Differential Infection of Juvenile Pacific Salmon by Parasitic Sea Lice

Cole B. Brookson[1], Brian P. V. Hunt[2], Sean C. Godwin[3], Martin Krkošek[1,4]

Background

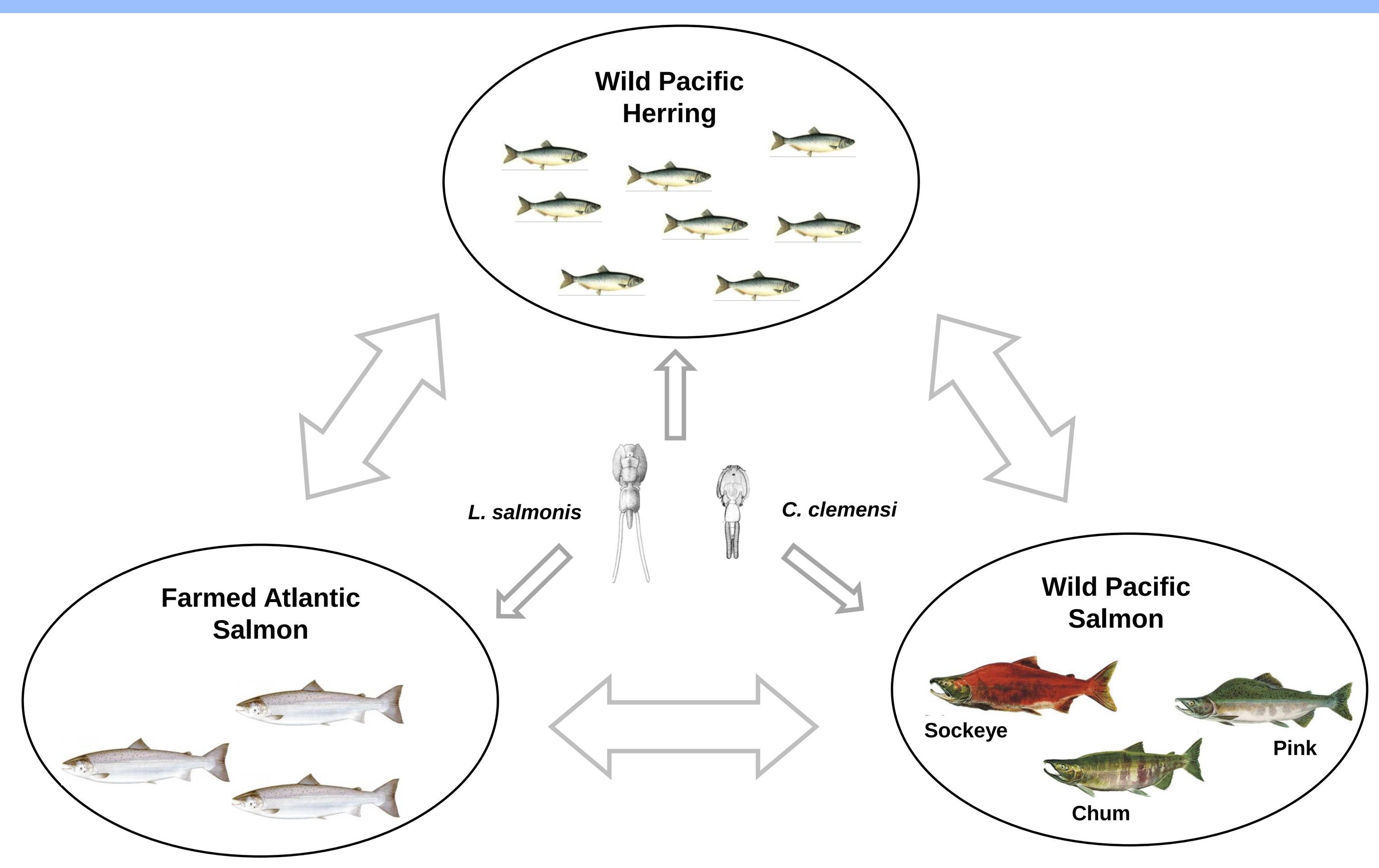

Figure 1: Study system depicting the various infection pathways of ectoparasitic sea lice onto sympatric fish species

Study Goals:

1. **Investigate differential parasite loads of *C. clemensi* and *L. salmonis* on pink, chum, and sockeye salmon**
2. **Determine what factors contribute to the differences in infection across different regions**

Figure 2: Adult lice on juvenile salmon

Methods

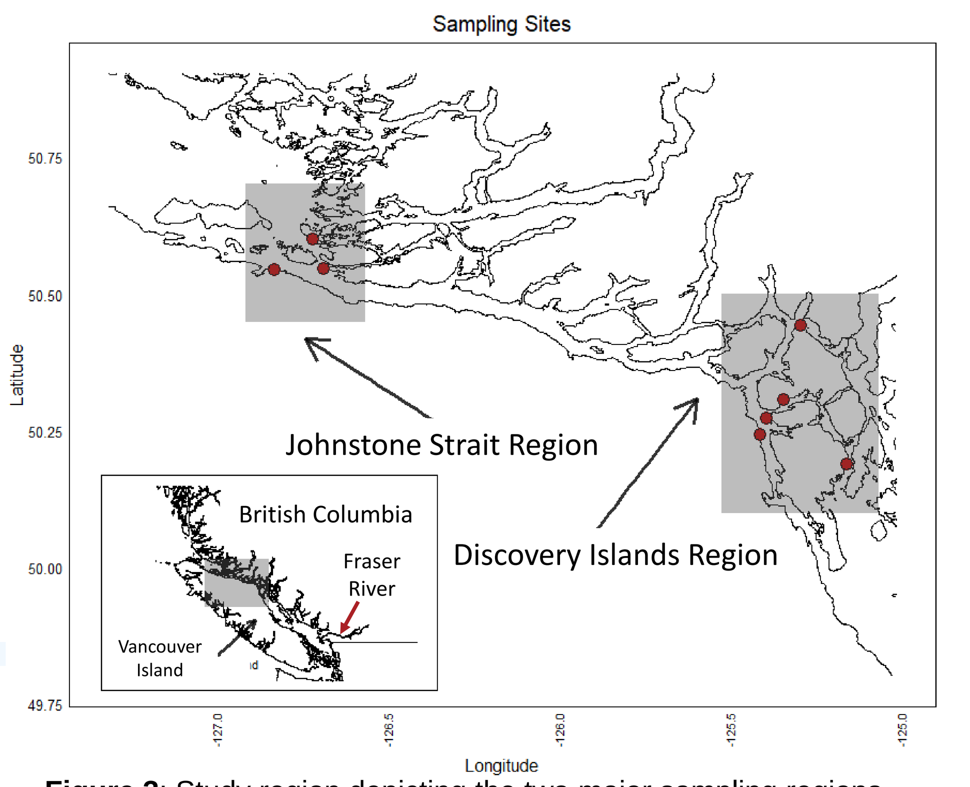

Figure 3: Study region depicting the two major sampling regions

Figure 4: Juvenile salmon sampling, Johnstone Strait, 2016

Field Sampling

- Individuals were sampled from May to July (2015 – 2018), in the Discovery Islands and Johnstone Strait
- Fish were measured and worked up for sea lice

Analysis

- GLMMs parsed out *species-level* and *region-level* differences in parasite loads
- Models were compared/selected based on AIC
- Hierarchical bootstrapping confirmed model predictions

Species-Level Results

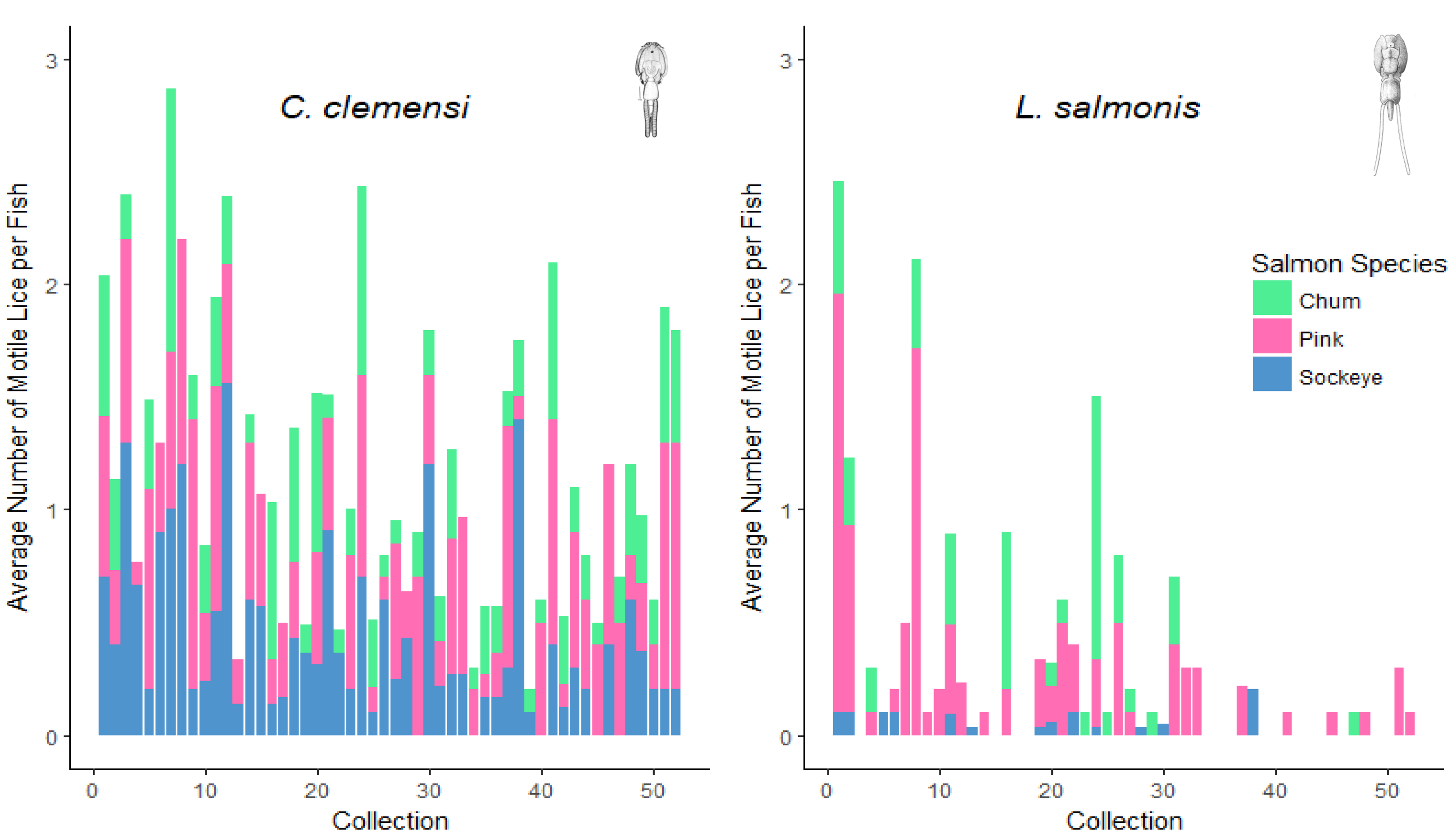

Figure 5: Average number of lice per fish in each collection, divided by louse species, and fish species. The two lice species are present at different abundances across all collections, with *C. clemensi* present ubiquitously and *L. salmonis* thinly dispersed across collections. Motile lice are adult lice that are easily identifiable by species.

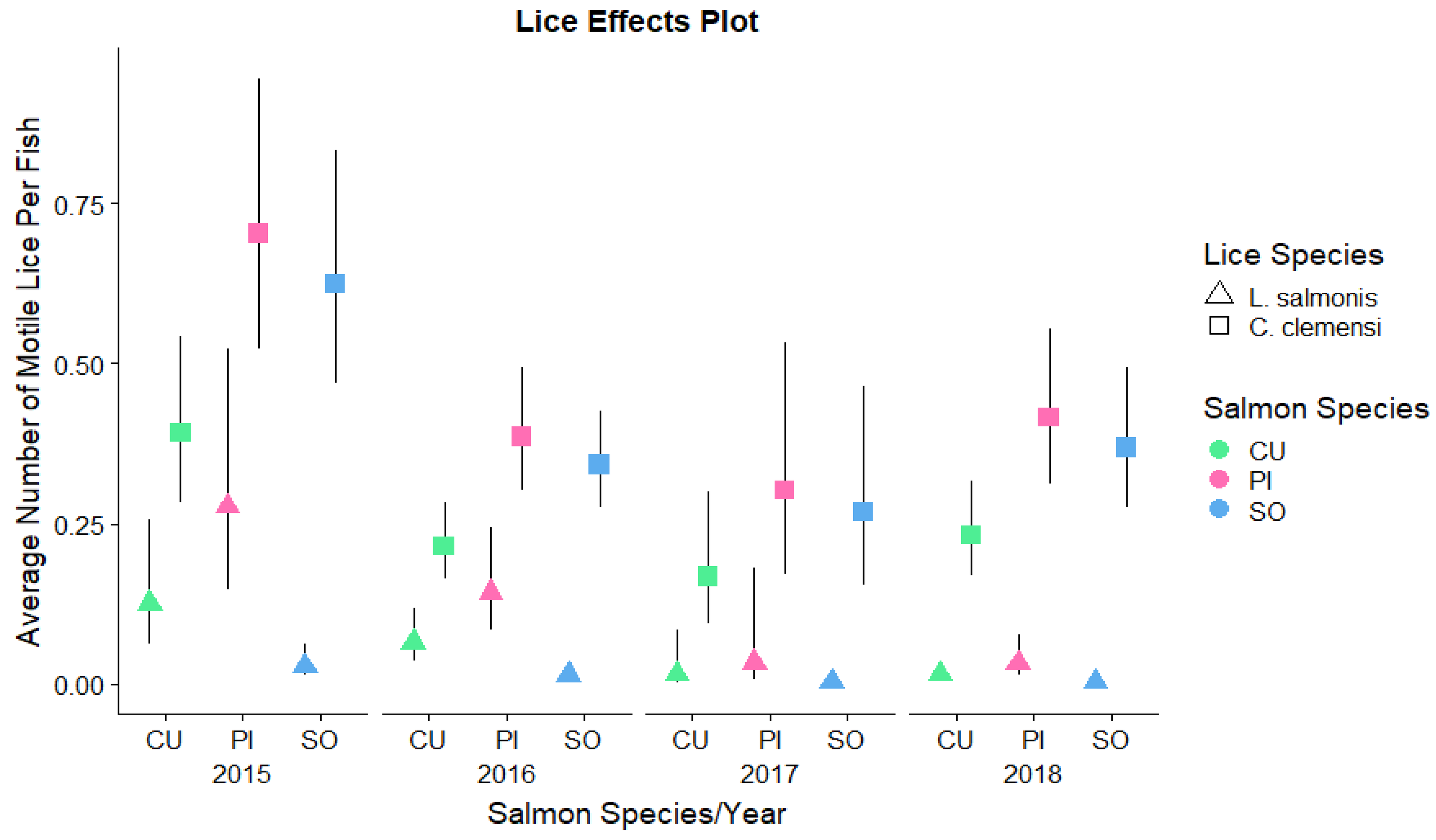

Figure 6: Estimated number of lice per fish for *C. clemensi* & *L. salmonis* calculated by back-transformation, divided by sampling year, as well as by salmon species, and grouped by site region. Pink salmon (PI) show highest estimated lice loads for all years and both lice species, with sockeye (SO) also showing high loads of *C. clemensi* and chum (CU) showing the lowest infection from both lice. 2015 shows higher parasite loads for almost all species combinations.

Table 1: AIC table for full model set. The full model fit our data best for both species of lice.

C. clemensi Model	Negative Log Likelihood	AIC value	Delta-AIC value	*L. salmonis* Model	Negative Log Likelihood	AIC value	Delta-AIC value
Null	-1509.7	3025.5	27.9	**Null**	-461.3	928.7	75.8
Year	-1502.8	3017.7	20.1	**Year**	-452.4	916.7	63.9
Species	-1497.3	3004.7	7.1	**Species**	-427.8	865.7	12.8
Species, Year	-1490.7	2997.6	0.0	**Species, Year**	-418.4	852.8	0.0

Region-Level Results

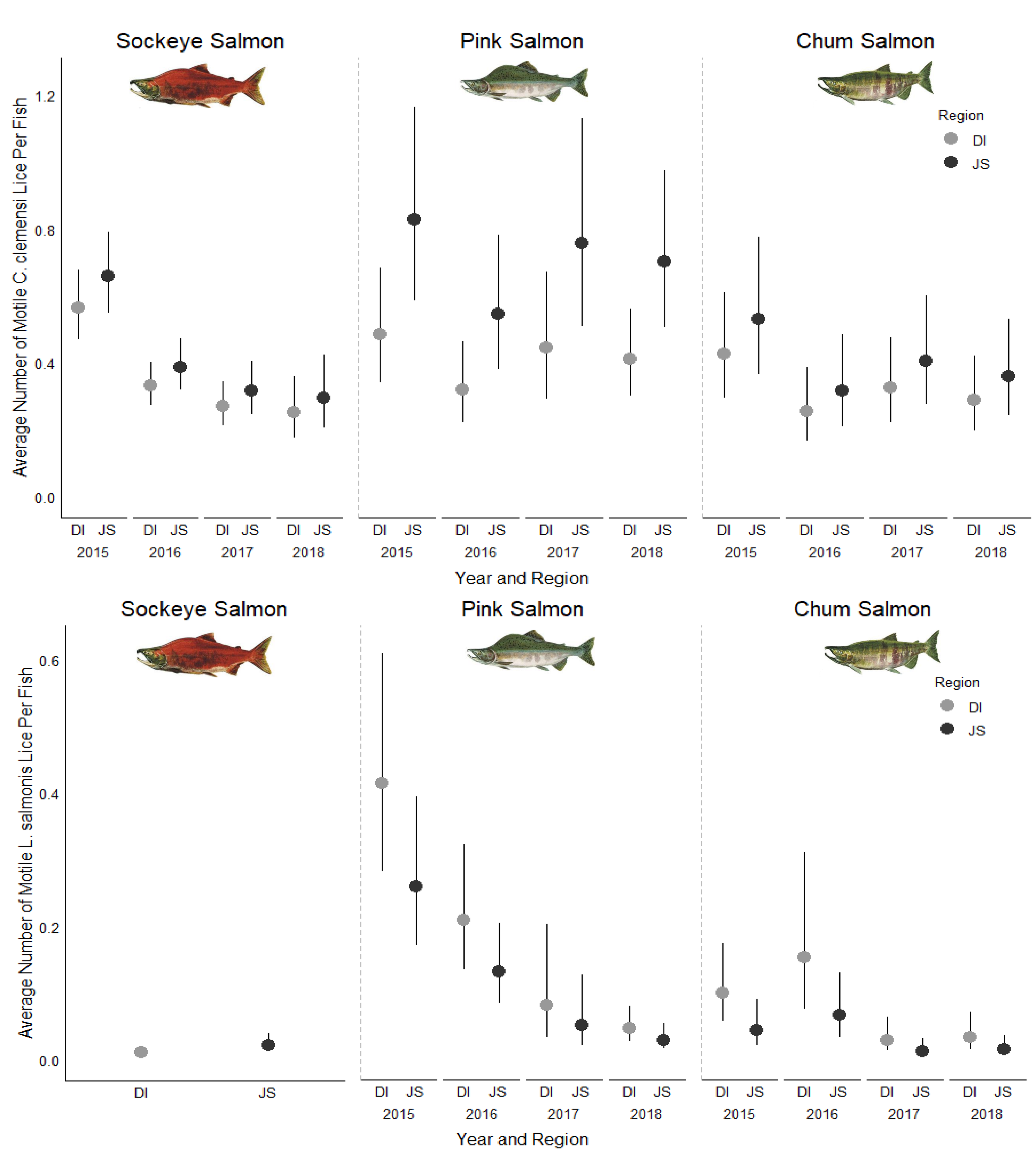

Figure 7: Estimated number of lice per fish for *C. clemensi* & *L. salmonis* in each region, according to the respective best fitting model. Parasite prevalence differed between sites in nearly every species comparison. AIC scores indicated the full model fit best for all data except Sockeye/*L. salmonis*. Discovery Islands (DI) showed higher estimated per-fish louse abundance for *C. clemensi* than for Johnstone Strait (JS), with the opposite in *L. salmonis* except Sockeye.

Conclusions

- **Sea lice show different infection pressures on different salmon**
- **Inverse region-level differences between lice species indicates that Herring might play a larger role than previously thought in determining infection pressures**
- **Basic infection patterns were consistent across years indicating internal dynamics are driving infection patterns**

Acknowledgements

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Citations -- 1. Hunt et al. 2018, *Juvenile Salmon Program;* 2. Johnson & Albright, 1991. *J. Mar. Biol. Assoc. UK;* 3. Costello, 2006. *Trends Parisitol;* 4. Krkosek et al. 2007. *Science*

Affiliations:

1: Department of Ecology & Evolutionary Biology, University of Toronto, Toronto, Ontario, Canada
2: Department of Earth, Ocean, and Atmospheric Sciences, University of British Columbia, Vancouver, BC, Canada
3: E2O Research Group, Department of Biological Sciences, Simon Faser University, Burnaby, BC, Canada
4: Salmon Coast Field Station, Simoom Sound, British Columbia, Canada