**Methods**

To test whether *Lepeophtheirus salmonis* (hereafter called ‘sea lice’) are associated with reduced productivity of pink and chum salmon populations in Kitasoo-Xai’xais (KXx) territory, we will couple spawner-recruit data from the North and Central Coast of British Columbia (BC) with sea-louse infestation data from wild and farmed salmon in KXx territory, and employ a similar hierarchical Ricker spawner-recruit analysis to those used by Krkosek et al. (2011) and Peacock et al. (2013, 2014).

***Data sources***

Our analysis will use three datasets: 1) a sea-louse monitoring dataset from the salmon farming company MOWI, which will provide total sea-louse counts on Atlantic salmon farms in KXx territory throughout their years of operation (from 2001 through 2019); 2) a sea-louse monitoring dataset from the KXx Nation, which is comprised of sea-louse counts on out-migrating juvenile pink and chum salmon in KXx territory from 2005 through 2019; and 3) a spawner-recruit dataset from the Pacific Salmon Foundation (PSF), which includes annual estimates of spawner and recruit abundances for streams in DFO management areas 3 to 9 (i.e., the mainland North and Central Coast of British Columbia, Canada) for 1954 through 2015 brood years for pink salmon and for 1954 through 2012 brood years for chum salmon. If, prior to publication of our analysis, the PSF dataset is updated to include more recent brood years, we will include these in our analysis.

The sea-louse counts in the MOWI dataset were collected by industry staff in a standardized manner as mandated by the license conditions of the farms. For each counting event, at least 20 stocked fish were collected in three net pens by seine net. The captured fish were then anesthetized in a bath of tricaine methanesulfonate (TMS or MS-222) and assessed for sea lice by eye. These counts focus on the motile (i.e., pre-adult and adult) life stages rather than the attached juvenile stages of the lice.

The detailed field-collection and louse-enumeration methods for the KXx dataset are described in Butterworth et al. (2008) and Saksida et al. (2011). Briefly, juvenile pink and chum salmon were captured by beach seine (15 m x 2 m, with 6 mm and 13 mm mesh in the bunt and tow, respectively) throughout KXx territory (Fig. 1) from 2005-2009. Between 10 and 100 juvenile salmon from each collection were euthanized and frozen in a ZiplocTM or Whirl-Pak® bag. The frozen samples were transported to the BC Centre for Aquatic Health Sciences in Campbell River, BC, where they were assessed for sea-louse infestation by dissecting microscope. The sex, life stage, and species of each louse were identified by trained technicians. We will exclude the 2005 sea-louse data from our analysis because they provide a small and unrepresentative sample for that year (n = 194 fish from two sites).

The spawner and recruit estimates in the PSF dataset were generated using the North and Central Coast escapement, age, and exploitation-rate data from the Pacific Salmon Explorer (Pacific Salmon Foundation 2020), which relies on DFO datasets. The PSF dataset is the only one that provides coastwide spawner-recruit data via a standardized approach and it will be regularly updated, allowing for updates to our analysis. Spawner-recruit data for each stream were generated by coupling escapement data from DFO’s New Salmon Escapement Database System (NuSEDS) with Conservation Unit-level exploitation rate data from English et al. (2018). Age composition of each year’s returns was assumed to be constant among years and among streams within a Conservation Unit (English et al. 2018). The proportion of chum spawners returning at age six was assumed to be zero in order to maximize the length of the time series; the actual proportion of age-6 spawners was <1% for all the Central Coast Conservation Units (mean = 0.2%). The KXx Nation may be able to provide an additional spawner-recruit dataset that estimates recruit abundance using local estimates of catch appropriate for each watershed in KXx territory rather than a conservation-unit-level exploitation rate applied to each watershed (L. Greba pers. comm). If we are provided this dataset, we will re-run our analyses using the KXx spawner-recruit data for KXx streams and the PSF spawner-recruit data for non-KXx streams (for which the more detailed estimates are unavailable). We will compare the results from this updated analysis to those from our original analysis using the PSF dataset, drawing inference from both analyses with the appropriate caveats.

***Data analysis***

We will estimate the total number of adult female sea lice on farmed fish in KXx territory prior to the juvenile outmigration by multiplying the averaged MOWI counts of lice per fish in March and April (contingent on data quality and migration timing) by the number of stocked fish, and then summing across all active farms. To examine the relationship between lice on wild and farmed fish, we will regress the estimated abundances of lice on wild juvenile salmon with the estimated total number of adult female lice on farms using data transformations as necessary to ensure normality of the residuals.

We will estimate the mean number ofsea lice on wild juvenile salmon in KXx territory for each year from 2006-2019 using the hierarchical modelling approach presented in Bateman et al. (2016). This approach is designed to account for inter-annual variation in sampling, unbalanced sample sizes, and repeat sampling (pseudoreplication). The associated generalized linear mixed-effects model (GLMM) will include fixed effects for year and louse stage and random effects for week-of-year (to account for spatially coherent seasonal variation in louse counts) and location-year combination (to account for infestation variation among locations due to farm activity or environmental factors). The model will be fit using Bayesian tools and will employ a negative binomial error distribution to account for parasite clustering, a log link function, and uniform priors. We will pool pink and chum salmon observations as in Bateman et al. (2016) because the salmon-species data are missing or inaccurate for 2006-2008 in the KXx sea-louse dataset. To ensure pooling does not introduce bias into the sea-louse estimates, we will first generate the estimates separately for pink and chum salmon for 2009-2019; if these estimates are comparable between salmon species then we will pool the 2006-2019 data conventionally; if not, we will employ a species-correction factor when pooling the data.

If the relationship between wild and farmed sea lice is clear, we will impute the wild-salmon sea-louse estimates by generating predicted abundances of lice on wild salmon for 2001-2005 using the farm sea-louse data, and we will gauge sensitivity of spawner-recruit analysis results to this imputation by comparing a wild-count-only model to a model where all sea-louse estimates have been replaced by their imputed values.

We will pre-screen the spawner-recruit estimates, excluding populations (i.e., species-stream combinations) with fewer than 18 spawner-recruit data pairings across the time series. Since pink salmon have genetically distinct odd- and even-year lineages due to their obligatory two-year life cycle, we will analyse even- and odd-year runs separately for each stream, as is standard practice (Dorner et al. 2008, Irvine et al. 2014). We will also ignore measurement error associated with spawner observations as in Peacock et al. (2013, 2014) because this allows us to use the same modelling framework as found in previous work, and more elaborate (e.g. state-space) models would be unlikely to substantially improve parameter estimates (Su and Peterman 2012).

We will model salmon productivity separately for pink and chum salmon using a hierarchical Ricker spawner-recruit model as in Peacock et al. (2013, 2014):

(1)

where is the spawner abundance in population (i.e., species-stream combination) *i* in brood year *t*, is recruit abundance for fish spawned in brood year *t*, *a* is the mean Ricker productivity parameter, is population-specific density dependence, and is the estimated mortality of salmon due to sea lice. We will fit the model using a Bayesian approach with Monte Carlo (MC) fitting methods and uniform priors in R (R Core Team 2020) using the package RStan (Stan Development Team 2020).

The model will follow previous work (Peacock et al. 2013, Peacock et al. 2014) and account for environmental stochasticity and synchrony in productivity among populations at larger scales using four random effects: 1) , the spatially coherent year-to-year variation common to all populations, 2) , the temporally coherent population-to-population variation, 3) , the temporally coherent variation among genetically distinct sets of populations called Conservation Units (Holtby and Ciruna 2007, Fisheries and Oceans Canada 2020), and 4) , the variation common to populations within management areas in a given year. The residual variation, , represents random noise (attributed to deviations due to return-rate mis-estimation, natural environmental variability, and model form) that is independent across populations and years. The random effects and residual variation will each be random normal variables of mean zero and variance to be estimated.

We will test for an effect of sea-louse infestation on salmon productivity using the covariate , which represents parasite exposure for exposed population *ie* in year *t+1* (i.e., the year that juvenile pink and chum salmon emerge from freshwater and migrate past salmon farms). As in Peacock et al. (2014), we will examine two different forms of this covariate: 1) the estimated total number of adult female sea lice on salmon farms in April, and 2) the estimated average number of sea lice (of all stages) on wild juvenile salmon. While the second form of the covariate is intuitive, as it is a direct measure of infestation on wild salmon, the first form may better reflect parasite exposure if wild salmon have high mortality rates from infestation. The latter would occur if high louse counts on wild fish induce mortality during out-migration, therefore rendering high louse loads unobservable. We will be unable to estimate sea-louse abundances on wild juvenile salmon in the region prior to 2001 due to a lack of data, but small-scale Chinook farming did occur in KXx territory in 1993-1995, and Atlantic salmon farming began there in 1999. Consequently, we will treat as missing data for 1993-1995 and 1999-2000 (i.e., we will exclude the 1992-1994 and 1998-1999 brood years for exposed populations from the analysis). In the years when no salmon farming occurred in KXx territory, all populations will be classified as ‘baseline’ (but will still be subject to population-, region-, and year-specific variation in the model). While *L. salmonis* do infest wild juvenile salmon in non-farming regions of BC, their prevalence and abundance are extremely low (Beamish et al. 2009), especially on the Central Coast (Gottesfeld et al. 2009); we will therefore follow Peacock et al. (2013) in assuming that, for both forms of the covariate, is equal to zero for baseline populations and the variation associated with background louse levels in wild salmon will be accounted for in the random effects. For both forms of the covariate, the strength of the relationship between parasite exposure and overall salmon survival will be determined by the parameter *c*, and the estimated percentage mortality due to sea lice, in fish that would otherwise return to spawn, will therefore be equal to (Krkosek et al. 2011, Peacock et al. 2013).

In the absence of the detailed hydrodynamic modelling available for other salmon-farming regions (e.g., Stucchi et al. 2011, Foreman et al. 2012), we will be conservative in our classification of populations to ensure that we do not classify baseline populations as exposed. A population will be considered exposed in a given year if its juvenile salmon are forced to pass within 20 km of an active salmon farm. In the Broughton Archipelago, BC, salmon farms are associated with increased infestation pressure on wild juvenile salmon for 30 km (Krkosek et al. 2005, Krkosek et al. 2006). Exposure designations for populations may change year to year based on the location of active salmon farms in the region. Depending on hydrodynamics, farm louse abundances, and migration direction, some populations that may be exposed to sea lice from salmon farms will be conservatively classified as baseline in our analysis. Consequently, we will also identity ‘potentially exposed’ populations whose juvenile salmon *may* swim within 30 km of an active salmon farm. We will examine the distributions of of the potentially exposed populations post-hoc, and if these are clustered and generally negative we will infer a possible louse effect. We will then re-fit the model with an additional *cp* louse-impact parameter for potentially exposed salmon populations and report associated results alongside the primary results (i.e., those from the original model fit). Regardless of the estimated louse effect on salmon survival, we will perform a similar power analysis to the one performed by Peacock et al. (2014) to determine our statistical power to detect a louse effect if it indeed existed.

As a secondary analysis, we will determine whether wild juvenile salmon with more sea lice have lower body condition in KXx territory using the length and weight data in the KXx dataset. Juvenile salmon, like most fish, have a tight log-log length-weight relationship (Perry et al. 1996, Wechter et al. 2017). We will fit seven mixed-effects models to the log-weight data with different combinations of potential louse correlates. The null model will have fixed effects for log-length and species, as well as random effects for site and for week-of-year nested within year. The six additional models will have the same fixed- and random-effects structure as the null model, plus different combinations of four sea-louse covariates. These four louse covariates will be: 1) *L. salmonis* abundance, 2) motile *L. salmonis* abundance, 3) *C. clemensi* abundance, and 4) motile *C. clemensi* abundance. Four of the models will have just one louse covariate, another model will have both the *L. salmonis* and *C. clemensi* abundance covariates, and the final model will have both the motile abundance covariates. The error distribution of the models will depend on the data. We will perform model selection using the Akaike Information Criterion (Akaike 1974).

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