dynamics, so these scenarios are limited to 5 locations only within this preliminarily study.

2.3.1. Baseline scenario: current active sites

The current DMAs are designed with nearshore–open-pen aquaculture in mind. The methodological process used to define these DMAs has shown that they are robust and fit for purpose over the last 20 yr. We explore if the inference from the bio-physical model based on local hydrodynamics suggests that a different connectivity may occur, that is not accounted for in the current DMA framework. To do this, we release particles from all 215 active salmon seawater farms in 2018 (n = 9 391 200, Fig. 1) and compare the inference from the model output to the DMA output for the same farms.

2.3.2. Near-future scenario: nearshore exposed sites

Aspirations towards expansion means, in the short to medium term, businesses may look towards expanding the scale of current sites by increasing biomass, or they may look at farming in more exposed waters. Here we assume that preferred sites will be relatively close to existing sites to utilise current infrastructure. A key criterion is that any new development will not cause existing DMAs to join. To theorise on potential development, we have identified DMAs that have a single active farm. For this exploration, we assume all seawater areas are suitable for industry expansion and will not cause adverse environmental effects and/or that no other planning constraints exist. We define suitable nearshore exposed locations using 6 criteria: within a current DMA with only 1 other site; suitably placed so that it does not join the DMA to another DMA; minimum distance from shore of 1.5 km; maximum distance from shore of 3 km; minimum current speed of 0.05 m s^{-1}; and maximum current speed of 0.5 m s^{-1}.

Choosing DMAs with only 1 other site assumes that businesses may look to increase biomass on current sites prior to developing new infrastructure. DMA separation is an important criterion for maintaining biosecurity on sites. Minimum and maximum distance from shore is an arbitrary definition to distinguish nearshore and offshore within this simulation study. Minimum current speed is based on existing conditions around farms, which must allow enough flushing, while maximum current speeds must reflect conditions that are suitable for fish swimming against currents. Using ArcGIS version 10.6, 5 potential nearshore exposed site locations within existing DMAs with only 1 active site were identified. Particles were continuously released from these 5 hypothesised nearshore exposed site locations at a rate of 5 h^{-1} for the full climatological year (n = 218 400). We compare the inference from the model output to the DMA output for the same hypothesised nearshore exposed site locations.

2.3.3. Long-term future scenario: offshore sites

Ongoing technological innovations in response for the need to produce more food with fewer resources has led to pilot studies for offshore farms (e.g. Off-Aqua; Scottish Association for Marine Science 2018, Morro et al. 2021). As the development and implementation of new technologies and the build-up of expertise continues, we expect to see fish farm applications for farms further offshore in the longer term. In previous studies assessing the locations of offshore farms, minimum distance from shore ranged from 0.7 to 46.3 km (mean ± SD: 9.6 ± 15.4 km), minimum water depth from 15 to 45 m (28.9 ± 9.2 m), and minimum current speeds from 0.05 to 0.31 m s^{-1} (Froehlich et al. 2017). For the purpose of this analysis, we assume that all new farms will have an open-pen design and will need to be placed in suitable locations for fish welfare. Thus we define suitable offshore locations using the 5 following criteria: suitably placed so that it does not join a DMA to another DMA; minimum distance from shore of 3 km; maximum distance from shore of

12 km; minimum current speed of 0.05 m s^{-1}; and maximum current speed of 0.5 m s^{-1}. Using ArcGIS version 10.6, we randomly selected 5 potential offshore sites out of the areas that met the above criteria for this study. Particles were continuously released from these 5 hypothesised offshore site locations at a rate of 5 h^{-1} for the full climatological year (n = 218 400).

2.4. Comparison of inference from maps

There are 2 approaches that may be used to assess inference from the pattern produced after 12, 24 and 48 h of particle tracking, in order the compare model output to the hypothesised DMA map for these same farms. Mean monthly density hulls of the maximum distance particles travelled from origin may be used. This method subsets the data to allow the maximum spread only be assessed, which may be less computationally expensive, and thus may be of interest to managers; however, by subsetting the data, inference may be lost. Here we are interested in the total spread through various DMA locations, thus we use all particle locations after 12, 24 and 48 h of particle tracking, in order to compare model output to the hypothesised DMA map for these farms. This analysis was carried out in R version 3.6.3 (R Core Team 2018) using the equivalent spatial join tool to ArcGIS, called 'over' from the package 'sp' (Pebesma & Bivand 2005, Bivand et al. 2013) in R.

Each particle location at the 3 different times was further explored to evaluate the potential risk of infection. We assessed the proportion of particles which crossed into another DMA 12, 24 and 48 h respectively to quantify risk of infections crossing from one DMA to another, using the 'over' function from the package 'sp' in R.

DMAs are currently based on a given radius which infers a set distance is travelled by viable particles; it is necessary to assess the difference in inference between modelled output and the currently accepted DMA distance. Thus we measured the displacement from origin for each particle after 12, 24 and 48 h for each month. To investigate if the displacement from origin is significantly different in different regions or different months, we investigated the interaction between the region and month using linear regression models fitted using the lm function in R (R Core Team 2018). We then compared the distances travelled by particles in the model to the radius within the current DMA framework using a simple ANOVA test in R (R Core Team 2018).

3. RESULTS

Results are described for the 3 time frames (12, 24 and 48 h) for each of the 3 scenarios (baseline, near-future and long-term).

3.1. Baseline scenario: current active sites

The current DMAs have thus far proved effective at containing and eradicating outbreaks of disease (Murray et al. 2010); it is important to understand how the inference from the bio-physical model approach differs from the current DMA approach to then inform future scenario testing. Fig. 2 highlights the numbers of DMAs in which particles are found after 12, 24 and 48 h, using all particle locations and the 'over' function in R. If particles are found in 2 or more DMAs, there is potential for transmission across boundaries; however, this is a maximal interpretation of potential that does not take account of decay or
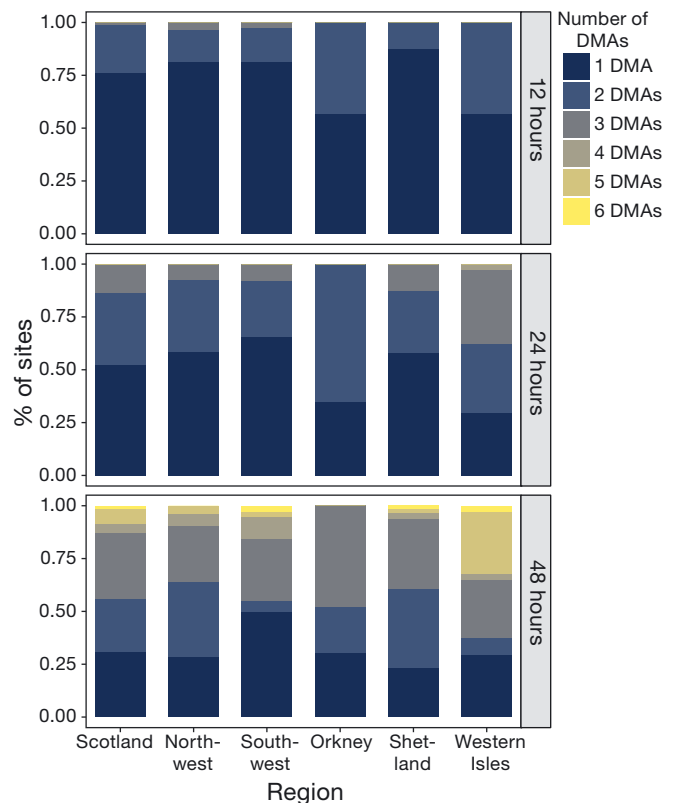

Fig. 2. Percentage of sites that potentially interact with 1 or more disease management areas (DMAs) using inference from the bio-physical model, in all of Scotland (n = 215) and the 5 regions of Northwest (n = 53), Southwest (n = 38), Orkney (n = 23), Shetland (n = 64), and Western Isles (n = 37), and for 3 viability timescales of interest (12, 24, 48 h) using all particle locations and the 'over' function in R

dilution of particles whereby pathogen concentration may drop below minimum infectious dose. This figure does not show the proportion of sites that spread particles into the wider model domain in areas of sea not covered by any DMA. On average over the year, the bio-physical model inferred that in the first 12 h of a particle's lifespan, 76.3% of sites (n = 164/215) do not spread particles into other DMAs and either retain all particles in their DMA or spread to areas outside any DMA designation (Fig. 2). Only 22.3% of sites (n = 48/215) spread particles into a second DMA, while <2% (n = 3/215) of sites spread particles into a third DMA within the first 12 h of the particle's lifespan, irrespective of the state of the tide, as particles are released continuously (Fig. 2).

After 24 h, further spread into neighbouring DMAs occurred from a higher proportion of sites. The number of sites in which particles are retained within a single DMA, or spread into open water, is reduced after 1 d to around 52.1% (n = 112/215). In 24 h, 34.4% of sites (n = 74/215) show particles which have the potential to spread to a second DMA, a further 13% of sites (n = 28/215) highlight particles

which may spread through 3 DMAs, and 0.5% (n = 1/215) highlight particles that may move through 4 DMAs (Fig. 2).

After 48 h, the number of sites which retained all particles or spread only to open water was reduced to 31.2% (n = 67/125). Within 48 h, 24.7% of sites (n = 53/215) have particles which have shown the potential to spread to a second DMA, while a further 31.2% of sites (n = 67/215) show particles which may spread through 3 DMAs, with 4.7% of sites (n = 10/215) suggesting particles that may move through 4 DMAs, ~7% of sites (n = 15/215) showing particles which may potentially spread through 5 DMAs and finally 1.4% of sites (n = 3/215) showing particles with the potential to move through up to 6 DMAs (Fig. 2).

This is further broken down to show the percentage of sites in each region that interact with multiple DMAs (Fig. 2). The Western Isles, for example, shows spread into a higher proportion of sites than other regions after 48 h, which must be taken within the context of the percentage of particles in each area, shown in Fig. 3. This means that in 24 and 48 h
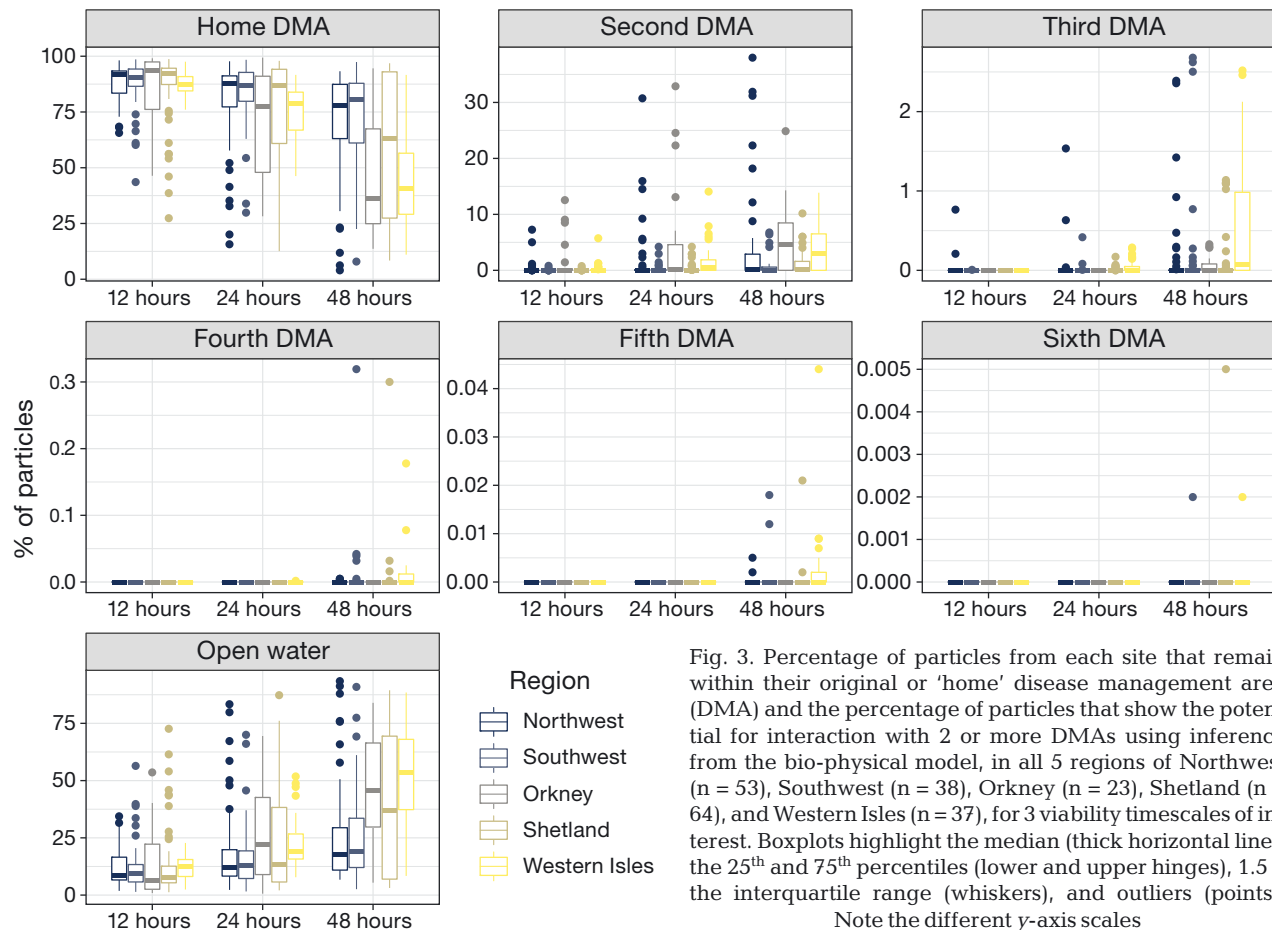

Fig. 3. Percentage of particles from each site that remain within their original or 'home' disease management area (DMA) and the percentage of particles that show the potential for interaction with 2 or more DMAs using inference from the bio-physical model, in all 5 regions of Northwest (n = 53), Southwest (n = 38), Orkney (n = 23), Shetland (n = 64), and Western Isles (n = 37), for 3 viability timescales of interest. Boxplots highlight the median (thick horizontal line), the 25th and 75th percentiles (lower and upper hinges), 1.5 × the interquartile range (whiskers), and outliers (points). Note the different *y*-axis scales

respectively, the potential for particles to spread and potentially impact sites within different DMAs increases; however, more research is required into all relevant epidemiological factors, such as dilution and pathogen viability, to fully quantify the risk of disease transmission.

The proportion of particles that crossed into another DMA was analysed to quantify the risk. Fig. 3 summarises the percentage of particles in each area listed for each region after the time stamp given. On average, 87.03% ± 11.81% (mean ± SD) of particles were retained within the home DMA, 12.65% ± 11.54% of the particles moved to open water, whereas 0.31% ± 1.42% of the particles entered a different DMA. Fig. 3 further breaks this down by region, showing that after 12 h, the majority of particles are retained in their home DMA; Western Isles retained 87.4% ± 5.8%, Shetland Islands 87.0% ± 12.2%, Orkney 85.0% ± 15.9%, the Southwest region 86.7% ± 14.9%, and the Northwest region 88.2% ± 8.0%. After 12 h, the proportion of particles entering a second DMA in any region is fairly small, ranging from 0.02% ± 0.1% in Shetland to 1.6% ± 3.5% in Orkney, with the other regions sitting in between. Naturally, the numbers of particles retained in the home DMA decreases after 24 and 48 h respectively. After 24 h, Western Isles retained 75.4% ± 11.6%, Shetland Islands 83.1% ± 15.5%, Orkney 68.7% ± 24.7%, the Southwest region 75.4% ± 22.6%, and the Northwest region 79.1% ± 19.7%. After 48 h, Western Isles retained 44.6% ± 22.0%, Shetland Islands 71.7% ± 21.8%, Orkney 47.2% ± 27.1%, the Southwest region 60.0% ± 32.0%, and the Northwest region 69.7% ± 24.7%. When the location of particles after 24 and 48 h respectively is considered, the proportion of particles moving outside their origin DMA into open water increases to 21.66% ± 18.65% and 36.68% ± 26.81% in turn, while 1.36% ± 4.39% of the particles entered a second DMA in 24 h and 2.68% ± 5.47% of the particles entered a second DMA in 48 h. The average percentage moving to a third DMA in 24 h is 0.02% ± 0.12%, which increases to 0.22% ± 0.55% in 48 h. Notably, Fig. 3 highlights the proportion of particles that spread into open water, not shown in Fig. 2. Particles, when leaving their home DMA in any region, are most likely to enter open water, and as the proportion of particles in the home DMA decreases, the proportion of particles in open water increases (Fig. 3). The proportion of particles moving into the second DMA increases from 0.3% ± 1.4% after 12 h, to 1.4% ± 4.4% after 24 h, and 2.7% ± 5.5% after 48 h in all DMAs, with some regional variation occurring particularly after the longer times. The proportion of particles reaching any further DMAs is minimal (Fig. 3).

Inference of the average displacement from origin by particles after 12, 24 and 48 h respectively is shown in Fig. 4. In 12 h, 95% of particles were retained within 5.78 km of origin, the maximum distance any particle travelled in 12 h was 11.47 km, and the minimum distance was 0.51 km. In 24 h, 95% of the particles stayed within 11.18 km, and the range of displacement from origin was 0.56 to 12.98 km. After 48 h, 95% of particles had travelled less than 19.85 km, ranging from 0.57 to 23.18 km.

Table 1 summarises the average distance (±SD) and 95th percentile of displacement from origin across all sites in Scotland and then broken down by each region. These values represent the average value across all months.

There is a statistically significant difference (p < 0.01) in displacement from origin by particles from sites in different regions and different months (Fig. 5). Results are based on the climatological hydrodynamic output, thus these distances represent an 'average' year.

The displacement from origin by particles after the 3 viability timescales was consistently higher in the winter months (December, January and February; Fig. 5). The particles originating from farms in the Orkney region tended to travel furthest on average, followed by the particles originating from farms on the Western Isles (Fig. 5).
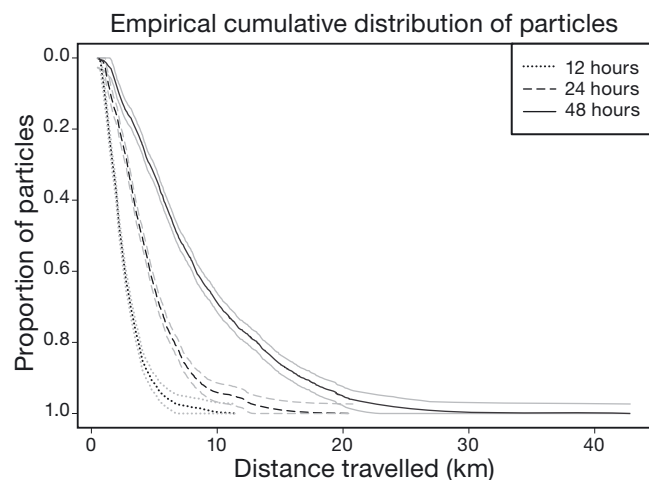

Fig. 4. Empirical cumulative distribution of displacement from origin by particles after 12, 24 and 48 h. Confidence intervals (grey lines) calculated using Dvoretzky–Kiefer–Wolfowitz inequality equation (Dvoretzky et al. 1956)

Table 1. Summary of the average distance of displacement from origin by particles for all sites, broken into each region across all months. n: the number of sites included; 95 %ile: 95th percentile

Region	n	Distance travelled (km)					
		After 12 h		After 24 h		After 48 h	
		Mean ± SD	95 %ile	Mean ± SD	95 %ile	Mean ± SD	95 %ile
Existing sites							
All active sites	215	2.689 ± 1.648	5.781	4.66 ± 3.010	11.184	8.455 ± 5.896	19.949
Northwest	53	2.652 ± 1.373	5.226	4.429 ± 2.785	10.145	7.477 ± 5.433	15.947
Southwest	38	2.228 ± 1.094	4.588	3.855 ± 2.152	7.746	6.682 ± 3.879	14.879
Shetland	64	1.959 ± 1.185	4.447	3.196 ± 1.936	7.188	5.22 ± 3.401	11.673
Orkney	23	4.810 ± 2.495	9.628	9.014 ± 3.782	15.749	16.795 ± 5.873	26.174
Western Isles	37	3.158 ± 1.191	5.273	5.642 ± 2.064	9.112	12.087 ± 4.882	20.036
Hypothetical sites							
Nearshore exposed	5	3.017 ± 1.297	5.706	5.309 ± 2.536	11.254	9.031 ± 3.353	14.976
Offshore	5	4.842 ± 2.896	10.6	8.580 ± 5.538	18.894	16.174 ± 10.457	34.45

3.2. Near-future scenario: 'nearshore exposed sites'

The inference from the bio-physical model output was compared to the DMA output for the hypothesised nearshore exposed site locations in terms of spread and displacement from origin. The hypothesised nearshore exposed sites 1 and 2 kept particles within their originally placed DMA, while hypothesised nearshore exposed sites 3, 4 and 5 occasionally spread particles to 2 adjacent DMAs. In 12 h, 95 % of particles were retained within 5.71 km of their origin; the maximum distance any particle travelled in 12 h was 7.64 km, and the minimum distance was 1.47 km. Table 1 summarises the average distance (±SD) and 95th percentile of displacement from origin for all hypothesised nearshore exposed sites for all months, while Table A1 in the Appendix gives further details on each site. The average displacement from origin after 12 h for the hypothesised nearshore exposed sites was not significantly higher than the average displacement from origin for current active sites.

3.3. Long-term future scenario: 'offshore sites'

The hypothesised offshore sites 1, 2 and 4 did not spread particles to any current DMAs, while hypothesised offshore site 3 occasionally spread into 2 nearby current DMAs, and hypothesised offshore site 5 occasionally spread into 1 current DMA. In 12 h, 95 % of particles were retained within 10.32 km of their origin, the maximum distance any particle travelled in 12 h was 11.55 km, and the minimum distance was 1.49 km. Table 1 summarises the distance metrics for hypothesised offshore site across all months, while Table A2 in the Appendix gives details on each site. The average displacement from origin after 12, 24 and 48 h respectively for the hypothesised offshore sites was significantly higher ($p < 0.01$) than the average displacement from origin for current active sites.

4. DISCUSSION

As computational power increases, spatial management and associated tools are considered an integral element of fish health protection in reducing and preventing disease outbreaks (Viljugrein et al. 2009, Salama & Murray 2011, Foreman et al. 2015, Murray & Gubbins 2016, Bravo et al. 2020). Where other studies such as Foreman et al. (2015) or Bravo et al. (2020) focused on specific pathogens, namely IHNV and piscirickettsiosis respectively, we instead explore the utility of bio-physical modelling to support and inform potential changes in future DMA structure in Scotland's aquaculture more generally. Here, we analysed the number of sites in which particles are retained within a single DMA for 12, 24 and 48 h respectively. The spread of particles after 12 h is important, as many pathogens survive a short time in the marine environment if no host is available, whereas more robust pathogens may survive longer. DMAs are used in the containment and eradication of serious notifiable disease such as ISA. Other diseases, such as pancreas disease (PD) (Kilburn et al. 2012) caused by the salmonid alphavirus (Weston et al. 1999), or complex gill disorder (Noguera et al. 2019) are considered endemic
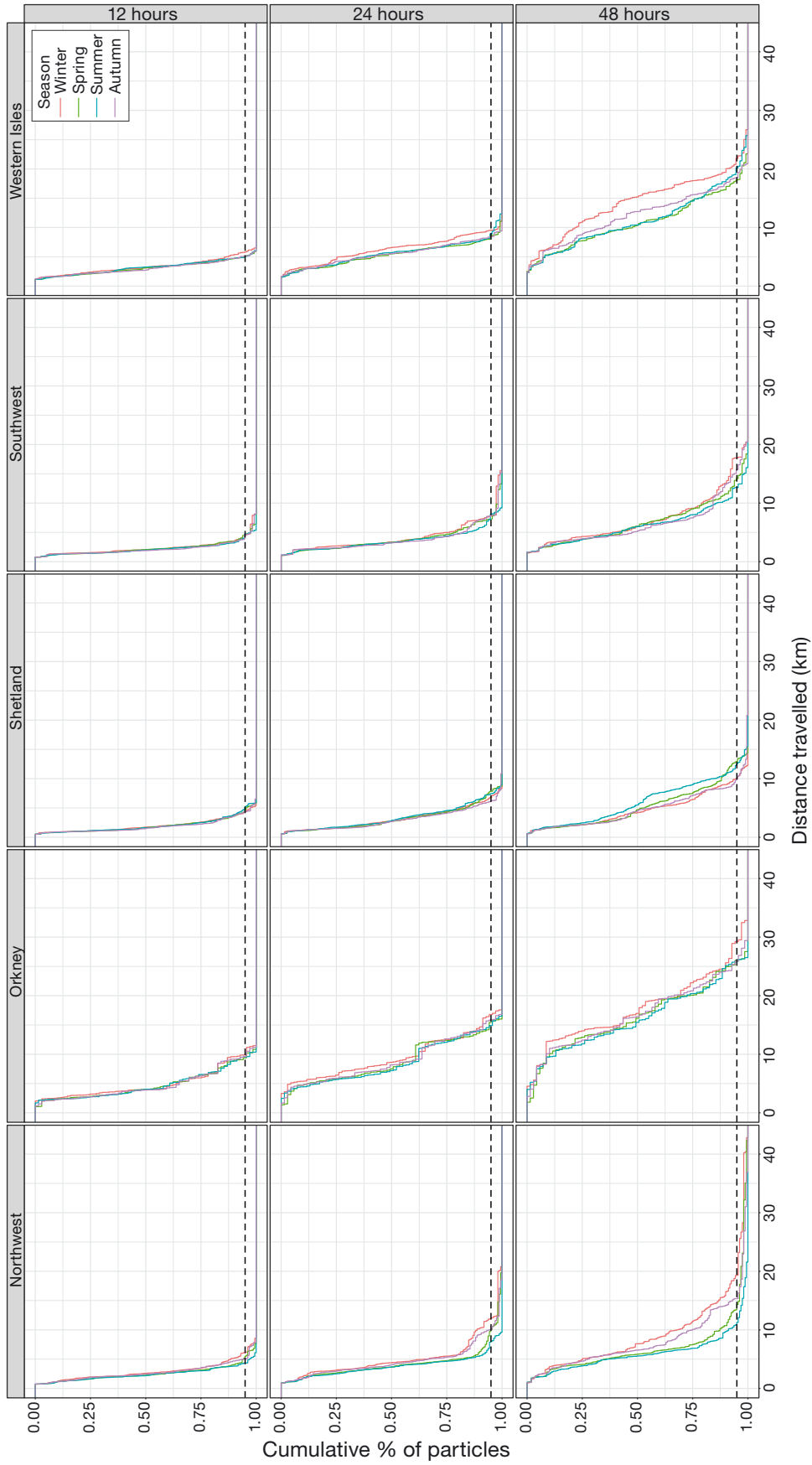
Fig. 5. Cumulative frequency of average distance particles travelled from each site in each season for the 5 regions in Scotland (Northwest, n = 53; Southwest, n = 38; Orkney, n = 23; Shetland, n = 37; Western Isles, n = 64) for the 3 viability timescales of interest (12, 24, 48 h)

and are not controlled through the DMA structure and depopulation, although they can cause high levels of mortality. Bacterial kidney disease, although notifiable in salmon, is controlled at the farm level through movement restrictions and is not at the area level, since the causative pathogen, *Renibacterium salmoninarum*, survives poorly in the environment, thus transmission to neighbouring farms is not considered as important to its epidemiology (Murray et al. 2012). Other diseases like infectious pancreatic necrosis caused by the widespread pathogen infectious pancreatic necrosis virus (IPNV) are relatively robust (Oidtmann et al. 2018), thus potentially making DMAs less effective for their control (Murray et al. 2006). IPNV specifically has not been managed using DMAs, and is now non-notifiable and is not subject to official controls.

We explored the inference of the maximum spread of particles after 12, 24 and 48 h respectively as this allows us to better understand the area that may potentially be impacted by notifiable diseases such as ISA and VHS. Thus it is allowing us to be conservative in our recommendations in terms of control of these listed diseases and to provide recommendations for further research to better understand the risk of disease spread, particularly in changing climates. In this exploratory analysis, inert particles moved through various DMAs driven by the physical properties of the hydrodynamic model, such as ocean current. Thus this does not account for abundance of a pathogen, its decay or mortality, as the maximum spread was of interest. Nor does this account for other epidemiological factors for which the separation of DMAs is important in containing serious notifiable disease, should this occur.

The overall pattern of dispersion of particles within the baseline scenario of the bio-physical model provided inference that the current DMAs are generally conservative enough to reduce the spread of notifiable diseases to other DMAs, but not large enough to capture the spread into the wider sea, as all 215 sites show varying degrees of spread not captured by the current DMA.

The sites showing particles spreading through multiple DMAs were assessed to explore the potential risk likely to occur (Fig. 3). This highlighted that the risk posed from all sites where particles were found to move into a secondary DMA within 12 h is likely to be minimal. The percentage of particles that enter more than 3 DMAs is less than 0.001%, thus unlikely to pose any risk of infection. The potential risk this may cause will be dependent on how robust

the pathogen is, given various other environmental factors such as water temperature.

We explored the inference of average displacement from origin by particles after 12, 24 and 48 h respectively in each month of the year to assess if particles travel further on average at certain points of the year (Fig. 5). This analysis added to the inference gleaned from the spread discussed above by allowing a comparison of average distances particle travel from all sites and the set distance used in the current DMA methodology, which is based on epidemiologically relevant fixed separation distances around active farms. There is a statistically significant difference (p < 0.01) in displacement from origin by particles from sites in different regions and different months. The winter months of December, January and February showed consistently higher distances travelled by particles than in other months (Fig. 5), which relates to stronger wind forcing during these months, as all particles stay near the surface in this model. Greater mixing due to stronger wind may mean that viral particles do not remain at the surface, and thus this assumption should be challenged if inference from bio-physical modelling is proposed as a supporting tool in informing DMAs. Regional differences showed the particles originating from farms in the Orkney region tended to travel furthest on average (Fig. 5), although particles were more likely to end up in open water than another DMA (Fig. 3). Particles originating from farms on the Western Isles travelled the next furthest in distance (Fig. 5); again, more particles ended up in open water than entered another DMA (Fig. 3). This suggests that perhaps a regional approach to inferring epidemiologically relevant fixed separation distances for disease area management may be more applicable, particularly if our hypothesis of moving to more exposed areas is correct. However, this analysis only looks at one component of disease transmission, namely the movement of particles in the coastal-oceanic zone. This may provide a useful indirect measure of efficacy of current biosecurity measures, but cannot conclude on whether changes are required in DMAs, as this would require all aspects of disease transmission be included. The hypothesised near-future scenario with nearshore exposed sites and long-term scenario with offshore site locations highlighted that particles spread further and reach larger distances in more exposed areas. While this is not surprising, it is an area for consideration, alongside other epidemiological aspects of relevance for disease transmission, when new farm locations are suggested in exposed areas.

4.1. Model assumptions, limitations and recommendations

The hydrodynamic model output used in the study is an average 1 yr climatology based on the 25 yr period 1990–2014. This means that specific extreme (e.g. storm) events were not included and inter-annual variability cannot be estimated. The results from this study will therefore represent an average year for the above given time frame. This is appropriate to management of clusters of farms that will be in place over many years, particularly for management of occasional large outbreaks whose coincidence with extreme conditions is a very low probability. There is currently no scenario of the SSM available to simulate extreme weather conditions. This is a limitation of this study, but inclusions of storm events (e.g. 1 in 100 yr) could provide inference on particle tracking that would suggest different results. This should be considered prior to changing the existing methodology or implementing a stepwise change within the industry to offshore site locations.

The particle-tracking model uses the integrated grid output version of the SSM, which combines the coarser- and finer-resolution model outputs. However, this is a very computationally expensive exercise, which required high-powered computing resources, thus is not something that is easily repeated, and particle-tracking runs were performed offline.

For the pathogen behaviour in the particle-tracking simulations, a number of assumptions and simplifications were made, such as the pattern and duration of spawning and length of the pelagic duration and settlement window. No mortality was built into the particle-tracking model, due to the differences between various pathogens in specific environmental conditions. Thus, all particles 'survive' the duration of the simulations, although to quantify survivorship correctly, we would have also needed an estimate of numbers of viral particles released, which was not available. The number of particles released from each area aims to replicate the movement of a potential pathogen from a site, in order to understand the spatial extent of pathogens shedding from farm sources only. Therefore it does not reflect an absolute number of a given pathogen and the rate at which the particles are released does not reflect the quantitative temporal distribution of a pathogen's reproduction. Horizontal diffusivity of $10 \, \mathrm{m^2 \, s^{-1}}$ was specified within this analysis. This parameter will require testing, validation and a sensitivity analysis prior to changing the current DMA methodology, as this level of diffusivity may impact inference of particle behaviour, by sug-gesting more or less random movement than seen in nature by virus particles. All particles were released on the surface in this study; in previous studies with particles representing viruses, there was little difference between particles released at the surface, mid-depth and bottom (Wolf et al. 2016b); however, this is another area representing model uncertainty. We recommend a full sensitivity analysis on key model parameters such as horizontal diffusivity, minimum number of particles released and timing required to capture physical parameters of importance, such as current velocity, and also epidemiological factors prior to considering whether changes are required for the current methodology of assigning DMAs.

Empirical data which tracks virus particles in water is not practical to collect; however, the observational data from active farm sites shows that the current DMAs are effective, in that they were effective as part of the programme of bringing ISA under control and then eradication when it first occurred in Scotland in 1998 and in the containment and eradication of a second occurrence in 2008, and used to contain and eradicate VHS in 2012; thus any changes to DMA structure must follow a conservative approach and should treat the current epidemiological zone as a minimum acceptable area. This needs to be considered if bio-physical models are to be used in driving area-based management changes for pathogen control in Scottish waters.

The near-future and long-term scenarios are limited to 5 locations only, thus this first look does not provide a definitive statistical analysis. New technologies are likely to emerge through various industry innovations, which may change the types of cages and thus the transmission dynamics from sites. Further work is required to fully evaluate the transmission dynamics from offshore farms within future climate scenarios. This requires additional understanding of potential offshore cage types and logistics, which is outside the remit of the current work.

4.2. Conclusions

Diversifying impact mitigation for pathogen control in marine environments involves increasing host resilience to disease, reducing pathogen abundance and managing environmental factors that facilitate disease. Here we have shown the current DMA methodology is robust for the movement of particles from farms in nearshore, relatively sheltered areas, building on previous research (e.g. Murray et al. 2006, Salama & Murray 2013, Murray & Gubbins

2016). This work highlights the need to fully investigate if changes are required to the current DMA structure if the industry seeks to develop in offshore areas where pathogens are likely to have an increased spread, as in this analysis, the particles tend to spread further on average from more exposed areas. We do not consider all relevant epidemiological factors for disease transmission in Scottish waters; thus this bio-physical modelling exercise is a first step which helps to investigate if there is an increased risk associated with offshore farms in terms of pathogens. This work may be useful in assessing potential new offshore farm locations in the context of particles which may be pushed to nearby nearshore sites. Thus, if the industry plans to develop further offshore, then it may be prudent to further investigate the epidemiologically relevant fixed separation distance radius required for DMAs on these farms.

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Appendix.

Table A1. Summary of the average distance of displacement from origin by particles for each hypothesised nearshore exposed site across all months. 95%ile: 95th percentile

Hypothesised site name	Distance travelled (km)					
	After 12 h		After 24 h		After 48 h	
	Mean ± SD	95%ile	Mean ± SD	95%ile	Mean ± SD	95%ile
All nearshore exposed sites	3.017 ± 1.297	5.706	5.309 ± 2.536	11.254	9.031 ± 3.353	14.976
Nearshore Exposed 1	2.149 ± 0.326	2.643	3.778 ± 0.770	5.086	7.431 ± 2.181	10.310
Nearshore Exposed 2	2.608 ± 0.882	3.898	5.056 ± 1.977	8.436	8.435 ± 2.383	10.524
Nearshore Exposed 3	4.342 ± 1.714	7.286	7.647 ± 3.326	13.186	10.33 ± 2.184	13.975
Nearshore Exposed 4	2.067 ± 0.234	2.456	3.342 ± 0.567	4.207	5.333 ± 0.662	5.995
Nearshore Exposed 5	3.921 ± 0.589	4.785	6.726 ± 1.898	9.503	13.627 ± 1.364	14.976

Table A2. Summary of the average distance of displacement from origin by particles for each hypothesised offshore site across all months. 95%ile: 95th percentile

Hypothesised site name	Distance travelled (km)					
	After 12 h		After 24 h		After 48 h	
	Mean ± SD	95%ile	Mean ± SD	95%ile	Mean ± SD	95%ile
All offshore sites	4.842 ± 2.896	10.6	8.580 ± 5.538	18.894	16.174 ± 10.457	34.45
Offshore 1	5.743 ± 0.574	6.527	9.502 ± 1.943	12.355	17.780 ± 1.937	19.589
Offshore 2	2.04 ± 0.16	2.296	3.508 ± 0.331	4.085	5.679 ± 0.509	6.571
Offshore 3	4.526 ± 1.306	6.4	7.754 ± 2.985	12.042	13.289 ± 1.144	14.108
Offshore 4	2.238 ± 0.564	3.103	4.223 ± 1.305	6.148	9.405 ± 2.531	13.062
Offshore 5	9.665 ± 1.53	11.861	17.911 ± 2.138	21.067	34.717 ± 3.893	41.458