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Definition of sanitary boundaries to prevent ISAv spread between salmon farms in southern Chile based on numerical simulations of currents

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ABSTRACT

The infectious Salmon Anemia virus (ISAv) is a pathogen that mainly affects the Atlantic Salmon (*Salmo salar*). It was detected in Norway in 1984 and in June 2007 appeared in Chile, producing a drop of more than 30% in the country's production level. It is expected that with certain regularity, outbreaks will continue to appear in Chile without the need of reintroducing the virus from foreign countries. We present a numerical study of the influence of winds and tides in the dispersion of lagrangian particles to simulate the transport of ISAv in the Aysen region, in southern Chile. This study combines the use of numerical models of the ocean and atmosphere, lagrangian tracking and biological aspects of ISAv infections. As in previous results, a wider dispersion of ISAv was observed during spring tides. Temporal changes in wind significantly modified the transport of viral particles from an infected center. Under similar forcing conditions, the areas of risk associated to culture sites separated by a few kilometers could be very different. Our main results remark the importance of the use of a detailed knowledge of hydrographic and atmospheric circulation in the definition of boundaries for sanitary management areas. We suggest that a methodology similar to the one presented in this study should be considered to define sanitary strategies to minimize the occurrence of native outbreaks of ISAv.

1. Introduction

The Infectious Salmon Anemia virus (ISAv) is a pathogen that mainly affects the Atlantic Salmon (*Salmo salar*). Since it was first diagnosed in 1984 in Norway, the ISAv has provoked epizootics in Scotland, Faroe Islands, the east coast of Canada and United States of America. In Chile, the first outbreak was detected in June 2007 and by November 2008 the virus had already spread along 500 km of coastline between 41.5 S and 46.5 S, affecting more than 60% of the country's salmon farms (Katz et al., 2011). One factor that complicates the control of the disease is the genetic variability in the virus. Different strains of ISAv can exist in a fish population, and even within the same fish, each one characterized by different degrees of virulence (Mjaaland et al., 2005; Ritchie et al., 2009). In Norway, where high prevalence of non-virulent strains of ISAv is commonly found (Raynard et al., 2001; Ritchie et al., 2001), the outbreaks have been linked to the mutation of non-virulent strains into virulent ones (Aldrin et al., 2010). In Chile, where sites with high prevalence of the non-virulent HPR0 strain have also been found, it is presumed that the initial outbreak of ISAv probably originated from a *in situ* mutation of the Norwegian strain, introduced a couple of years earlier (Kibenge et al., 2009; Vike et al., 2009). The aforementioned constitutes a scenario whereby, with certain regularity, new outbreaks of ISAv would occur, even without the re-introduction of the virus from outside the country. Under these conditions, eradication becomes extremely difficult, and the control of ISAv in Chile must include a strategy to effectively isolate spontaneous, and unpredictable, outbreaks of the disease (Vike et al., 2009).

The principal mechanism by which fish are infected involves the entry of ISAv through the gills (Totland et al., 1996; Mikalsen et al., 2001). This is possible because the infected fish start to shed viral

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particles in detectable quantities 7 days after the infection has occurred, increasing to massive amounts a few days prior to the fish death (Gregory et al., 2009). Since the particles shed into the sea water maintain their infectious capacity for more than 20 h (Nylund et al., 1994), the disease can spread not only from one cage to another within a salmon farm, but also between farms separated by kilometers (Lyngstad et al., 2008). Operations like the transport of fish, fish remains, or water that has contained infected fish, can make this logistic network an efficient way of viral dissemination between farms (Murray et al., 2002; Scheel et al., 2007). On the other hand, the survival of viral particles in the water also permits dispersion of the disease among sites that are hydrodynamically linked (Jarp and Karlsen, 1997; Gustafson et al., 2007a). Although the relative influence of each of these factors on the development of an epizootics is a subject of debate (Aldrin et al., 2010), it is clear that strategies for controlling each process are of a different nature. When an outbreak is dispersed by a shared logistic network, the actual process of pathogen transport can be controlled. In contrast, in current-based dispersion, because marine currents cannot be changed, the only option left is to modify the location of farms from which ISAv is released, e.g. setting distances between then that are larger than the distances swept by currents over the duration of the infection period.

With the aim of improving epidemiological control throughout the entire fjord zone of southern Chile, the Chilean Fisheries Agency (SUBPESCA) established a system of Sanitary Management Areas (SMA). According to present regulations, farms belonging to the same SMA must coordinate production cycles and comply with common rules regarding maximum densities, therapeutic procedures, mortality disposal, and transport of live fish or fish remains. All these measures are attempts to ensure that logistic networks are shared only within a same SMA, and are isolated from the networks used by farms in other SMA. The limits of each SMA were set up before these rules were discussed. At the core of this decision was the assumption that a separation of 11.1 km between farms belonging to different SMA, effectively prevents dispersion of pathogens by currents. This study aims to contribute relevant information to evaluate that assumption, based on numerical simulations of the transport of viral particles forced by a hydrodynamic model.

2. Materials and methods

Water circulation in the fjord region of Chile (Fig. 1) was simulated using the numerical model ROMS (Shchepetkin and MacWilliams, 2005; Penven et al., 2005). ROMS solves primitive equations of fluid dynamics using the hydrostatic approximation, considering a free surface and sigma (terrain–following) vertical coordinates. A 2D version of this model has already been used for studying circulation in the fjords region of Chile (Aiken, 2008), where an adequate representation of sea level in the zone was obtained. To represent propagation of the tides within the region of the austral fjords, ROMS was implemented on the full domain with a spatial resolution of 1.2 km. The results of this simulation were used to force a sub–model, or subdomain, with an approximate resolution of 0.36 km (Fig. 2), using the ROMS2ROMS tool (Mason et al., 2010). Both domains possess 16 vertical levels, distributed so as to provide a more detailed representation of the surface layer. Bathymetry of both domains was generated with GEBCO_08 (IOC et al., 2003), in a 30 s grid (0.83 km) resolution. This bathymetry was compared with charts 7000 and 8000 of the SHOA (Servicio Hidrográfico y Oceanográfico de la Armada de Chile: Hydrographic and Oceanographic Service of the Chilean Navy). Some of the main channels and straits of the zone of interest were corrected by hand.

Given the vast area of the study zone and the limited hydrographic information available, it was decided to initialize the temperature and salinity fields with information taken from the World Ocean Atlas 2001 data base (Conkright et al., 2002). The same information was used to calculate the geostrophic currents at the open boundaries of the model. Tidal forcing was incorporated through the coefficients calculated by the TPX07 model (Egbert and Erofeeva, 2002). Given that the effect of freshwater discharge from the major rivers in the area was not included, it is considered that the model only represents variations in sea level and barotropic currents, as well as the effect of wind on the surface layers. Initial conditions were derived from the WOA data base and a spin–up time of 4 months was prescribed, during this spin–up time the forcing for the December/September scenario was repeated every month. This was done to develop the high resolution features of the velocity fields that were not present in the initial condition.

To describe the climatological atmospheric forcings, information from the COADS (Da Silva et al., 1994) data base was used, interpolating linearly between monthly climatological averages. Temporal variability of atmospheric circulation was represented using the MM5 atmospheric model (Dudhia, 1993). A domain with a spatial resolution of 27 km (Fig. 1), 23 vertical levels and a time step of 70 s was used. Boundary and initial conditions were obtained from reanalysis (Kalnay et al., 1996) for the simulated months. Physical parameterizations selected included the Grell scheme (Grell, 1993) for cumulus parameterization, the planetary boundary layer MRF (Troen and Mahrt, 1986) and the Dudhia ice scheme for cloud microphysics (Dudhia, 1989). Surface sea temperature (SST) was maintained constant during the simulation period using an optimal interpolated SST corresponding to the week prior to when simulation began (Reynolds and Smith, 1994). The hourly outputs of this model were used to force the free surface of the ROMS subdomain in the scenarios that used this atmospheric forcing (Table 1).

Four physical scenarios were generated, each one was simulated for 30 days to study the potential effect of tide and wind as forcings of surface circulation and, as a result, of the areas swept by the viral particles shed by each salmon farm (Table 1). Although the COADS climatology in the study area shows wind blowing predominantly from the west, it presents significant seasonality in the northern component, with predominant wind from the northwest in winter and the southwest in summer. To include this seasonal variation, a scenario was created where the circulation was forced by late–-winter climatological wind (September) and another scenario, with mid–summer climatological wind (December). On the other hand, given the time scale over which the ISAv retains its infectious capacity, daily variations in wind also could have the potential to significantly modify the areas swept by the particles. This source of variability was included by generating two more scenarios. One of them was forced with MM5 simulated wind, using synoptic boundary conditions extracted from reanalysis for September, 2008. The other scenario, incorporated synoptic conditions for December 2008. These periods were selected because they included the passing of a strong low pressure system (September scenario) and a high pressure system (December scenario) through the study area.

An evaluation of the nested model was carried out by comparing simulated velocities at 10 m depth with ADCP measurements taken at the same depth, between 2008 and 2009, in 5 mooring sites within the study area (Fig. 2, Table 2). Since no meteorological information associated with these measurements is available, it was not possible to quantify the effect that local wind could have on the surface current. It is expected that daily variations in wind may introduce noise in the simulation that would lead to an