

University of Prince Edward Island

Faculty of Veterinary Medicine
Summary of Dissertation

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Modeling sea lice dispersal from salmon farms in the Broughton Archipelago, British Columbia, Canada

Here we present results from a sea lice dispersal study, which simulated larvae releases from 20 salmon farms in the Broughton Archipelago, British Columbia, Canada. This was done by utilizing a coupled biological and physical model for a time period of wild salmon smolt out-migrations (March - July), simulating the physical conditions of 2009. The output from the physical model was then used as input for a particle-tracking model. Each of the 20 salmon farms simulated a release of 50 particles every hour for 129 days. The particles were also assigned a biological model, mimicking “pre-parasitic” nauplii maturing into parasitic copepods.

From this output, the connectivity patterns through space and time were analyzed. The underlying pattern of connectivity showed certain clusters of farms strongly connected via biologically-modeled particles. There were also some farms that had low connectivity to all other farms. There was high temporal variability in the farm connectivity, with overall low connectivity for the study period, interrupted with pulses of high connectivity. These pulses coincided with warming events. Thus, it would be ideal to manage the farms with a plan for these spikes. Furthermore, the sea lice larvae’s survival was suppressed throughout the simulation due to the freshet event, where the snowmelt from the surrounding mountains deluged the fjords of the BA. The fresh, cold water of the freshet acts as a sea lice control aid, and highlights the risks associated with the possible loss or lessening of the freshet event due to climate change. Finally, we found support for the simulation’s patterns in the observed sea lice abundance data set. The similarities provided some confidence in the reliability of the simulation and thus the management recommendations that emerged from the analysis. Additionally, the methodology employed here could be applicable to many questions around marine disease dispersal pathways.