Comparison of juvenile pink and chum salmon foraging ecology, behaviour and interactions during early marine migration through dynamic regions of coastal B.C. (*Thesis title*)

**Chapter 1:** Trophic interactions and foraging ecology of juvenile pink and chum salmon across a range of ocean conditions along their coastal migration route (*i.e.* ***SPATIAL*** *DATA CHAPTER*)

* 1. **Introduction**

Pacific salmon species have complex life history strategies that impact survival from smolts to adults, and species interactions during the early marine phase are still not well understood. Pink salmon are the smallest salmon to begin the marine migration (as small as 0.2 g \*), due to their short, restricted life cycle of two years. Chum salmon are the second smallest species when leaving freshwater habitats, with various amounts of time spent rearing in estuaries. Smaller salmon smolts are often the most vulnerable to predators and require sufficient food resources to grow to a critical size during this period to survive their first winter in the ocean.

Pink and chum salmon have the highest abundance and biomass (respectively) of all five Pacific salmon species and pink have shown competitive dominance over food resources. (\*) Many studies have found biennial patterns in planktivorous species growth and survival, indicating competition with pink salmon over and above oceanic trends in food availability. (\*) Although, only a few studies have investigated pink salmon and other species diet contents and interactions in depth across spatial and temporal scales with varying ocean factors such as temperature, salinity and levels of mixing. (\*) Furthermore, chum salmon have shown to prey shift in times of low food availability, demonstrating consistent foraging strategy flexibility. (\*) Chum salmon have been shown, in different life stages and all across the Pacific Ocean, to consume gelatinous prey items such as jellyfish, which tend to have lower nutritional content than other types of zooplankton. Comparing multiple species diets can determine how animals can co-exist in the same environment and utilize the prey resources competitively or neutrally.

The migration pathway of Discovery Islands and Johnstone Strait is a long and arduous portion of the route for Pacific salmon through the Strait of Georgia towards the open ocean.

This research study aims to understand and characterize the relationships between ocean conditions, juvenile pink and chum salmon diets, and interactions between species. The salmon migration route of Discovery Islands and Johnstone Strait is a highly dynamic coastal environment, providing a suite of conditions to compare the diets of pink and chum. Oceanic conditions influence prey availability and thus, resource partitioning between species reveals different foraging strategies of each species and their relationships to the environment.

Furthermore, comparing stomach fullness of juvenile pink and chum salmon across a large section of early migration route can show foraging hot spots and more challenging pathways. Therefore, this study will describe juvenile pink and chum salmon ecology and interactions across a migratory path with varying amounts of ocean mixing and foraging opportunities.

* 1. **Methods**
     1. **Field sampling**

Field sampling was performed as part of the Juvenile Salmon Program, a collaboration between the Hakai Institute, the University of British Columbia and Salmon Coast Field Station. Annual sampling of juvenile salmon, zooplankton tows and oceanographic data is executed every May to July during the outmigration of salmon. The Discovery Islands region is sampled annually from the Hakai Institute research station at Quadra Island and the Johnstone Strait area is sampled by the Salmon Coast Field Station, situated near Echo Bay in the Broughton Archipelago.

* + 1. **Stomach content analysis**

The stomach content analysis protocol is similar to the UBC/Hakai protocol methods outlined and described in King et al., 2018. Following extraction and preservation of stomachs by Hakai at the Quadra Island research station, it was transported to UBC and processed by me. The first step was to remove the stomach from the 95% ethanol, blot with a paper towel and store in water for 30 minutes to rehydrate before processing to make the sample less brittle. Weights were taken of the full stomach before dissection, the food contents after removal and the empty stomach lining, weighed on an analytical balance to the nearest 0.01 milligrams. (\*) A visual estimate of fullness was recorded (in 25% increments) but gut fullness indices were calculated from food bolus weight divided by the weight of the fish for a quantitative measure.

The prey items were sorted in groups according to species (or as close to species as possible), digestion state (an index from 1-4: fresh, semi-fresh, partially digested and fully digested), life stage and size class of prey (<1 mm, 1-2 mm, 2-5 mm, 5-10 mm and >10 mm). Each prey grouping was then enumerated, measured for minimum and maximum length using an ocular micrometer in the microscope, photographed for future reference and then weighed. The contents were then preserved and stored in ethanol for potential future DNA extractions.

* + 1. **Data analysis**

Stomach content data was recorded in a notebook and input into a csv file and all the oceanographic data was provided by the Hakai Institute (<https://github.com/HakaiInstitute/jsp-data>). Data transformations, analysis and visualizations were all performed in R (version 3.6\*). Full taxonomic details of prey were included in the multivariate statistics, unless prey occurred in less than 3 stomachs, in which case that prey group was grouped in with the higher taxa level (for example, if only one *Acartia clausi* was found, it would be merged in with the *Acartia spp.*).

Proportional wet weight (biomass) of prey was used over abundance in the analysis due to the high prevalence of gelatinous prey which could not be accurately enumerated and thus would be lost in any measures of abundance metrics. The data was transformed using an arc sine square root transformation, common for proportional data metrics to correct skewed data. Bray-Curtis dissimilarity metrics were then calculated for clustering and ordination analyses, to determine and visualize the differences in diets between the salmon species, sites and regions.

* 1. **Results**
     1. Stomach fullness

* + 1. Dietary composition

* + 1. Species comparison

* + 1. Environmental variables

* 1. **Discussion**
     1. Resource partitioning

* + 1. Survival implications

* + 1. Limitations

* 1. **Conclusion**