Characterization of the live salmonid movement network in Ireland: Implications for disease prevention and control

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ABSTRACT

Live fish movement is considered as having an important role in the transmission of infectious diseases. For that reason, interventions for cost-effective disease prevention and control rely on a sound understanding of the patterns of live fish movements in a region or country. Here, we characterize the network of live fish movements in the Irish salmonid farming industry during 2013, using social network analysis and spatial epidemiology methods, and identify interventions to limit the risk of disease introduction and spread. In the network there were 62 sites sending and/or receiving fish, with a total of 130 shipments (84 arcs) comprising approx. 17.2 million fish during the year. Atlantic salmon shipments covered longer distances than trout shipments, with some traversing the entire country. The average shipment of Atlantic salmon was 146,186 (SD 194,344) fish, compared to 77,928 (127,009) for trout, however, variability was high. There were 3 periods where shipments peaked (February–April, June–September, and November), which were related to specific stages of fish. The network was disconnected and had two major weak components, the first one with 39 nodes (mostly Atlantic salmon sites), and the second one with 10 nodes (exclusively trout sites). Correlation between in and out-degree at each site and assortativity coefficient were slightly low and non-significant: −0.08 (95% CI: −0.22, 0.06) and −0.13 (95% CI: −0.36, 0.08), respectively, indicating random mixing with regard to node degree. Although competing models also produced a good fit to degree distribution, it is likely that the network possesses both small-world and scale-free topology. This would facilitate the spread and persistence of infection in the salmon production system, but would also facilitate the design of risk-based surveillance strategies by targeting hubs, bridges or cut-points. Using Infomap community detection algorithms, 2 major communities were identified within the giant weak component, which were linked by only 4 nodes. Communities found had no correspondence with geographical zones within the country, which could potentially hinder the implementation of zoning strategies for disease control and eradication. Three significant spatial clusters of node centrality measures were detected, two in county Donegal (betweenness and outcloseness) and one in county Galway (incloseness), highlighting the importance of these locations as hot spots of highly central sites with a higher potential for both introduction and spread of infection. These results will assist in the design and implementation of measures to reduce the sanitary risks emerging from live fish trade within Ireland.

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1. Introduction

Aquaculture is an important contributor to the Irish economy, providing jobs and revenue particularly along the western seaboard of the country. During 2013, the value of Irish aquaculture products reached €117 mill, with salmon farming accounting for 50% of that figure (BIM, 2014).

Salmon farming seeks to mimic the natural life cycle of salmon, with fish undergoing an intricate network of movements as they grow. Reproductively mature fish are transported from the sea into freshwater broodstock facilities in late summer/early autumn, to be 'stripped' of their gametes later on winter. Fertilized eggs are

produced, which are then either incubated on an on-site hatchery or transported directly to other hatcheries, for development through several juvenile stages (alevin, fry, and parr). At 6–12 months of age, fish will go through smoltification, the process of adapting for life in the ocean. Further movements may also occur during the period between egg and smolt, where fish may be sold or moved to other freshwater sites. After smoltification, fish are transported to seawater net pens, where they will grow until harvest time, with the possibility of being moved to other sea sites in between. At the time of harvesting, fish may be slaughtered on site or moved one final time, using well-boats, to a harvest station for slaughter and processing.

In Ireland, all eggs for commercial trout production are imported either from Denmark, USA or the UK. Eggs are hatched at the importing site, then kept until ready for processing or sold or otherwise moved to other sites for further growing. Some farms will also sell fish to 'Put and Take' fisheries for recreational purposes. Currently Irish trout production is entirely conducted at freshwater sites.

Although an essential aspect of salmonid production, movement of live fish could be an important mechanism for introduction and spread of infectious agents. Live fish transport has been implicated in facilitating the spread of infectious salmon anaemia (ISA) in Scotland (Murray et al., 2002) and Chile (Mardones et al., 2014), and in the widespread dissemination of bacterial kidney disease (BKD) in the UK (Green et al., 2009; Hall et al., 2015). In Ireland, fish movement has been implied with the spread of infectious pancreatic necrosis virus (IPNV) (Ruane et al., 2007, 2009b). Therefore, characterizing the salmonid movement network structure and patterns is critical for the prevention and control of infectious agents.

Social network analysis (SNA), defined as the study of the relationships amongst social entities and the patterns and implications of these relationships (Wasserman and Faust, 1994), can assist in characterizing the live salmonid transport network in Ireland, and understanding the implications of this network for disease prevention and control. In preventive veterinary medicine, the use of SNA started in the early 2000's but is rapidly increasing. As examples, see the reviews by Martinez-Lopez et al. (2009b) and Dubé et al. (2009), and the application of this methodology for livestock and poultry diseases such as foot-and-mouth disease or avian influenza (Kao et al., 2006; Kiss et al., 2006b; Ortiz-Pelaez et al., 2006; Robinson et al., 2007; Dent et al., 2008). There are few examples of its use in farmed salmonids, with most studies conducted in Scotland, where node and network properties were investigated (Green et al., 2009, 2011, 2012; Munro and Gregory, 2009). Further, network analysis has been incorporated into simulation models for disease spread between salmonid sites in England and Wales (Jonkers et al., 2010). Recently, Mardones et al. (2014) estimated the effect of farm connectivity measures on the risk of infectious salmon anaemia (ISA) positivity in Chile, based on the idea that centrality of nodes (farms) could be considered as a proxy of holdings that are influential in mediating the flow of animals in the network. Such highly connected premises (hubs) are at risk of becoming infected and transmitting infection to others (Shirley and Rushton, 2005). However, to the best of the authors' knowledge there are no studies conducted for salmon industries that are predominantly organic, which imply, among other features, more restrictive stocking densities and use of chemotherapeutic treatments. This production system is expected to have distinct movement patterns and characteristics than intensive production systems, which certainly will impact the risk of disease introduction and spread.

In this paper we characterize, for the first time, the network of live fish movements in Ireland, a country where most of the production (more than 80%) is certified organic (BIM, 2013). The results of this study will inform the Irish salmonid farming stakeholders in the design and implementation of preventive and intervention strategies to limit the risk of disease introduction and spread, keeping organic salmon production sustainable in the long term.

2. Material and methods

According to EU Council Directive 2006/88/EC, Member States shall ensure that aquaculture production businesses (APBs) are registered, keeping record of all movements of aquaculture animals and products into and out of the farm (Anon, 2006). In Ireland, these data are stored in a database administered by the Irish Marine Institute (MI). MI provided 2013 data for analyses in this study, which consisted of a dataset of live fish movement with the following variables: date of movement, origin and destination sites with geographic coordinates, life stage, species and quantity of fish moved.

The directed network of salmonid fish movements was defined here as a group of nodes or sites (epidemiological unit) connected by unidirectional arcs, corresponding to at least one (and potentially several) shipments with a sender and receiver, which represent direct contact between sites due to fish movement. Direct contact does not imply transmission of infection if present, but is nevertheless a prerequisite for it. Sites may be sources of infection (posing a risk of onward spread), sinks for infection (at risk from introduction of infection), or both (Green et al., 2009).

For the network of direct contacts (i.e., fish movements) among farms, the characteristics and temporal-spatial patterns of the network were analyzed, including the number of contacts per month, Euclidean (straight line) distance of shipments based on the geographical coordinates of the farms, shipment size, mixing pattern, characteristics of the giant strong and weak components (GSC and GWC, respectively), and centrality measures of the salmon farms, namely degree, betweenness, and closeness, all of which were estimated considering the directed nature of the network and standardized by their theoretical maximum. Definitions and computation details of these centrality measures have been described previously, for example by Dubé et al. (2009) and Martinez-Lopez et al. (2009b). For evaluating the mixing pattern of the network, we estimated the assortativity coefficient, using the same approach as the one used by Green et al. (2009). Briefly, this consisted of assessing if sites with high in-degree send fish shipments to sites with high out-degree more frequently. An assortative mixing pattern (i.e., positive assortativity coefficient) would mean that sites with high in-degree tend to send fish to sites with high out-degree, potentially boosting the spread of infection and implying a higher basic reproduction number, R_0. On the other hand, a disassortative mixing pattern (i.e., negative coefficient) would be associated with a lower R_0 (Green et al., 2009). Further, we estimated a jackknife estimate of the variance of the assortativity coefficient (Newman, 2003) and used it to obtain a 95% confidence interval (95% CI) around this estimate. We also estimated the correlation between a node's in and out-degree. Again, we used a jackknife estimate of variance (Efron, 1979) of this quantity to estimate a 95% CI, considering that in and out-degree distributions were severely right-skewed.

Summary statistics of centrality measures and distances were stratified by type of farm (broodstock, freshwater, seawater, and fisheries) to evaluate the differences among them. Highly connected areas were identified using a spatial scan statistic for the node centrality measures based on a normal model (Kulldorff et al., 2009).

To assess if the overall network possessed a small-world topology, we estimated its transitivity (clustering coefficient) as estimated by Green et al. (2009), and average path length, both estimates considering the directed nature of the network, and compared these with the same measures estimated for a directed