



Seasonality in live fish movements and its effects on epidemic dynamics



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ABSTRACT

Live fish movements between salmon farms risk spreading pathogens, and movements between freshwater farms (FW–FW) or from freshwater to seawater (FW–SW) show clear seasonality. In this study, we quantify the effects of seasonality of live fish movements on epidemic dynamics, using a network model populated with data from live fish movements between Scottish salmon farms from 2002 to 2004. We used three types of networks: A) timing and pair-wise movements between farms were as observed; B) as network A, but with a random reordering of FW–FW and FW–SW movements; and C) number of movements were kept the same as in the data, but connection between nodes was random. We compared the time-course of simulated epidemics in a stochastic model for all three networks. We showed that seasonality had the strongest effect in networks B and C, especially when local transmission was high, and this effect was stronger in SW farms compared with FW farms.

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1. Introduction

Scotland is the third-largest producer of Atlantic salmon (*Salmo salar*) after Norway and Chile, and produced approximately 154,000 tons in 2010 (Marine Scotland Science, 2011). However, the Scottish industry is threatened by disease outbreaks such as those of pancreas disease and infectious salmon anaemia (ISA). Movements of live fish provide a route for spreading pathogens between otherwise isolated farms, which has been associated with the spread of several diseases (Mardones et al., 2009; Murray et al., 2002) and is a potential route for introduction of exotic pathogens (Peeler and Thrush, 2004). However, movements are common in aquaculture and are required for both economic and biological reasons (e.g., movement of salmon smolts from freshwater to marine farms).

Epidemic network models can be used to assess the risk of these live fish movements on the transmission of pathogens and can easily take into account heterogeneity in the number of movements between farms (Kiss et al., 2005; Webb, 2005). A movement network can represent live animal movements between farms; these are connected by “edges” (undirected contact) or “arcs” (directed contact) representing potentially infectious contact (Martinez-Lopez et al., 2009); movements of fish are inherently directed.

Epidemics that start during periods with increased movement activity have a higher probability of becoming more widespread than epidemics starting during other periods of the year (Kiss et al., 2006).

This was one reason why the British outbreak of foot-and-mouth disease in 2001 was so large: because it started at a busy time of year for sheep trading via livestock markets (Gibbens et al., 2001; Kiss et al., 2006). In a previous study, Scottish live fish movements were shown to be seasonal, but these seasonality patterns differed across production phases (Werkman et al., 2011a). Movements between freshwater (FW) farms mainly occurred from May to July, while seawater (SW) farms were supplied with smolts mainly during February to March and October to November (Werkman et al., 2011a).

During periods of the year when many movements occur, early recognition of disease is important. Sites known to be infected with a notifiable disease are prohibited from moving fish to other farms (Joint Government/Industry working Group, 2000), but are allowed to send fish for processing. However, diseases can go unnoticed when the prevalence is low or when there are no clinical signs, and fish might therefore be moved while they are infected with a notifiable disease (Graham et al., 2006; Jonkers et al., 2010; Lyngstad et al., 2008; Murray and Peeler, 2005).

In addition to fish movements, pathogens may also be transmitted between farms through the environment, principally by water movement (Jonkers et al., 2010; OIE, 2009). Survival time of the pathogen outside of its host, in water, differs between pathogens and is dependent on factors such as water temperature or chemistry (OIE, 2009) and on available natural reservoirs (such as wild fish) in the proximity of fish farms (Uglem et al., 2009).

In the current study, we investigated the effects of seasonal patterns of FW–FW and FW–SW movements between salmon farms on the course of simulated epidemics. Descriptive statistics from an earlier study (Werkman et al., 2011a) were used as a base to estimate parameter values for seasonality in the numbers of movements per

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farm. As the transmission of pathogens between farms can vary largely according to the characteristics of the environment, host or pathogen, a wide range of transmission rates and removal rates was studied. This model was aimed to be as parsimonious as possible, while still being capable of describing the features of interest in a particular system (Jørgensen and Bendoricchio, 2001; Murray, 2008).

2. Materials and methods

Pathogen transmission was modeled through both live fish movements and through local spread, to investigate the effects of seasonality of live fish movements on the course of epidemics.

2.1. Long-distance movements

Scottish fish farmers are obliged to record live fish movements *onto* and *off* their farms. The records from 1 January 2002 to 31 December 2004 were used in this study (2401 live salmon movements) (Munro and Gregory, 2009; Werkman et al., 2009). Over this period there were $N_{fw} = 186$ active FW farms (i.e., farms in a production cycle either having stock or fallowing), and 314 active SW farms of which 304 farms had movements onto or off their farm. Nine research farms had both FW and SW facilities available. For the purpose of this study we classified these farms as SW farms ($N_{sw} = 323$). The total number of all salmon farms (N_{total}) was 509.

The effect of seasonality of live fish movements on the course of epidemics was studied for three different types of networks. For all situations, a directed dynamic contact matrix A_{ijt} was developed of size $N_{total} \times N_{total} \times \text{time } t$ ($1 \leq t \leq 159$ weeks). An element A_{ijt} contained 1 when there was a movement between farm i and j at time t and 0 otherwise.

For all three networks, we compared two scenarios: a) the network with the seasonality preserved; and b) seasonality removed by altering the movement timings such that the number of FW–FW and FW–SW movements was distributed homogeneously over the time period. The timing of SW–SW, SW–FW and ‘other’ movements did not show clear seasonal patterns (Werkman et al., 2011a) and was preserved under scenario b).

2.1.1. Network A: real-life network

Network A included the real-life situation as recorded in the data: the movement network structure and the relative ordering of movements in the data (Werkman et al., 2011a) were preserved for both the seasonal and non-seasonal network.

In the non-seasonal network, all movements were placed in chronological order based on the date they occurred. The study period was 3 years and each year contained 53 weeks, resulting in 159 time steps. Movements were allocated evenly across weeks in the order they occurred. For FW–FW movements this resulted in $1181 / t \approx 7$ movements per week. For the first week, the first 7 FW–FW movements of the chronological movement list were selected; for week 2, movements 8 to 14 were selected, etc.

Movements were only allowed once per week such that $A_{ijt} \in \{0,1\}$ (Werkman et al., 2011a); when network A was transformed to a non-seasonal network, it resulted in a few cases where two movements occurred between a pair of farms in the same week. For these cases, movements were changed to the first movements in the following week in order to keep the sequence of the movements in the non-seasonal network as close as possible to the sequence of the movements in the seasonal network.

2.1.2. Network B: real-life network with random order of movements

For the seasonal version of network B, the original movements of network A were matched to a new timing list. In this list the original timings of movements (i.e., week numbers) were put in a random order and one-by-one matched to a movement. The movement

network structure and seasonal pattern of network B was the same as network A, but the sequence of FW–FW and FW–SW movements was altered by letting them occur in a random order. Comparison with network A allowed investigation of the importance of the precise ordering of the contacts on disease dynamics.

For the non-seasonal version of network B, another timing list was made where each week number occurred with equal frequency, such that the totals matched the number of movements per production phase in the original data. As with network A, movement was restricted to once per week: during matching of movements to the list of time points, where $A_{ijt} = 1$, the next time point was attempted until the criterion was met or possibilities exhausted. In the latter case, this movement was discarded (a maximum of two movements was missing over a three-year period for all network types in less than 5% of the created networks). This resulted in a network where the movements were randomized and the number of movements per week was equal over the whole time period.

2.1.3. Network C: simulated network

The last network, network C, was designed in such a way that the number of movements going onto and off farms were preserved, but not the pairwise connectivity between specific farms. The order of movements was not taken into account, but the in–out degree correlation was preserved.

During 2002 to 2004, there were in total 1181 movements between FW farms recorded. To build the long-distance movement network between FW farms, two lists of farms were constructed. The first list contained 1181 stubs (i.e., one half of an arc), which represented the source farms. There were 108 farms with movements off their farm that were selected at random from the FW farms and were repeated as often as they had movements off the farm (varying from 1 to 38 times).

The second list contained the destination farms: 161 were selected and repeated as often as they had movements on their farms (varying from 1 to 52 times), again resulting in 1181 stubs. Of these 161 farms, 92 farms were also in the source list and 69 farms were selected at random from the remaining FW farms. Nine farms remained without any simulated FW–FW movements on or off their farm. As in the original data, these farms had only movements to SW farms, to or from farms with both FW and SW facilities, or were supplied with broodstock from SW farms.

An additional list was made which included the timings of the movements as described for network B. The source list, destination list and the timing list were each put in a random order. One by one, each farm from the source list was connected to one farm from the destination list and one week number from the timing list. The farms were only matched when $A_{ijt} = 0$ and $i \neq j$. Otherwise, the next farm on the source list was selected until the criteria were met or after 50 unsuccessful attempts, in which case the second movement between i and j at time t was removed without replacement. A similar approach was used for FW–SW movements ($N = 810$).

2.2. Local contacts

An additional undirected contact matrix B_{ij} of size N_{total} by N_{total} that was developed represented spread between farms by local contact other than recorded movements. To create this matrix, the maps from the Scottish salmon and sea trout catches (Fisheries Research Services, FRS, 2003) were used in conjunction with geographic data for the farms and management area maps from the Joint Government/Industry Working Group (2000) as updated by Fisheries Research Services for 2003 to take into account the opening and closure of farm site over the intervening three years. Scotland is divided into 62 salmon fishery statistic districts, which can contain single or multiple river catchments that were combined with adjacent coastlines. Salmon FW farms were dispersed over 39 salmon fishery statistic districts each containing between one and 23 farms (Fig. 1).

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