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Is between-farm water-borne pathogen dissemination an important driver in the epidemiology of salmonid rickettsial septicaemia in Chile?

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Abstract

Although the bacterium *Piscirickettsia salmonis* has been detected in many salmon-producing countries around the world, losses caused by salmonid rickettsial septicaemia (SRS) are mostly occurring in the Chilean aquaculture industry. Horizontal transmission of SRS between salmonid farms was suggested, based on the existence of spatiotemporal correlation in the level of disease between neighbouring sea farms. However, it remains unclear to which extent between-farm water-borne pathogen dissemination is important in the epidemiology of SRS in Chile. Such information is critical to assess the level of risk of transmission of SRS from one farm to another at different mortality incidence levels and to apply appropriate and cost-effective mitigation measures. In this study, we used weekly SRS mortality data from all salmonid farms in the Los Lagos region between January 2012 and September 2018 to model the spatiotemporal autocorrelation in the SRS-attributed mortality in the study area. A generalized additive regression modelling framework was adopted, using a linear functional component to model the influence of other farms on the target farm. Several nested statistical models were built to compare the significance of different covariates. Predicted values of SRS mortality on the target farm, conditional on different distance, time lag and mortality values from the source farms were estimated from the best model. The results showed that there was a statistically significant association between the weekly mortality incidence at source farms and the mortality incidence at target farms during the same week and during the previous weeks. This study did not provide evidence that the spatiotemporal correlation observed in SRS mortality may be due to water-borne pathogen dissemination between farms and alternative explanatory mechanisms should be investigated. It remains possible that the patterns of lagged correlation observed between source and target farm mortality may be due to a model artefact. In addition, there was no evidence of a threshold effect above which farms pose a substantially larger health risk to their neighbours. Stronger evidence for or against between-farm transmission of *P. salmonis* may be obtained by different methods.

Keywords:

Salmonid rickettsial septicaemia,Atlantic salmon,Rainbow trout,Retrospective study,Spatial correlation

Introduction

Salmonid rickettsial septicaemia (SRS[1]) is an infectious disease caused by the bacterium *Piscirickettsia salmonis*. The disease was first identified in Chile in coho salmon farms in 1989 (Bravo and Campos, 1989), and has since caused substantial losses to the industry in all salmonid species. Although smolt stocks are disease-free at sea entry, a previous study of regulatory data showed that about 80% of production batches will be diagnosed with SRS during the sea production phase (Hillman et al., 2020). The occurrence of horizontal transmission between farms has been suggested in Chile for SRS and other pathogens, as well as for ectoparasites such as sea lice (Rees et al., 2014; Kristoffersen et al., 2013; Price et al., 2017; Arriagada et al., 2017). These suggestions were based on detecting spatiotemporal correlation in the level of disease or infestation between neighbouring sea farms, a phenomenon also called 'infection pressure' by some authors. However, the distances between sites and the site densities for which this correlation poses a substantial health risk have not been characterized. In addition, it remains unclear whether the available evidence of spatiotemporal correlation between farms is due to direct horizontal transmission between farms or to infection by a common environmental reservoir of *P. salmonis*. In the latter case, the SRS mortality on neighbouring farms would be correlated due to such farms sharing similar environmental and spatial characteristics. Under the hypothesis of horizontal transmission between farms, the pathogen circulation could be mediated by a vector or occur via bacteria suspended in the flowing saltwater column. The latter would be possible given the extended survival time of *P. salmonis* in salt water, which can be up to 50 days (Olivares and Marshall, 2010). In addition, the role of wildlife reservoirs is unclear as *P. salmonis* has been identified in native fish species in Chile (Contreras-Lynch et al., 2015).

Comprehensive management of SRS outbreaks requires direct application of control measures in affected farms to limit the local transmission of SRS and hence reduce mortality within a farm. Moreover, control measures should effectively mitigate the risk of SRS spreading from one farm to other farms. The Chilean National Fisheries and Aquaculture Service (Servicio Nacional de Pesca y Acuicultura, Sernapesca) sets regulatory thresholds for SRS mortality incidence rates that, if exceeded, trigger mandatory responses to control outbreaks of SRS and hence reduce the risk of transmission to nearby farms. These regulations rely on the assumption that the infectivity of a farm for neighbouring farms is correlated with the mortality incidence on the infected farm. However, the level of risk of transmission of SRS from one farm to another at different mortality incidence thresholds is yet to be characterized for the Chilean salmon farming industry.

This study was the fifth in a series of epidemiological studies to examine risk factors for SRS and evaluate the effectiveness of interventions to control the disease (Happold et al., 2020a, Happold et al., 2020b; Hillman et al., 2020; Meyer et al., 2019). This work aimed to generate information that supports Sernapesca in evaluating the current regulatory threshold for on-farm interventions (Sernapesca, 2012). Our specific objective in this work was to examine the plausibility of the hypothesis that spatiotemporal correlation of SRS mortality between farms in Chile is caused by water-borne pathogen dissemination between farms.

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