Transmission Dynamics of Parasitic Sea Lice from Farm to Wild Salmon

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Parasitic sea lice infestations of juvenile salmonids have been correlated with salmon farming and are concurrent with declines in affected populations, worldwide. However, these relationships are correlative only and their causal nature is unclear. Scientific understanding and consensus has largely been limited by an inability to track parasite movement from farmed to wild salmon.

This report looks at lice infestations on wild juvenile pink and chum salmon as they migrated past an isolated salmon farm down a long and narrow migration corridor in the Broughton Archipelago, British Columbia, Canada (see Box 1). Mathematical models were used to analyze these data (see Box 2) and revealed juvenile salmon were initially infected with sea lice originating from two host populations: farm salmon and naturally occurring hosts. The calculations suggest the infection pressure near the farm was approximately 70 times greater than natural ambient levels and exceeded ambient levels for 30 km of migration route (see Box 3). This amounts to a total direct contribution of sea lice from the farm that was approximately 30,000 times greater than the natural production of sea lice in the length of habitat occupied by the salmon farm.

The results also show that once lice were transmitted to wild juvenile salmon, they were transported down the migration route where they reproduced and re-infected the wild juvenile salmon. Inclusion of this second generation of lice raises the farm-origin infection pressure above natural levels for approximately 75 km of migration route resulting in a total direct and indirect contribution of sea lice that was 200,000 times greater than the natural production of sea lice in the length of habitat occupied by the salmon farm. This transport and reproduction of farm-origin lice raises the possibility for disease growth and spread to other wild salmon populations up and down the coast.

Sea Lice (*Lepeophtheirus salmonis* and *Caligus clemensi*)
Sea lice have two distinct phases in their lifecycles – planktonic and parasitic. Planktonic larvae float freely in the water and allow lice to be transmitted between wild and farmed salmon. During the second, parasitic phase, lice attach themselves to a host salmon and feed on the surface of the fish – leading to increased disease and sometimes death in their infected hosts (See Box 2).

Scientific Conclusions

The peer-reviewed primary scientific literature on sea lice interactions between wild and farmed salmon in British Columbia makes the following conclusions: (1) infection rates on wild juvenile pink salmon were greater in salmon farming regions than in regions without salmon farms[1]; (2) within a salmon farming region most lice on wild juvenile pink and chum salmon originated from farmed salmon[2]; and (3) transmission of lice from farmed to wild salmon leads to population growth and spread of lice in wild salmon populations. Salmon aquaculture likely has negative impacts on wild salmon populations and the next scientific challenge is to quantify this impact.

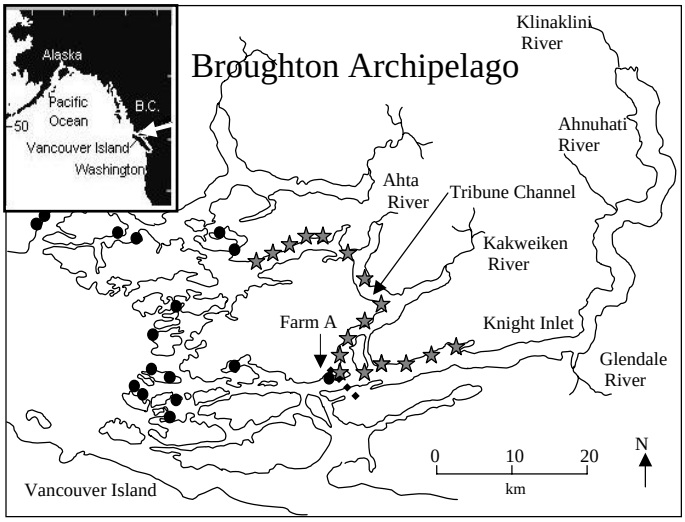
Policy Implications

There is sufficient scientific evidence to compel precautionary action by regulators. The premise of industrial-scale open net aquaculture in wild salmon habitats needs to be reconsidered and the proposed expansion of the industry throughout BC must be halted until the full ecological costs of this industry are understood. There is a clear potential for severe and irreversible damages to be inflicted upon wild salmon populations and their dependent cultures, ecosystems, and economies.

References

[1]Morton, A., Routledge, R., Peet, C., & Ladwig, A. 2004 Sea lice (*Lepeophtheirus salmonis*) infection rates on juvenile pink (*Oncorhynchus gorbuscha*) and chum (*O. Keta*) salmon in the near shore marine environment of British Columbia, Canada. *Canadian Journal of Fisheries and Aquatic Sciences.* 61, 147-157.

[2]Krkošek, M., Lewis, M. A., & Volpe, J. P. 2005 Transmission dynamics of parasitic sea lice from farm to wild salmon. *Proceedings of the Royal Society of London Series B.*



Box 1. Study Area

- ✶ **Sample sites**,
- **Active salmon farms**

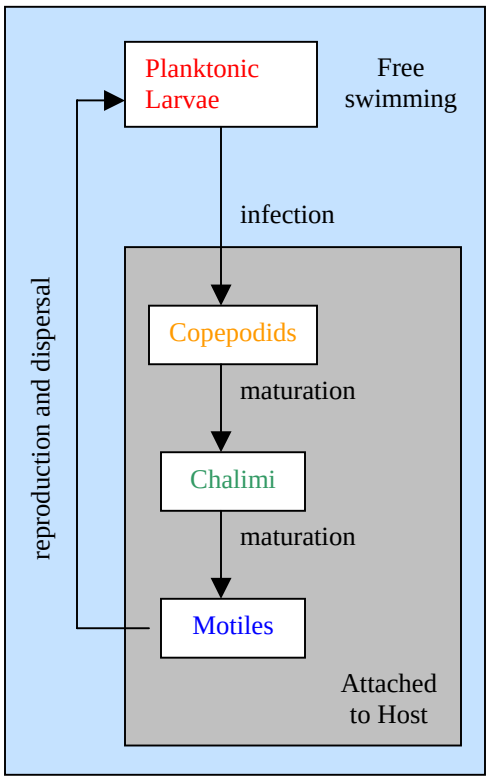
Salmon Migration Juvenile pink and chum salmon originate in freshwater streams in Knight Inlet. They must then travel south and west down the inlet toward Tribune channel and either continue down Knight Inlet or travel through Tribune Channel on their way to sea.

Sample Sites Farm A is the first salmon farm juvenile salmon would encounter along their migration and is the focus of this analysis. presented here.

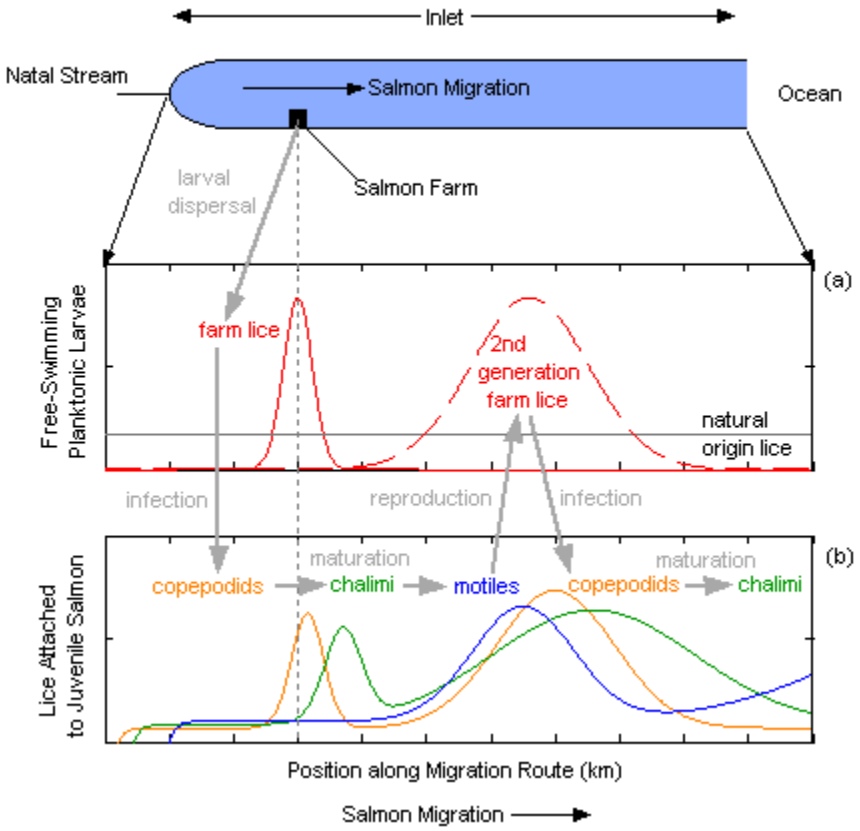
Data All sites were sampled within a 14 day period in May 2003 resulting in a high resolution dataset of sea lice infection levels on juvenile pink and chum salmon as the passed an isolated salmon farm (Farm A). Please refer to the source paper[iv] and Krkošek et al 2005b[v] for the full methodology and analysis.

Box 2. Louse Lifecycle and Transmission Dynamics

Louse Lifecycle



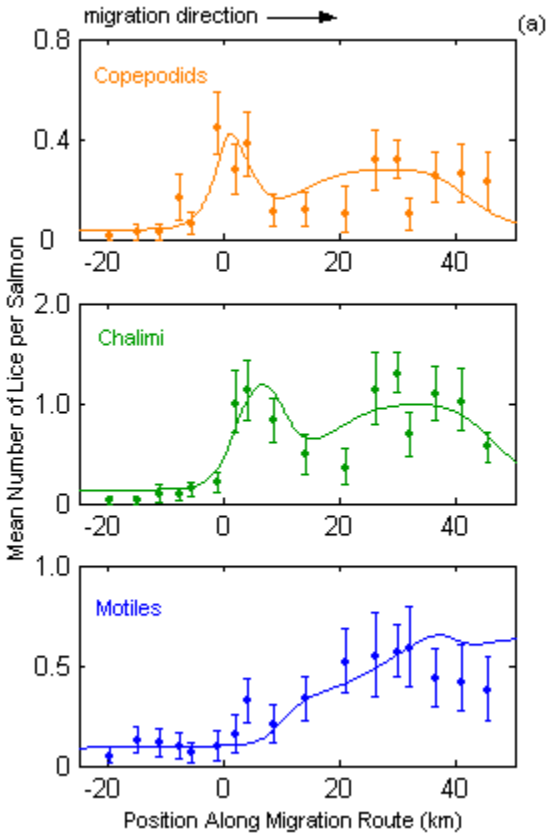
Transmission Dynamics Model

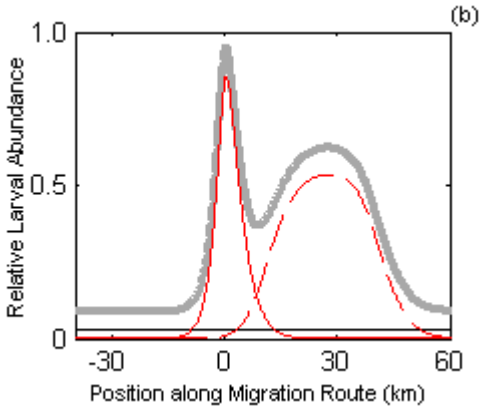


Life Cycle The two main stages are free-swimming planktonic larvae and attached parasites. Free-swimming larvae must attach to a host fish and the first attached stage is the copepodid (orange), which then develops through chalimus (green) and motile (blue) stages. Motile lice include sexually reproductive adults whose progeny are released into the water column as planktonic larvae, completing the lifecycle.

Transmission Dynamics The model combines the sea lice lifecycle with interactions among farmed salmon, alternate natural hosts, and wild out-migrating juvenile salmon. The graphs illustrate how juvenile salmon, which enter the marine environment free of lice, migrate past salmon farms and are infected with sea lice. The second spike in lice is from reproduction by the farm-origin lice on the wild fish, after the wild fish have moved on past the farm.

The transmission dynamics of lice between farmed and wild juvenile salmon follow the progression shown by the thick grey arrows. Larvae are produced by farmed salmon, disperse into the surrounding environment, infect juvenile salmon, and subsequently mature and reproduce on the wild fish.





Box 3. Model Predictions Agree With Field Data

Panels (a) on the left show actual louse abundances on juvenile pink and chum salmon as they passed Farm A, located at x=0. Points with 95% confidence bounds correspond to field data and the solid lines are the best fit of the model to the data.

Graph (b) shows the model's inferred origins and spatial profiles of sea lice larvae that would be required to produce the patterns seen in the data (a). The red lines depict the location and relative abundances of planktonic larvae whose origin can be traced back to farmed salmon either directly or through one generation of lice.