Do salmon aquaculture sites alter wild fish communities in the Broughton Archipelago?

by

Dane Stabel
B.Sc., University of British Columbia, 2005

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in the School of Environmental Studies

Supervisory Committee

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Dr. Thomas A. Okey (School of Environmental Studies)
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Abstract

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Open net-pen aquaculture allows for free exchange of materials between farm and wild environments. Increased habitat complexity in the form of farm infrastructure produces effects similar to fish aggregating devices and artificial reefs, altering the distribution and abundance of fish species within the greater area. The continuous input of nutrients via fish waste and uneaten food pellets can amplify such effects, leading to large and persistent aggregations of wild fish near aquaculture sites. These aggregations have been quantified in numerous geographical locations but data are lacking for salmon farms in coastal British Columbia. The footprint of the attractive effects is also poorly understood in all cases as research has focused on fish populations directly associated with the infrastructure. In this study wild fish populations were quantified at shallow rocky ecosystems adjacent to salmon farms in the Broughton Archipelago and compared to paired reference sites with similar habitat characteristics to test for aggregating effects. Two SCUBA divers performed visual surveys along six 25x4x4m transects at each site, three at each of two depth ranges: deep (12-16m) and shallow (6-10m). Species, abundance, and estimated total length, as well as temperature, salinity, rugosity, and visibility were examined. A combination of multivariate and univariate statistical analysis were performed to compare the physical characteristics, community composition, number of individuals, and biomass between farms and reference sites. The overall community composition was significantly different at farm sites despite no difference found in the physical habitat characteristics between treatments. This difference was predominantly driven by five fish species, yellowtail rockfish (*Sebastes flavidus*), copper rockfish

(*Sebastes caurinus*) quillback rockfish (*Sebastes maliger*), shiner perch (*Cymatogaster aggregata*) and striped perch (*Embiotoca lateralis*). Presence/absence data showed no significant difference in species identity between farms and references, implying that the difference in community composition was primarily driven by changes in abundance rather than species identity. The total number of fish and biomass of all fish species was also significantly higher at farms. These results suggest that salmon farms in the Broughton Archipelago alter the community structure and increase the abundance of near-field wild fish populations. The aggregating effects are asymmetric within the community, with higher trophic level species showing the greatest increases in abundance. The potential implications of these results include a greater risk of disease and parasite transfer between farm and wild fish, as well as within each population. The ecological relationships among species may also be compromised with predator amplified communities potentially exhibiting top-down effects on the rest of the food web. Changes to wild fish communities seen up to 170m away from farm infrastructure suggest that the mechanism of the attractive effects may be driven more by nutrient subsidies than the presence of infrastructure. This work underscores the need to determine the full spatial extent and mechanisms of attractive effects as well as the ecological implications of persistent aggregations of wild fish near salmon farms.

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Acknowledgments

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Chapter 1 Introduction

1.1 Background

Nutrient availability plays a major role in determining community composition in aquatic ecosystems (Polis et al. 1996). Primary producers are most often limited by phosphorus and nitrogen, and bottom-up changes in the concentrations of these nutrients can significantly alter abundance and biomass of primary and secondary consumers (Micheli 1999, Havens et al. 2001). As a result fish density is often correlated with nutrient availability (Wu et al. 1999). Fish production in Canadian freshwater lakes has been closely correlated with the concentration of phosphorus and the subsequent annual phytoplankton production (Downing et al. 1990). Similarly, marine fish production is controlled by the conversion of nitrogen into phytoplankton biomass and subsequent transfer through the food web (Iverson 1990). Although inputs into nutrient limited ecosystems often increase the overall productivity and species diversity of affected communities, nutrient subsidies can also negatively impact the biological and chemical characteristics of an ecosystem. Toxic algal blooms can occur with heavy nutrient loading leading to decreases in oxygen concentrations. Sediment can also become anoxic and contain increased concentrations of sulphides and other harmful chemicals (Diaz and Rosenberg 2008). These conditions can overshadow the positive effects of nutrient enrichment, leading to subsequent abundance declines (Norkko and Bonsdoriff 1996). Nutrient subsidies may also benefit species asymmetrically, potentially leading to changes in community composition and decreases in species diversity (Hillebrand and Sommer 2000, Harlin 1995).

Habitat availability and character is another major determinant of community structure in marine ecosystems. Substrate type, rugosity, relief and other characteristics vary naturally and significantly affect the abundance and diversity of fish species (Bond et al. 1999, Gratwicke and Speight 2005). These characteristics are also subject to anthropogenic modification and manipulation. Fish aggregating devices (FADs) and artificial reefs are employed to increase the numbers and density of wild fish in a local area. FADs generally refer to man-made surface structures while artificial reefs are structures on the seafloor. Both have been shown to be effective in aggregating fish populations and subsequently increasing catch per unit effort (Dempster 2004, Santos and Monteiro 1998). Generally both function by providing increased habitat availability and complexity, shelter from predators, increased food availability and settlement points for larval fish, invertebrates and algae (Castro et al. 2004). There is debate whether artificial structures actually increase net production or simply attract and concentrate near-by individuals (Pickering and Whitmarsh 1997).

Open net-pen aquaculture sites can have similar effects to FADs (Dempster et al. 2002) altering the presence, abundance, diet and residence times of wild fish (Carss 1990). Large aggregations of wild fish are a ubiquitous feature of marine farms throughout the world (Carss 1990, Bjordal and Skar 1992, Dempster 2002, Boyra et al. 2004, Tuya et al. 2006, Valle et al. 2007, Dempster et al. 2009, Oakes and Pondella 2009). The decline of commercial fisheries has facilitated the rise of the global aquaculture industry which has had an average annual growth rate of 8.9% since 1970 (Tacon 2003) and a total production of 52.5 million metric tonnes in 2008 (FAO 2010). The large scale of open net-pen aquaculture may therefore result in significant effects on the distribution and behaviour of wild fish populations in some areas or regions. More than half of the total aquaculture production in Canada occurs in British Columbia, where Atlantic salmon operations represent over 90% of the total value of all aquaculture activities (DFO 2011).

The putative mechanisms of attraction of aquaculture sites are similar to FADs. The infrastructure of the farm provides increased habitat availability and complexity in which fish can find shelter from predators, as well as a spatial reference which fish can use for orientation (Carss 1990, Tuya et al. 2006). Increased foraging opportunities are available through the abundance of fouling communities settled on the infrastructure as well as the increased susceptibility to visual predation of zooplankton in shadowed areas (Tuya et al. 2006). Aquaculture sites may also act as recruitment points for larval fish, which can in turn supply food for and attract larger fish (Tuya et al. 2006).

The continuous input of nutrients via uneaten food pellets and excreted wastes from open net-pen marine farms greatly enhances the attraction of the infrastructure alone (Sudirman et al. 2009) and many wild fish species directly consume these nutrient sources (Carss 1990). Tuya et al. (2006) reported fish abundances 25 times higher at active aquaculture sites compared to inactive sites where only infrastructure remained. Farm derived nutrient inputs can also increase primary productivity, further increasing foraging opportunity for planktivorous fish (Sommer et al. 2002). Wild fish may also be attracted to chemical signatures from the high densities of farmed fish (Tuya et al. 2006).

Aggregation sizes tend to increase with higher number of pens and proximity to shore (Dempster et al. 2002). More pens will produce increased underwater structure, supplying more artificial habitat as well as increased nutrient discharge and chemical cues from larger numbers of farm fish. The size of aggregated wild fish populations outside of the pens can vary across locations; it is generally greater in tropical and subtropical locations (100s-1000s of fish) compared to temperate regions (10s-100s) (Boyra et al. 2004). This difference may reflect increased nutrient or structure limitation in the tropics or differences in sampling technique (seine net vs. visual census) (Boyra et al. 2004). Assemblages at temperate aquaculture sites, though fewer in number, can have similar overall biomasses to those in the tropics reflecting larger average size of individuals (Dempster et al. 2009).

The potential effects of high density fish aggregations around aquaculture sites are numerous. The consumption of excess feed and particulate organic matter by wild fish can decrease the amount and alter chemical composition of exogenous nutrients reaching the seafloor (Dempster et al. 2009). The discharge of farm effluent can lead to eutrophication and subsequent changes in benthic community composition and species diversity (Subandar et al. 1993). Normally, organic matter deposited on the seafloor is utilized and decomposed by bacteria, ciliates, meiofauna and macrofauna. The scale of material released from industrial scale farms can overwhelm these processes, or modify them greatly (Tsutsumi 1990). Larger aggregations of wild fish may mitigate some of these impacts by converting a portion of the wastes to biomass and redistributing the rest over a larger area. This redistribution could lead to decreased concentrations of pollutants but a potential increase in the overall spatial distribution of farm effluent. Despite this phenomenon, nutrient loading continues to occur in areas adjacent to aquaculture sites, with approximately 19% of the total organic matter in salmon feed deposited in the sediment in the form of feces and uneaten food pellets (Stucchi et al. 2005). Wild fish feeding on farm pellets may bioaccumulate and/or bioamplify pesticides, antibiotics and heavy metals and subsequently expose human consumers (deBruyn et al. 2006). Species with long life spans, high site fidelity and high trophic levels are particularly susceptible to contamination from farms. Rockfish in coastal British Columbia exhibit these characteristics and subsequently have persistently higher levels of mercury contamination near farms than reference sites (deBruyn et al. 2006). The level of exposure can be controlled for farm fish but not for wild fish, with long-lived, philopatric species potentially accumulating particularly high levels of contaminants.

It is difficult to determine if increased fish density proximate to farms is driven by increased production or if farms simply attract existing individuals, resulting in no net production increase (Pickering and Whitmarsh 1997). Attraction and concentration of fish populations has been demonstrated near aquaculture sites but definitive evidence of increased production has not been shown (Dempster et al. 2002). Asymmetric attraction or production of certain species may affect the community composition of surrounding ecosystems and the ecological relationships between species (Dempster et al. 2004, Sepulveda et al. 2004). Increased abundance of higher trophic level species could produce top-down changes through the food web, and subsequent decreases in forage species. Increased abundance of lower trophic levels may induce bottom-up changes to the rest of the community. Wild fish aggregations themselves may attract and amplify local densities of predators such as diving birds, pinnipeds and otters around aquaculture sites (Carss 1990).

Increased fish production could benefit capture fisheries by leading to increased catch rates, but increased population densities around farms may also increase the susceptibility to fishing pressure, potentially leading to overfishing (Dempster et al. 2004). It has been suggested that restricting fishing effort near farms could create miniature marine protected areas where aggregated fish populations could increase fisheries production in adjacent areas through spill over effects and enhanced larval recruitment (Dempster et al. 2004).

Amplified densities of resident wild fish around aquaculture sites could have implications for parasite and disease transfer. Open net pen aquaculture sites are known to increase the prevalence of pathogens and parasites and subsequently transfers these to wild populations (McVicar 1997, Krkosek et al. 2006, Morton et al. 2004, Morton et al.

2008). Closer association with farm fish could facilitate the transfer of disease from wild to farm populations and vice versa (Diamant et al. 2007). Increased number and density of hosts in an area could also lead to higher disease and parasite prevalence within the wild population (Dempster et al. 2004).

Currently much of the research focusing on the aggregating effects of aquaculture sites has been done in tropical and sub-tropical latitudes, with modest efforts in northern Europe. Most studies have also quantified fish populations directly associated with the infrastructure and therefore may under-represent attractive effects. This study is designed to quantify wild fish populations at rocky ecosystems adjacent to temperate British Columbia salmon farms and reference sites in the Broughton Archipelago and quantify the strength of aggregating effects.

1.2 Research Questions

1) Does the presence of active salmon farms affect the community composition of wild fish in rocky subtidal ecosystems?

   b) Are the changes in community composition due to species identity, abundance or both?

   c) Which wild fish species accounted for the differences in community composition?

   d) Do the changes in community composition alter the relative proportions of trophic levels between farms and reference sites?

2) Does the presence of active salmon farms affect the mean abundance and biomass of wild fish in rocky subtidal ecosystems?

Chapter 2 Methods

2.1 Overview

Wild fish populations were quantified at 20 sites in the Broughton Archipelago between Knight Inlet and Penphrase Passage (Figure 1; Table 1) using visual SCUBA surveys along horizontal transects at each site. Visual surveys tend to underestimate abundances of cryptic species, and can lead to misidentification of taxa in ecosystems with high diversity (Dempster et al. 2002). Relatively low diversity within this study area minimized opportunity for misidentifications. Although visual surveys are subject to biases and limitations, these were consistent among all sites. Visual surveys can better estimate the overall density and biomass in a given area compared to trawl surveys, the most common alternative (Harmelin-Vivien and Francour 1992), and produce estimates consistent with video samples taken by remotely operated vehicles (Parry et al. 2002).

All sites were sampled between October 5th and November 30th 2009, and all surveys were conducted during daylight hours (9am-3pm) to minimize light as a confounding factor. Fall surveys were chosen in order to avoid poor visibility conditions during the spring and summer months. Winter sampling was also avoided due to the challenging weather conditions and underestimation of rockfish which often seek shelter in crevices and deeper depths during this season (Love et al. 2002). Habitats with rocky substrate were specifically chosen because it typically exhibits higher fish densities and species diversity than soft-bottom habitats (Bond et al. 1999).

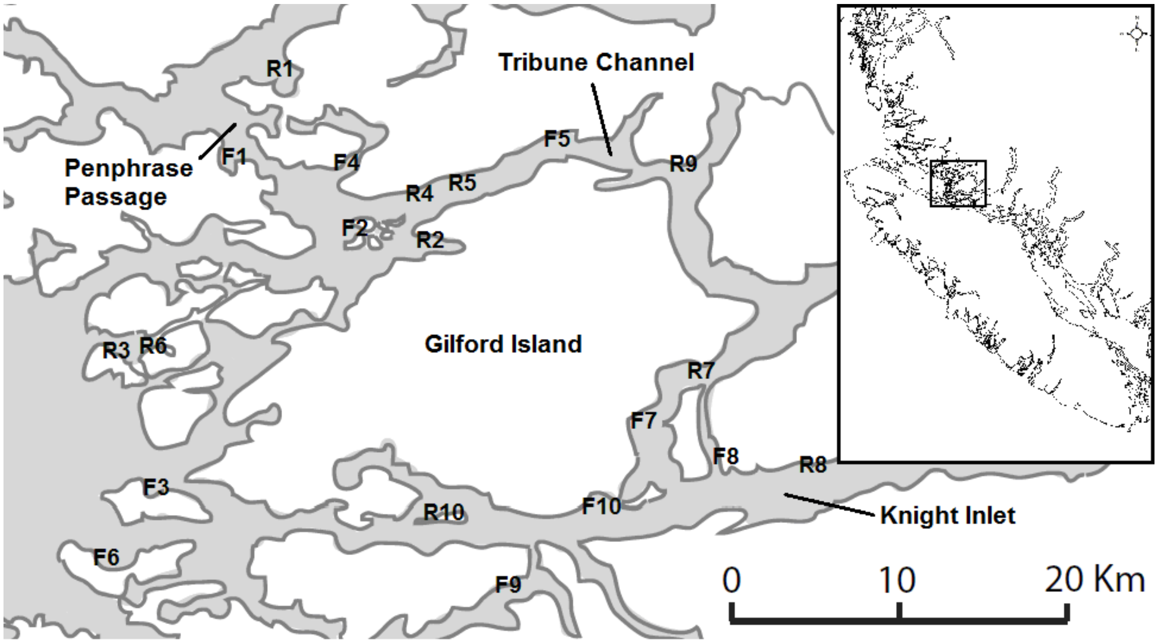


Figure 1. Location of farm and reference sampling sites in the Broughton Archipelago. See table 1 for identities of sites labelled F and R.

Table 1. Location of transect starting points of sampled farm and reference sites in the Broughton Archipelago.

Site	Map code	Treatment	Location
Sir Edmund Bay	F1	Farm	N 50.82.918 W 126.59.608
Moore Bay	R1	Reference	N 50.52.313 W 126.32.376
Burdwood Islands	F2	Farm	N 50.79.808 W 126.49.180
Viner Sound	R2	Reference	N 50.47.312 W 126.25.521
Midsummer Island	F3	Farm	N 50.39.141 W 126.39.558
Crib Island	R3	Reference	N 50.83.600 W 126.49.517
Cliff Bay	F4	Farm	N 50.50.087 W 126.29.433
Mouth of Tribune Channel	R4	Reference	N 50.81.884 W 126.43.887
Glacier Falls	F5	Farm	N 50.84.879 W 126.31.852
West Tribune channel	R5	Reference	N 50.49.308 W 126.24.433
Swanson Island	F6	Farm	N 50.61.810 W 126.70.604
Mars Island	R6	Reference	N 50.73.162 W 126.66.424
Humphrey Rock	F7	Farm	N 50.69.951 W 126.25.272
South Tribune Channel	R7	Reference	N 50.72.682 W 126.19.768
Sargeant's Pass	F8	Farm	N 50.67.084 W 126.18.335
North shore Knight Inlet	R8	Reference	N 50.67.115 W 126.12.158
Bennett Point	F9	Farm	N 50.60.935 W 126.35.944
Mouth of Bond Sound	R9	Reference	N 50.83.334 W 126.21.998
Doctor Islets	F10	Farm	N 50.65.131 W 126.28.796
Lady Islets	R10	Reference	N 50.64.509 W 126.42.504

2.2 Site Selection

Salmon farms that were actively rearing Atlantic salmon were selected and each paired with a reference site with similar physical and chemical conditions. Salmon farms in the Broughton Archipelago are typically located within 200m of shore and the rocky shoreline closest to the farm infrastructure where nutrient and habitat subsidies are likely to be most prominent were sampled. Increased proximity to the source of these subsidies can maximize the potential aggregating effects of the site. All ten farms had a minimum of six stocked net-pens during the time of sampling and based on the size of fish, had been active for a minimum of two months. The size of the pens, stocking density, age of fish and the duration of rearing varied among farms. This variation, along with the difficulty of estimating these conditions visually, did not allow for control for these site characteristics while maintaining a requisite level of site replication. Starting coordinates for each survey were randomly chosen using a random number generator. The number referred to the millimetre mark (1-60mm) of a ruler placed over a screenshot of a marine chart. Divers entered the water at the designated position and conducted preliminary dives near the surface to confirm the presence of rocky substrate while minimizing disturbance to fish. If the habitat was unsuitable, the divers continued along the shoreline until suitable habitat was found. In such cases the survey was initiated as soon as rocky habitat was confirmed to a minimum depth of 20m and length of 100m.

Each reference site matched the physical and biological characteristics of its paired farm site as closely as possible. Reference sites were chosen that as closely as possible duplicated wave and wind exposure (sheltered and exposed), substrate type (cobble, boulder, or solid rock), substrate relief (low, medium, and high), and presence/absence of bull kelp (*Nereocystis luetkeana*) of the farm site. All reference sites were a minimum distance of three kilometres away from any salmon farm or other pollution source, such as municipal sewage outfalls, and when possible shared the same shoreline as its paired farm. This three kilometre distance ensured that reference sites did not receive habitat or nutrient inputs from anthropogenic sources.

2.3 Survey methodology

Visual survey methodology was based on a modified version of techniques described by Harmelin-Vivien et al. (1985). Six transects were completed at each site, three shallow (between 6-10m) and three deep (between 12-16m) (Figure 2). Each transect was 25m long, 4m wide, and 4m deep. Each transect followed a single depth isobath identified using a random number generator. Two depths ranges were assayed in order to differentiate between fish communities that differentially structure by depth. For each transect, two divers descended to the predetermined depth. Swimming side by side along the randomly chosen depth isobath at a speed of approximately 5m per minute, all fish encountered up to 2m to each side and 2m above and below the transect were recorded for a distance of 25m. The 4m width and slow speed allowed for positive fish identification in even poor visibility conditions. The total time for the biological surveys on each transect was approximately 5 minutes and this was kept consistent between transects in order to ensure a consistent sampling effort. The transect was deployed simultaneously with sampling in order to prevent disturbing fish before they could be counted. Each diver recorded species, number, gender (if possible), and estimated total length of each fish using a scale bar on an underwater slate as a reference. When a school of more than ten individuals of the same species were encountered an average length for the entire school was recorded. Depth and direction were maintained using a compass and dive computer throughout each dive. Following each survey we recorded temperature, salinity, visibility, and rugosity at two randomly chosen points along the transect. Temperature was measured to the nearest 0.1 degree Celsius using a dive computer and horizontal visibility using a Secchi disc. Water samples obtained at depth (by opening and closing a sealed bottle) were brought to the surface to measure salinity using a refractometer. Rugosity was assessed by laying a negatively buoyant 5m chain along the contours of the substrate and measuring the straight, horizontal distance covered from one end of the chain to the other. Rugosity is defined by the ratio of this measurement to the total length of the chain. A rugosity of 1.0 indicates a completely flat surface while lower values indicate increasing substrate relief. Only rugosity measurements were repeated at both randomly selected sites of each transect. Substrate type, relief and basic community structure, with specific reference to macroinvertebrates and algae, were qualitatively described for each site. This entire methodology was then repeated twice more at the same depth and three more times at the pre-determined shallow depth for a total six transects per site. Consecutive transects were separated by approximately five metres between the end of one and the start of another in order to limit the disturbance to fish. Shallow transects were laid parallel to and directly adjacent to the deep transects.

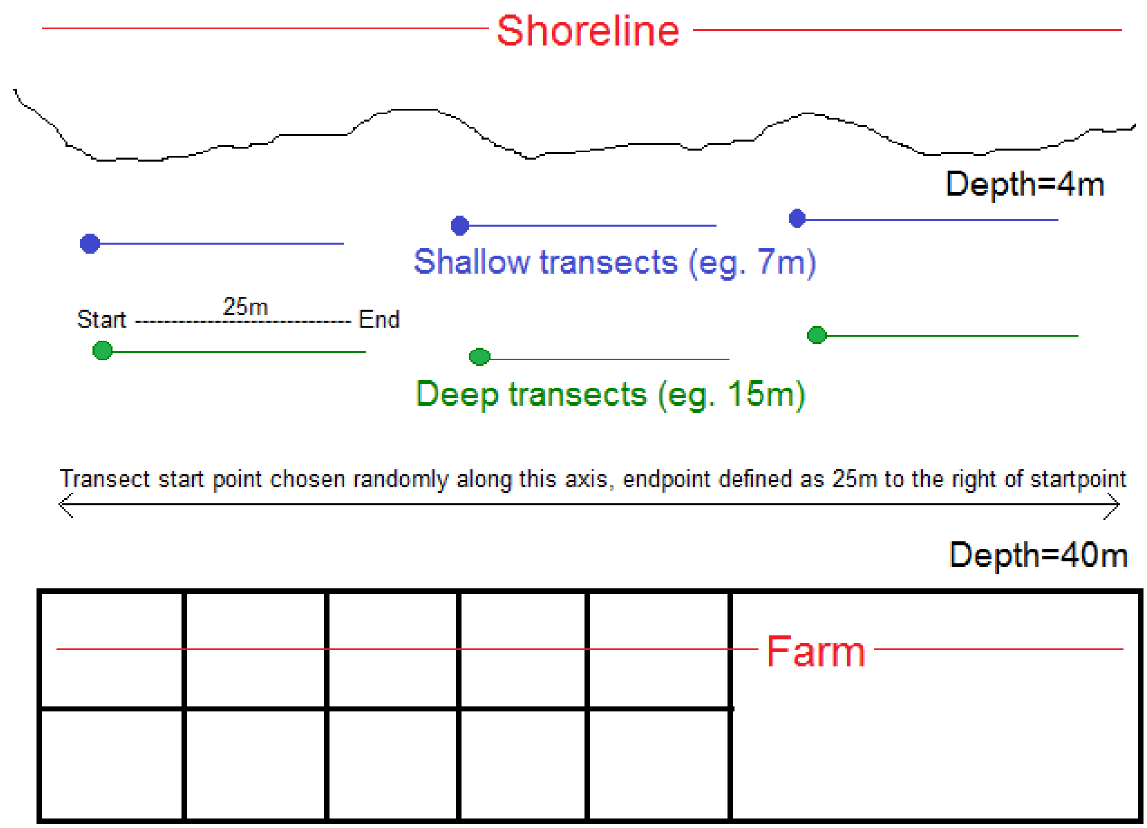


Figure 2. Diagram of transect orientations at a hypothetical farm site.

2.4 Statistical analysis

Differences in community composition between farm and reference sites were assessed using multivariate analyses with the statistical software Primer (Clarke and Gorley 2006). This approach allowed direct comparisons of both species identity and abundance simultaneously across the entire community. The data for the three transects per depth at each site were pooled to reduce the stress of multidimensional scaling and square-root transformed in order to increase the weighting of rare species as this can help to detect differences between sites (Cao and Larsen 2001). To compare changes in species composition among sites, Bray-Curtis (BC) similarity was chosen because it is robust in representing ecological distance (Faith et al. 1987, Legendre and Gallagher 2001) and is most often recommended for abundance data (Clarke and Gorley 2006). When directly compared to other similarity calculations such as the Canberra Metric and Morisita's index, BC similarity has been shown to more accurately reflect true similarity (Bloom 1981). The formula used for calculating BC similarity is:

$$S_{jk} = 100\frac{\sum_{i=1}^{p} 2\min(y_{ij}, y_{ik})}{\sum_{i=1}^{p}(y_{ij} + y_{ik})}$$

Where y_{ij} represents the abundance of the *i*th species in the *j*th sample and y_{ik} represents the same variable in the *k*th sample. BC similarity coefficients were visually represented using non-metric multidimensional scaling (nMDS) where a decreased distance between points represents increasing similarity. nMDS generally produces better ordinations than principal components analysis when using quantitative similarity measures (Fasham 1977). An analysis of similarities (ANOSIM) tested for statistically significant differences in similarity coefficients between farm and reference sites and compared these to differences within each treatment. ANOSIM produces an R statistic between -1 and 1 which is used to calculate the significance level of the multivariate difference between treatments (Clarke 1993). Positive values imply a greater difference between treatments than within treatments, negative values imply greater difference within treatments than between (O'Hara et al. 2010). Similarity percentages (SIMPER) were employed to quantify the contributions of each species to the overall differences between treatments. SIMPER describes the contribution of each variable to the average Bray-Curtis dissimilarity between groups and the average similarity within a group (Clarke and Gorley 2006).

The abundance data were transformed into presence/absence data to allow for comparisons of changes in species composition alone without considering numerical abundance. Bray Curtis similarity coefficients were calculated, visually represented using nMDS, and compared between farm and reference treatments by ANOSIM.

The physical characteristics of farm and reference sites were also compared using multivariate analyses. The data were square-root transformed and Euclidean distances were calculated for the variables temperature, salinity, rugosity, and visibility. Euclidean distances are often recommended for environmental and non-abundance data (Clarke and Gorley 2006). nMDS was used to visually represent the similarities and ANOSIM was used to test for a difference between farm and reference sites. This approach allowed for testing of the validity of reference site selection based on their similarity in physical characteristics to the farm sites (O'Hara et al. 2010).

The adult trophic level (TL) of each species was obtained from Fish Base (Froese and Pauly 2000) and used to test for asymmetries in the changes to community composition between low (TL=3.0-3.3), medium (TL=3.4-3.7), and high (TL=3.8-4.4) trophic level groups. Each species was grouped into one of these categories and the dataset divided accordingly. Multivariate analysis was then performed on each trophic level dataset individually. This included square-root transformations, calculation of Bray-Curtis similarities, nMDS visualization and ANOSIM to test for differences in the similarities between farm and reference sites. Comparison of the results of these three ANOSIM tests allowed for determining whether farm sites lead to changes in the relative abundances of species within each trophic level group.

Univariate analyses were performed in R (R Development Core Team 2010) to test specific differences between farm and reference sites. Data were square-root transformed to meet normality assumptions and t-tests were used for paired two-sample comparisons of the mean total number and biomass of fish. Biomass was quantified by estimating the total length of each fish and using length-weight formulas for each species to convert this value to biomass (Table 2). In cases where length-weight formulae were not available for a specific species, the formula available for the closest taxonomically related species was used. The mean length of copper rockfish and quillback rockfish were compared between treatments with two sample t-tests, and the length distributions of these populations were compared between the two treatments with two-sample Kolmogorov-Smirnov (KS) tests. KS tests were chosen over alternatives such as Chi-square because they are generally more powerful and can produce more valid results with small sample sizes (Lilliefors 1967). The data were pooled within each treatment for these latter two tests as sample sizes were not sufficient to allow for paired comparisons.

Table 2. Length-weight conversion equations and trophic levels (Froese and Pauly 2000) for each species of fish.

Species	**Equation**	**Trophic level**	**Trophic group**	**Source**
Copper rockfish (*Sebastes caurinus*)	W=0.0172*L3.018	4.1	High	Love et al. 2002
Quillback rockfish (*Sebastes maliger*)	W=0.0255*L2.920	3.8	High	Love et al. 2002
Yellowtail rockfish (*Sebastes flavidus*)	W=0.0287*L2.822	4.1	High	Love et al. 2002
Black rockfish (*Sebastes melonops*)	W=0.0043*L3.362	4.4	High	Love et al. 2002
Striped seaperch (*Embiotoca lateralis*)	ln(W)=-4.57282+3.03269*ln(L)	3.4	Medium	Pondella et al. 2002
Kelp perch (*Brachyistius frenatus*)	W=0.00491*L3.05	3.5	Medium	Odenweller 1975
Pile perch (*Rhacochilus vacca*)	ln(W)=-4.57282+3.03269*ln(L)	3.7	Medium	Pondella et al. 2002
Kelp greenling (*Hexagrammos decagrammus*)	W=0.000003586*L3.225	3.6	Medium	Froese and Pauly 2000
Pacific tomcod (*Microgadus proximus*)	W=0.0000106*L2.9919	3.6	Medium	Froese and Pauly 2000
Red irish lord (*Hemilepidotus hemilepidotus*)	W=0.0282*L3.00	3.5	Medium	Froese and Pauly 2000
Pacific staghorn sculpin (*Leptocottus armatus*)	W=0.000004*L3.00	3.5	Medium	Froese and Pauly 2000
Shiner perch (*Cymatogaster aggregata*)	W=0.00491*L3.05	3.0	Low	Odenweller 1975
Bay goby (*Lepidogobius lepidus*)	W=0.0083*L3.01	3.3	Low	Froese and Pauly 2000
White-spotted greenling (*Hexagrammos stelleri*)	W=0.0031*L3.428	3.3	Low	Froese and Pauly 2000
Buffalo sculpin (*Enophrys bison*)	W=0.000004*L3.00	3.3	Low	Froese and Pauly 2000
Crescent gunnel (*Pholis laeta*)	W=0.0043*L3.018	3.3	Low	Froese and Pauly 2000
Northern ronquil (*Ronquilus jordani*)	W=0.0028*L3.3288	3.1	Low	Froese and Pauly 2000
C-O sole (*Pleuronichthys coenosus*)	W=0.0321*L2.97	3.2	Low	Froese and Pauly 2000
Rock sole (*Lepidopsetta bilineata*)	W=0.0206*L2.858	3.2	Low	Froese and Pauly 2000

Chapter 3 Results

3.1 Physical Variables

The nMDS plot of Euclidean distance of the physical variables (temperature, salinity, visibility and rugosity) along deep transects suggests that farms were no more different from reference sites than they were from each other and vice versa (Figure 3A). Analysis of similarities produced a negative R statistic close to zero, suggesting that temperature, salinity, visibility and rugosity do not significantly differ between the two treatments (R=-0.073, p=0.934). How well the spatial configuration of points matches the data is represented by the “stress” value of the analysis, with a value of 0.0 being a perfect match and greater than 0.2 being a poor match (Kruskal 1964). In this case stress is 0.01, representing a good match between the plot and the actual data.

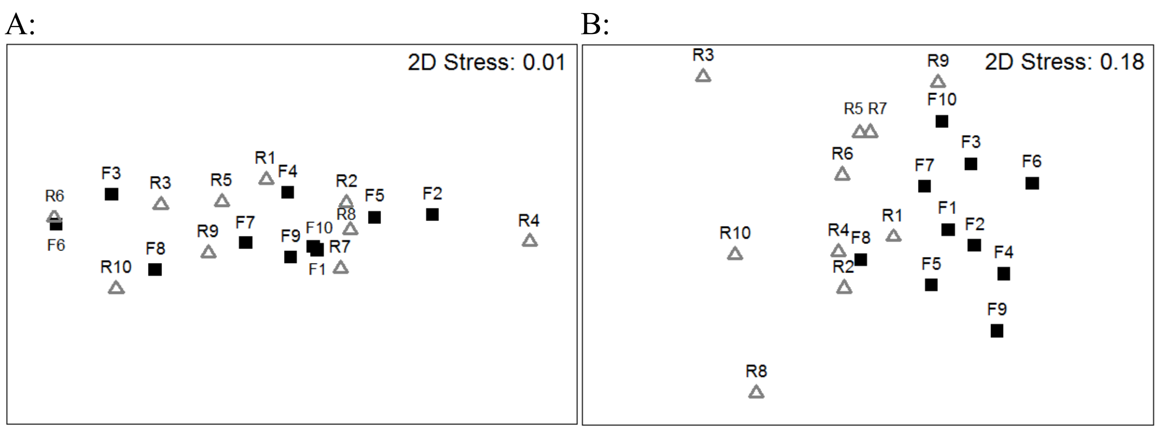


Figure 3. Panel A Physical Habitat: The consistent overlap of nMDS plots of Euclidean distances of physical variables (temperature, salinity, visibility and rugosity) near salmon farms (solid black squares) and paired reference sites (open grey triangles) along deep transects suggests no significant difference. Panel B Community Composition: nMDS plots of Bray-Curtis similarities of fish communities near salmon farms (solid black squares) and paired reference sites (open grey triangles) along deep transects. The spatial separation suggests a significant difference in community composition between farms and reference sites despite the lack of detected difference in physical habitat.

3.2 Community composition

The nMDS plot of Bray-Curtis similarities of community composition along deep transects suggests that farm sites were more similar to each other than they were to paired reference sites and vice versa (Figure 3B). The stress of 0.18 is high but within acceptable bounds for accurate depiction of data. Fish communities near salmon farms had significantly different compositions than those at reference sites (Global R=0.326, p=0.001). This result reflects not only a difference in the identity of species in the community but also the total number of individuals of each species. The plotted similarity for the Sargeant's Pass site (F8) did overlap with the reference sites (Figure 3B) as this was the most similar farm site to any reference site with a similarity of 77% to Reference Site 2 and 69% to Reference Site 4. No difference was seen in community composition between farms and references along shallow transects (Global R=0.043, p=0.214).

Wild fish communities at farm and reference sites were both predominantly characterised by the presence of the same five species (yellowtail rockfish [*Sebastes flavidus*], copper rockfish [*Sebastes* caurinus], quillback rockfish [*Sebastes maliger*], striped perch [*Embiotoca lateralis*] and kelp greenling [*Hexagrammos decagrammus*]). Within farm sites these species accounted for a total of approximately 93% of the similarity in species composition and abundance (58, 8, 17, 7, and 3% respectively). Within reference sites these five species accounted for approximately 92% of the similarity (37, 10, 16, 18, and 12% respectively). Within farm sites the average similarity was higher than within reference sites (46% and 33% respectively), while the average dissimilarity between farm and reference sites was 69%. Five of the 20 total species encountered (yellowtail rockfish, copper rockfish, quillback rockfish, striped perch, and shiner perch (*Cymatogaster aggregata*)) accounted for 75% of the differences in community composition between treatments (Table 3). Yellowtail rockfish were by far the most dominant contributors to the differences, alone accounting for 33%.

Table 3. The similarity percentages of individual fish species. Five species (yellowtail rockfish , striped perch, shiner perch, copper rockfish and quillback rockfish) accounted for 75% of the observed difference in site community composition. Column 1 refers to the species of fish. Columns 2 and 3 compare the average abundance of each fish species at farms and references for square root transformed data. Column 4 displays the calculated average Bray-Curtis dissimilarity between the two treatments for each species. Column 5 is the percent contribution of each species to the dissimilarity between treatments. Column 6 is the cumulative percent contribution of all previously listed species.

	Farm	Reference			
Species	Average abundance	Average abundance	Average dissimilarity	Contribution%	Cumulative%
Yellowtail rockfish	10.94	2.62	22.58	32.96	32.96
Striped perch	3.25	2.04	8.88	12.96	45.92
Quillback rockfish	3.6	1.17	7.55	11.02	56.94
Shiner perch	3.79	0	6.35	9.27	66.21
Copper rockfish	2.37	1.13	5.97	8.71	74.92
Kelp greenling	1.04	0.99	3.79	5.53	80.45
White-spotted greenling	0.48	0.95	3.07	4.48	84.93
Juvenile rockfish	0.71	0.28	2.29	3.35	88.28
Generic sculpin	0.54	0.2	1.73	2.53	90.81
Pile perch	0.46	0.42	1.63	2.37	93.18
Pacific tomcod	0.45	0.3	1.53	2.24	95.42
Buffalo sculpin	0.38	0	1.14	1.67	97.09
Crescent gunnel	0.2	0	0.51	0.74	97.84
Bay Goby	0.24	0	0.49	0.72	98.55
Red Irish Lord	0.17	0	0.25	0.36	98.91
Ronquil	0.1	0	0.24	0.36	99.27
Staghorn sculpin	0	0.1	0.21	0.31	99.58
CO Sole	0.1	0	0.14	0.21	99.79
Rocksole	0.1	0	0.14	0.21	100

The nMDS plot of Bray-Curtis similarities for presence/absence transformed data depicts consistent overlap between farm and reference sites (Figure 4). ANOSIM produced a negative R statistic close to zero, suggesting no significant difference in species composition between treatments ($R=-0.007$, $p=0.506$).

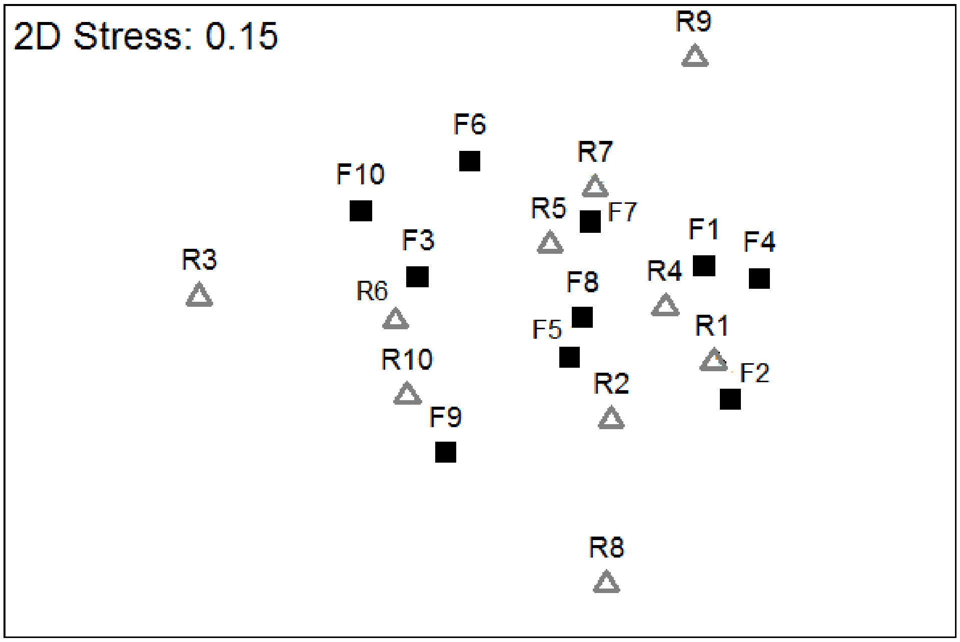


Figure 4. nMDS plot of Bray-Curtis similarities of farm (solid black squares) and reference sites (open grey triangles) for species presence/absence transformed data. The consistent overlap between treatments suggests that species identity is not driving the observed differences in community composition between farm and reference sites.

Multivariate analysis of abundance data subsetted by trophic level showed asymmetrical changes to the community composition between the high, medium and low categories. The cumulative average abundance was higher for all three trophic level groups at farms (17.7 vs 5.2, 5.37 vs 3.55, 5.93 vs 1.57 respectively). ANOSIM of Bray-Curtis similarities showed the difference in high trophic level species between farm and reference sites was statistically significant ($R=0.308$, $p=0.02$), while the difference in medium or low trophic level species was not ($R=-0.079$, $p=0.963$ and $R=0.093$, $p=0.083$ respectively).

3.3 Abundance and Biomass

The mean total number of fish (TNF) was significantly higher at salmon farms than at reference sites along the deep transects ($t=4.8863$, $df=9$, $p=0.0008639$, figure 6A). Although similar trends were present along shallow transects, the mean TNF was not significantly different at farms than at reference sites along the shallow transects ($t=2.2059$, $df=9$, $p=0.05482$, figure 6B). This result was most likely due to the high levels of variance in the data.

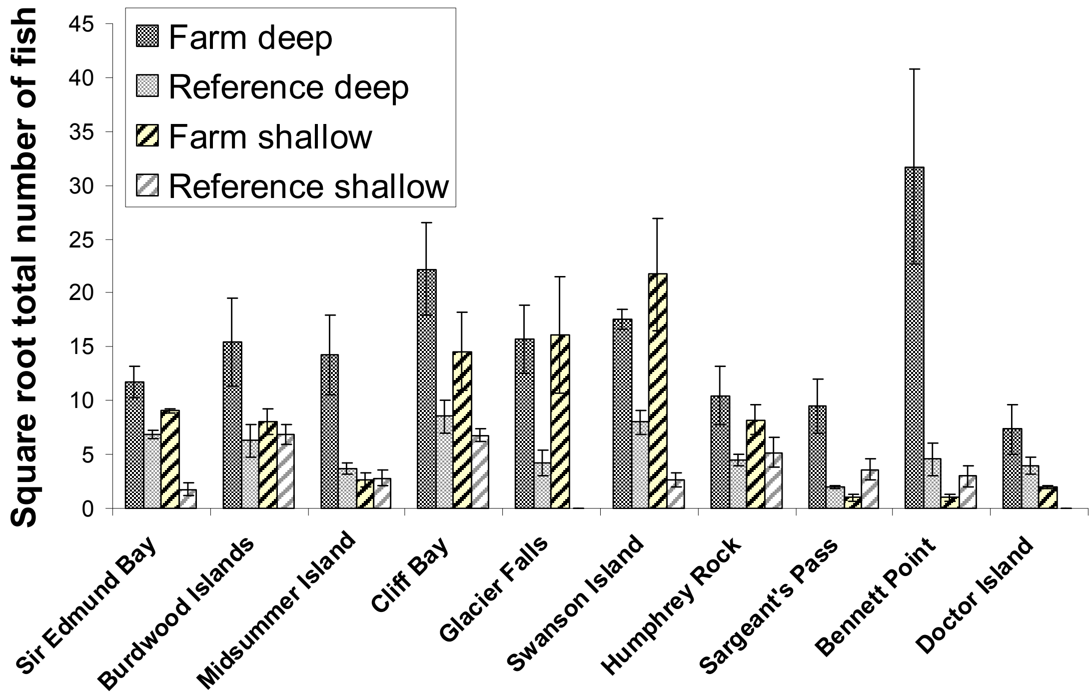


Figure 5. Square root of the total number of fish at ten farms and paired reference sites along deep and shallow transects. Aggregation sizes are consistently larger at farm sites than reference sites, especially along deep transects. Error bars represent standard error of the mean.

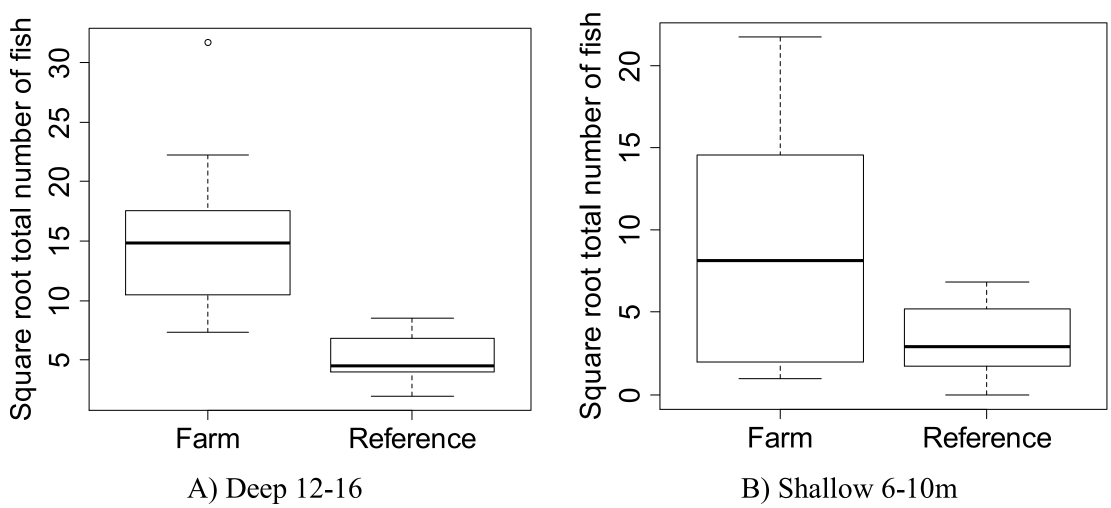


Figure 6. Boxplot of the square root of the total number of fish at salmon farms and reference sites along deep(A) and shallow(B) transects. The mean number of fish is statistically significantly higher at farms along deep transects but not along shallow. The horizontal bold line represents the median and horizontal box lines represent the 25th and 75th percentiles. The vertical dashed lines represent 1.5 times the interquartile range of the data and the dot is an outlier falling outside this range.

The largest increases in abundance at farms were seen in yellowtail, copper, and quillback rockfish as well as shiner and striped perch (Figure 7). The three rockfish species were seen at most site pairs and were consistently more abundant at most farm sites (Figures 8-10). Yellowtail rockfish had an average abundance 13.8 times higher at farms than references, while copper and quillback rockfish had average abundances 3.7 and 6.8 times higher at farms respectively. Shiner and striped perch also had higher average abundances at farms but the trend was not consistent at most sites. Shiner perch were not seen at most site pairs, occurring only at three farm sites and no reference sites. Striped perch were not consistently more abundant at farm sites, having higher abundances at four reference sites than paired farms.

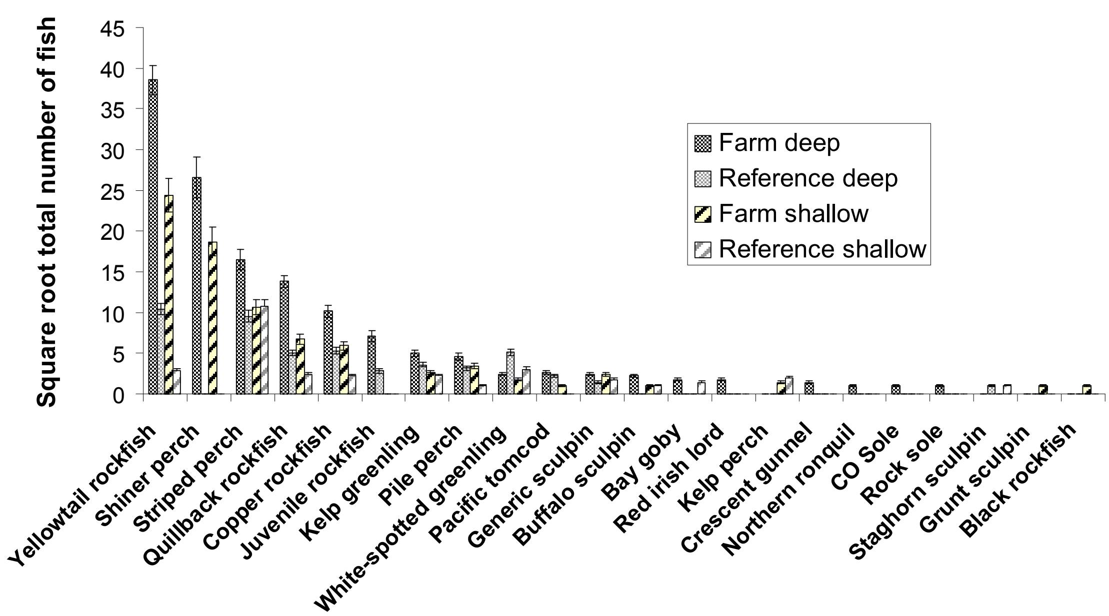


Figure 7. The square root of the total number of fish quantified at farms and paired references along deep and shallow transects. Three species of rockfish (yellowtail, quillback, and copper) and two species of perch (shiner and striped) showed the highest numerical increase between farms and references.

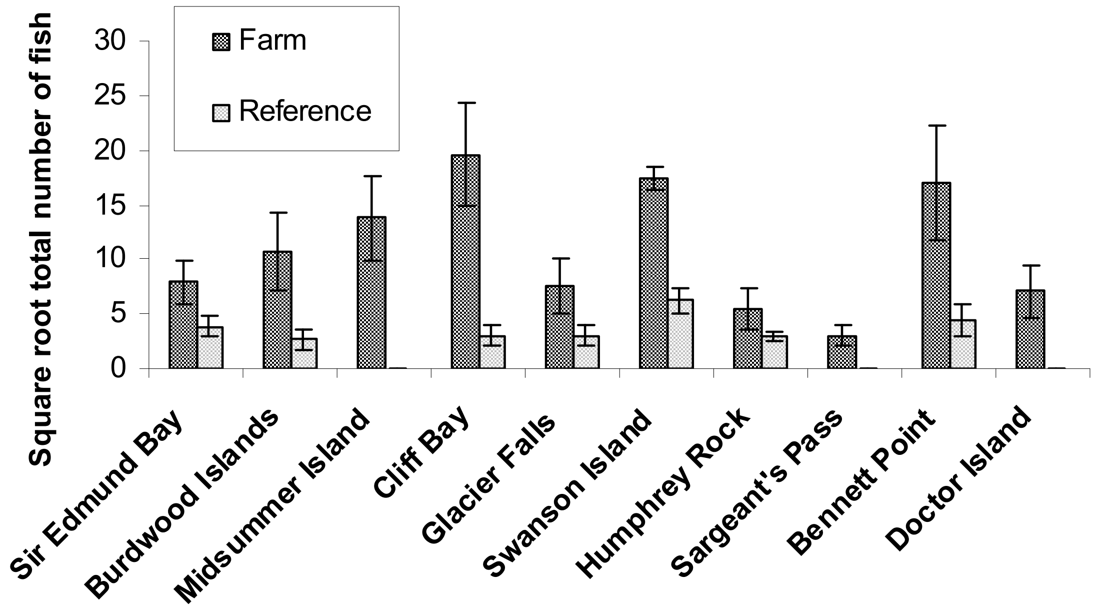


Figure 8. Total number of yellowtail rockfish at each farm and paired reference site along deep transects. Aggregations of yellowtail rockfish were present and consistently more numerous at all farm sites than references

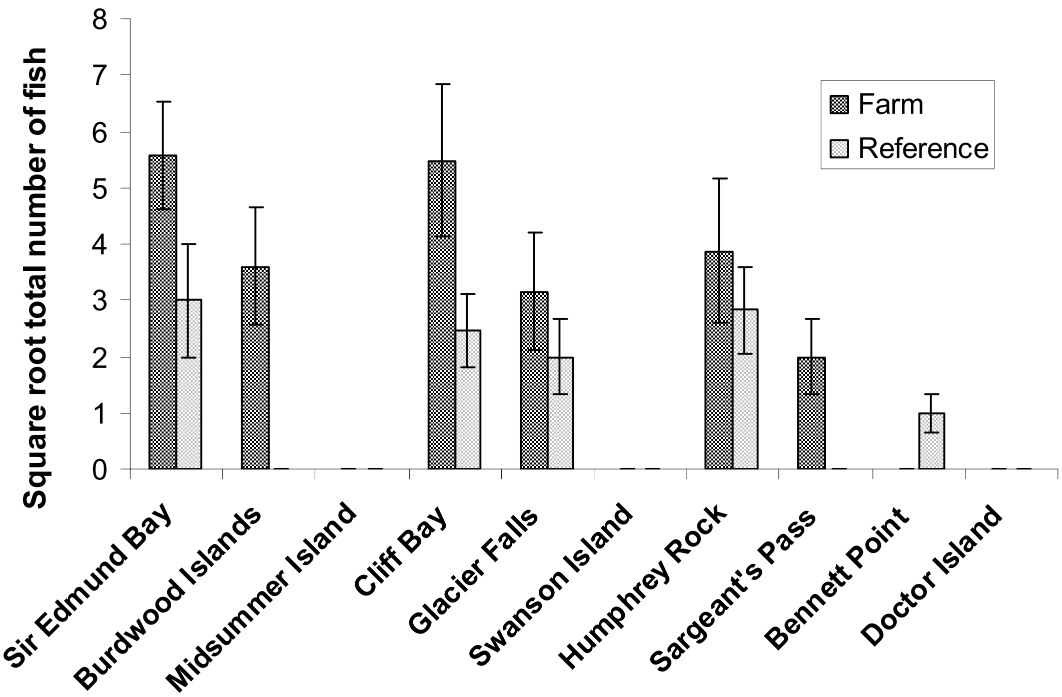


Figure 9. Total number of copper rockfish at each farm and paired reference site along deep transects. Aggregations of copper rockfish were present at seven site pairs and were more numerous at farms at all sites except Bennett Point.

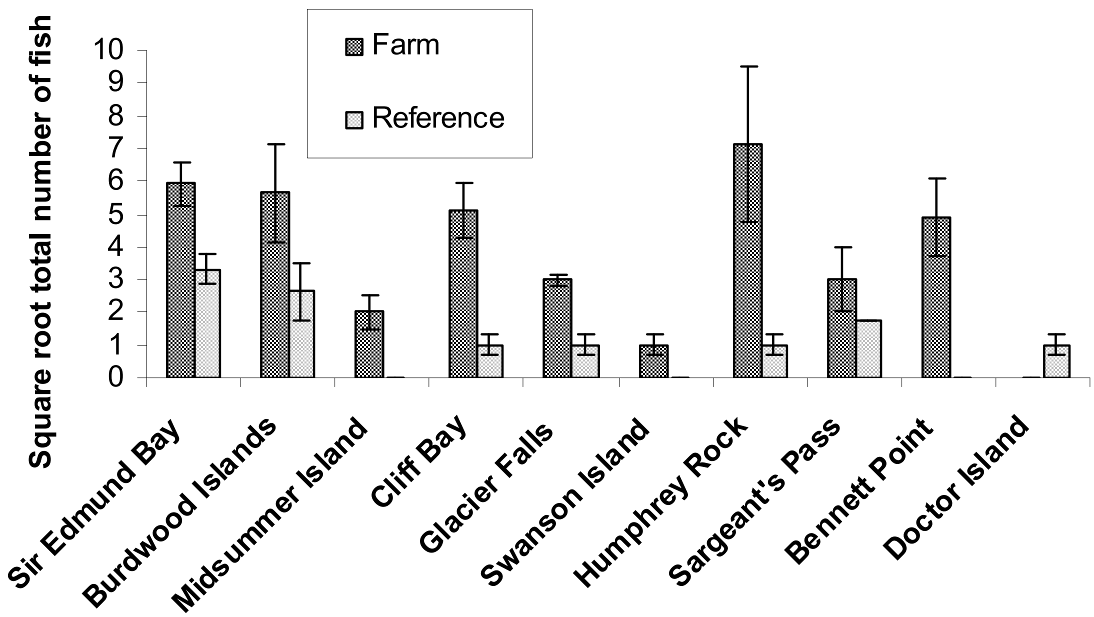


Figure 10. Total number of quillback rockfish at each farm and paired reference site along deep transects. Aggregations of quillback rockfish were present at nine farm sites and were consistently more numerous than at references except for Doctor Island.

The estimated biomass of fish communities varied considerably between farms and references sites (Figure 11). The total biomass was highest at the Swanson Island farm and lowest at the Sargeant's Pass and Doctor Island farms (Figure 11). The mean biomass was 6.3 times higher at farms (mean=8.64kg, S.E.=1.56) than references (mean=1.37kg, S.E.=0.28) along deep transects, and 10.2 times higher at farms (mean=3.72kg, S.E=2.25) than references (mean=0.36kg, S.E=0.13) along shallow transects (Figure 12). Paired t-tests determined that the difference in biomass along deep transects was statistically significant (t=6.7599, df=9, p=0.00008272) but was not along shallow transects (t=2.0027, df=9, p=0.07622 respectively).

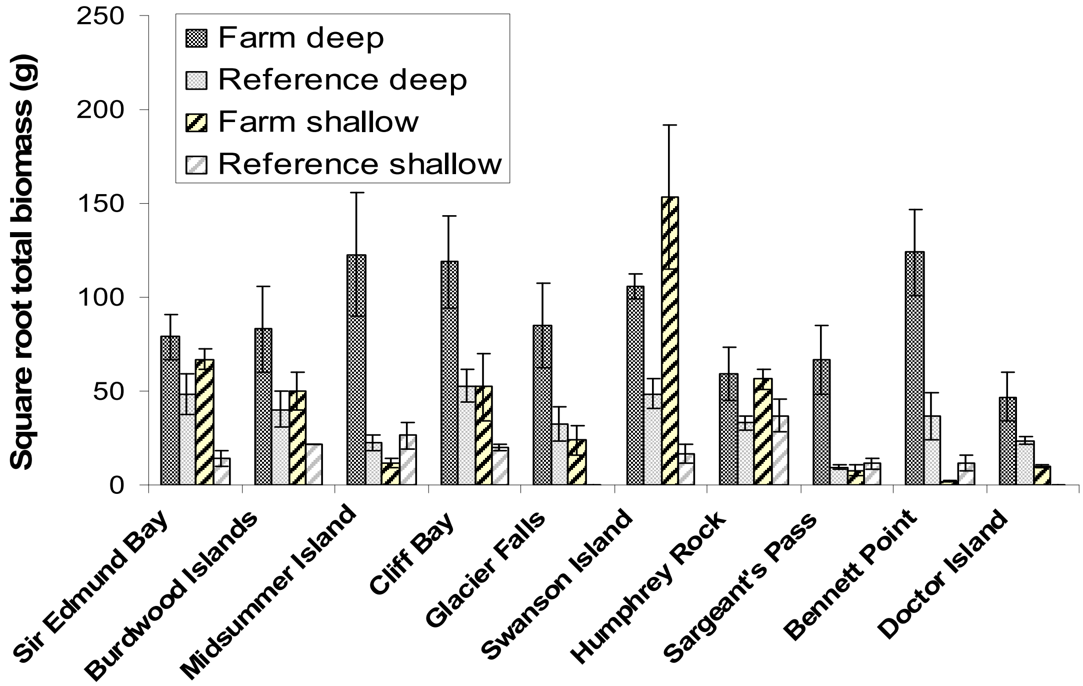
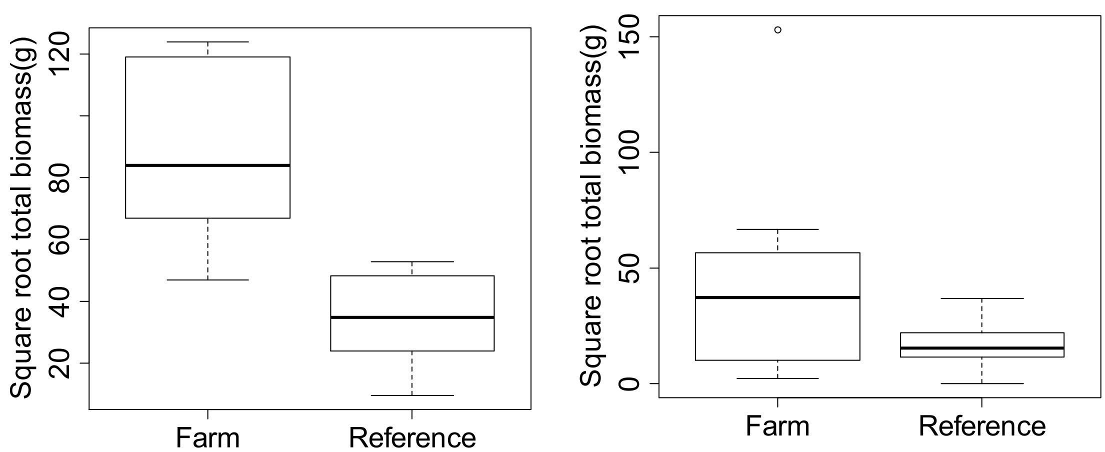


Figure 11. The square root of total biomass of fish quantified at deep and shallow transects at ten salmon farms and ten paired reference sites. The biomass was consistently higher at all farms sites along deep transects and at seven out of ten farm sites along shallow transects.



A) Deep 12-16 B) Shallow 6-10m

Figure 12. Boxplot of the square root biomass of fish populations at farms and reference sites along deep (a) and shallow transects (b). The mean biomass in both cases is higher at farms than reference sites.

A Kolmogorov-Smirnoff test determined that the length distribution of copper rockfish was significantly different between the two treatments ($D=0.486$, $p=0.001347$) with the farm populations having a significantly lower mean length ($t=-2.8098$, $df=68.102$, $p=0.006466$). There was no significant difference in the mean length of quillbacks ($t=0.288$, $df=26$, $p=0.7757$) or their distributions ($D=0.2405$, $p=0.3076$).

Chapter 4 Discussion

4.1 Overview

Open net-pen aquaculture sites have been consistently shown to alter the behaviour and distribution of near-by wild fish populations in many geographical locations (Carss 1990, Bjordal and Skar 1992, Dempster 2002, Boyra et al. 2004, Tuya et al. 2006, Valle et al. 2007, Dempster et al. 2009, Oakes and Pondella 2009). The resulting changes in community composition and population densities can have negative consequences for both wild and farm fish. These include increased susceptibility to disease and parasite transfer (Diamant et al. 2007), unregulated exposure of wild fish to contaminants and pharmaceuticals (Bustnes et al. 2010), and changes in the ecological relationships between species (Weir and Grant 2005). The current study quantified wild fish populations near salmon farms in the Broughton Archipelago, British Columbia and was consistent with studies in other locations. The community composition of wild fish populations was altered near farm sites, predominantly driven by increased abundances of a few species. The overall abundance and biomass of wild fish was much higher near farms than at reference sites, particularly in species with high trophic levels. These results offer important insights into the mechanisms and implications of the attractive effects observed at open net-pen aquaculture sites.

4.2 Community Composition

Analysis of community composition along deep transects shows similar results to Dempster et al. 2009, Tuya et al. 2006, and Boyra et al. 2004, with a clear separation between the farm and reference groups. This result implies that the farms were more similar to each other in terms of species identity and abundance than to their paired reference sites, and suggests that farms alter the community structure of local fish populations in predictable ways. Community composition did not differ significantly between treatments along shallow transects, most likely due to the loss of statistical power through increased variability in the data. This difference may also reflect the potential for decreased nutrient inputs from negatively buoyant food particles which may settle at deeper depths.

Along deep transects the Sargeant's Pass farm site did overlap slightly with its reference sites (Figure 2, F8). This is most likely the result of the relatively few fish quantified at this site, particularly the low number of yellowtail rockfish (9 vs 149 average at farm sites). This result may also be related to the lack of biological diversity noted for this site with invertebrates and macroalgae being qualitatively described as sparse. No significant difference was found in the physical and chemical properties of the sites, suggesting that these are not drivers of observed differences in community composition and abundance. SIMPER analysis showed that the differences between farm and reference sites were primarily driven by a few species (Table 3). Yellowtail rockfish was by far the greatest contributor to the observed differences between farm and reference, with a 13.8 times higher total abundance at farms along deep transects and a 74.2 times higher along shallow transects when compared to reference sites. Together with striped perch, quillback rockfish, shiner perch and copper rockfish, these fish species represented almost 75% of the dissimilarity between farm and reference sites due to their increased abundance at farms. Boyra et al. 2004 also found that a few species accounted for a large portion of the difference between farms and references. One species consistently contributed 11-17% of the total dissimilarity, and 50% driven by six species (Boyra et al. 2004). Dempster et al. 2009 found that six of fifteen species observed accounted for 70% of dissimilarities, with the largest contributor responsible for 21%. These results suggest that certain species are more attracted to farms than others and the aggregating effects of farms are asymmetric within the community.

This asymmetric attraction could be related to variations in behavioural or life history characteristics including site fidelity and migration patterns. Other species may also be attracted but may not be able to successfully compete for subsidies produced by the farms or may experience increased predation and subsequent population declines. Three species of rockfish and two species of perch were responsible for the majority of the difference between the treatments, but only the rockfish species were consistently seen in higher abundances at farms sites than references (Figures 8-10). Although shiner and striped perch were on average much more abundant at farms, this trend was not consistent across sites. Approximately 85% of shiner perch were seen in a single school along a single transect at the Bennett Point farm, thus representing a significant outlier from the rest of the data. The larger rockfish may be better competitors for the farm subsidies than other species as they are opportunistic generalists exploiting a wide variety of prey including zooplankton, benthic crustaceans and small fish (Love et al. 2002). The farm subsidies may be benefiting yellowtail, copper, and quillback rockfish through direct consumption of uneaten farm pellets or by increased prey abundance associated with higher productivity around the farms. Yellowtail rockfish were considerably more abundant than copper and quillback rockfish, and consistently aggregated in higher densities at all farms sites (Figure 8). This result may be related to the differences in residency and movement patterns among the species. Coppers and quillbacks have very limited home ranges (less than $30m^2$) in optimal habitat and larger home ranges ($400m^2$) in less desirable, low relief habitat (Matthews 1990). Although yellowtail rockfish can also have high site fidelity, tagging studies have also suggested considerable movements of hundreds of kilometres in both juvenile and adult populations (Stanley et al. 1994). This migratory behaviour may increase the likelihood of finding more productive habitat near salmon farms. It should also be noted the three rockfish species were generally larger and less cryptic than most others and therefore the higher abundances may be partially due to a higher level of detectability.

4.3 Abundance and biomass

Salmon farms had consistently higher total numbers of fish and biomass than paired references sites. The mean number of fish was 8.7 times higher at farms along deep transects and 6.9 times higher at farm sites along shallow transects. The mean biomass was also 6.3 times higher along deep transects and 10.2 times higher along shallow transects at farm sites. Although these differences were statistically significant along deep transects, they were not significant along at shallow depths. This is most likely the result of a lack of adequate statistical power to detect the difference at shallow depths due to increased variability in the data and large number of zero counts along shallow transects.

The variability in total number of fish and biomass among farm sites may be due to differences in habitat and community characteristics. The highest abundance and biomass was seen at Swanson Island farm, which was qualitatively described as having complex rocky habitat with numerous crevices and poor visibility possibly due to increase plankton abundance. Increased habitat complexity and productivity could explain the increased abundance and biomass at this site. The Sargeant's Pass and Doctor Island farm sites had the lowest abundance and biomass and were qualitatively described as having relatively few invertebrates and macroalgae. The lack of macroalgae may cause decreased habitat complexity while the lack of invertebrates may reflect decreased productivity at these sites. These were the only two farms sampled in Knight Inlet which is generally less sheltered than the other locations sampled and therefore can experience greater currents, wind, and wave exposure. Higher rates of flushing may disperse the nutrient subsidies at these sites over a greater area and therefore lead to lower productivity near the farms. These differences in abundance are not likely the result of temporal differences as all surveys were conducted at roughly the same time of day and all site pairs were sampled within a few days of each other.

The significantly higher biomass and number of fish at aquaculture sites are consistent with the results of Dempster 2002, Dempster et al. 2004, Dempster et al. 2005, Tuya et al. 2006, Carss 1990, Boyra et al. 2004, and Valle et al. 2007. The population sizes were most similar in numbers to studies conducted in temperate waters where 10s to 100s of fish were quantified near salmon farms (Carss 1990, Dempster et al. 2009). In tropical and subtropical latitudes, farm associated fish populations have generally been quantified in the 1000s to 10,000s (Tuya et al. 2006, Valle et al. 2007, Dempster 2002). These variations in population densities may reflect increased biodiversity levels in warmer waters (Boyra et al. 2004), or a greater presence of more numerous pelagic schooling species versus more solitary benthic species.

The effect size tended to be smaller in this study than most others, with less than an order of magnitude change in number of fish and biomass. These results are similar to those of Carss et al. (1990) who found average abundance and biomass approximately four times greater around salmon farms in Scotland. In Norway Dempster et al. (2009) described aggregations of fish associated with aquaculture sites as 1-3 orders of magnitude larger than near-by reference sites. At farms culturing sea bream (*Sparus aurata*) and sea bass (*Dicentrarchus labrax*) in the Canary Islands, Boyra et al. (2004) and Tuya et al. (2006) found abundances greater than one order of magnitude higher.

Valle et al. (2007) also found 2-3 orders of magnitude increase in fish abundance and biomass around sea bass and sea bream farms in Southeastern Spain.

This difference in effect size is most likely related to the proximity of sampling to the farms. Fish populations directly associated with the farm infrastructure are typically reported in previous studies, whereas this study sampled benthic populations along adjacent shorelines between 50 and 170m away from the infrastructure. The attractive effect of artificial reefs and aquaculture sites decrease rapidly with a distance of tens of metres from the infrastructure (Dempster et al. 2002). The increased distance from the nearest infrastructure produces decreased attractive effects and therefore suggests that the current results represent an underestimation of the true effect size of impacts of farms on fish. Although the magnitude of observed effect was smaller, increased population densities at distances of hundreds of metres from the farms were observed. This result suggests that the attractive effects of aquaculture sites can persist for longer distances than previously reported, and the total size of farm-associated fish populations may also have been previously underestimated by quantifying only those directly associated with the farm infrastructure.

The decreased effect size may also be the result of differences in the habitat characteristics of both farm and reference sites. The current study sampled along rocky shorelines near farm sites whereas the others sampled predominantly open water soft-bottomed habitats. Increased habitat complexity and availability generally leads to higher abundances and hard substrate generally supports greater numbers and diversity of species than soft substrate (Bond et al. 1999). Thus the gradient of complexity separating farm and reference populations in the current study was modest relative to most other studies where farm infrastructure greatly increased habitat complexity relative to reference sites with sandy or muddy bottoms. In this study substrate complexity and availability were similar between farm and reference sites, which are a powerful feature of this study that makes the revealed differences convincingly attributable to farms.

4.4 Species composition

Significant differences in species identity were not detected between farms and references when comparing presence/absence data. Fish communities at both farm and reference sites were predominantly made up of the same five fish species. These results suggest that the changes in community composition were primarily driven by changes in numerical abundance rather than changes in species composition. This may be the result of certain species being more strongly attracted to the farm sites or better able to compete for the subsidies produced by the farm, leading to a greater number of individuals but no increase in species richness. This result differed from that of Valle et al. (2006) and Dempster et al. (2002) who found increased species richness at farm sites compared to references. This difference again can be explained partially by the difference in sampling locations. These studies sampled populations directly below and adjacent to farm infrastructure where habitat complexity and nutrient subsidies are greatly enhanced. These populations were compared to those of soft-bottomed, open water reference sites which generally exhibit lower diversity than rocky substrate (Bond et al. 1999). The current study compared rocky shoreline communities near salmon farms to similar sites away from farms, producing negligible increases in habitat complexity and less direct nutrient subsidies. The difference in these results may also be related to a higher diversity of species in warm water ecosystems.

4.5 Trophic level

Upon division of the data into three trophic level categories, the only significant difference between farm and reference sites found was in the highest trophic level category. This difference in trophic levels suggests that there was not an equivalent increase in species of all trophic levels at farm sites. The increased abundance of high trophic level species was larger than increases seen in the medium and low trophic level categories. Although the average abundance was also larger at farms for low trophic level species, this was most likely inflated by the single large school of shiner perch seen at the Bennett Point farm and was not a statistically significant difference. Upon removal of this outlier, the average abundance of low trophic level species decreases from 3.8 times higher at farms than references to 1.9 times higher. Some of the largest and most consistent numerical increases at farm sites were found in copper, yellowtail and quillback rockfish. These three species had the highest trophic levels and accounted for over 50% of the observed change in community composition between farms and references. The larger size and predatory nature of these abundant rockfish may allow them to out-compete smaller fish for the farm subsidies. Increased predation on smaller fish species may also explain why species with higher trophic levels tended to have higher abundance at farm sites while lower trophic level species did not. This phenomenon has been described for artificial reefs where the altered trophic structure of fish communities lead to increased predator populations and subsequent decline in prey populations (Claudet and Pelletier 2004, Sosa-Lopez et al. 2005).

4.6 Mechanisms of attractive effect

The results of this study suggest that the attractive effects of salmon farms extend well beyond the immediate area surrounding the infrastructure. The mechanism of attraction is most likely a combination of various factors including increased habitat availability from the infrastructure and nutrient inputs from feed and waste (Boyra et al. 2004). The infrastructure provides increased substrate complexity, giving protection from predators and habitat for settling communities (Tuya et al. 2006). Increased habitat availability from underwater structures such as artificial reefs, FADs and aquaculture sites are known to increase fish population densities (Dempster et al. 2009). Populations in this study were quantified between 50 and 170m away from the infrastructure. Since the attractive effects of artificial infrastructure have been shown to decrease rapidly within tens of metres from the source (Dempster et al. 2002), increased habitat subsidies do not appear to be the main driving force for the increased fish population densities seen in this study.

Increased density of fish adjacent to salmon farms is more likely attributed to nutrient subsidies to the surrounding environment. Uneaten food pellets from farms are often consumed by wild fish, and this behaviour has been described as a major contributor to the attractive effect of the farm (Sudirman et al. 2009). Although intact food pellets generally settle on the bottom close to the farm, faeces and smaller food particles can be spread to a larger area. Kutti et al. (2007) found that most of the nutrient waste settled within 250m of salmon farms but traces could be found as far as 900m. The current populations studied are within these ranges and can therefore be expected to receive direct nutrient inputs from the farm. Many of the species seen in this study forage over a large area and could also be feeding nearer to the infrastructure and returning to the rocky shoreline habitat for protection. Since nutrient availability plays a major role in determining the abundance and density of marine populations (Polis et al. 1996), nutrient subsidies could explain the larger fish populations seen near salmon farms. This explanation is consistent with Tuya et al. (2006) who found that nutrient inputs greatly enhanced the attractive effects of the infrastructure alone.

Populations without direct access to nutrient subsidies from the farm may still benefit from a general nutrient enrichment of sediments and the water column. Increased nutrient concentrations from aquaculture sites can increase near-by plankton and invertebrate populations (Costa-Pierce and Bridger 2002). Increases in prey populations could themselves attract larger aggregations of fish.

The increased density of fish adjacent to farms may not receive any benefit from the farm subsidies and could be the result of a spill-over effect from populations directly associated with the infrastructure. This phenomenon has been well documented at sites adjacent to artificial reefs and marine protected areas (Francini-Filho and Moura 2008). Fish populations directly associated with the infrastructure may occur in higher densities through direct benefit from food and habitat subsidies. Predators, such as marine mammals and diving birds, are generally more abundant around farms and therefore may represent an increased mortality risk for fish directly associated with the infrastructure (Carss 1990). Increased competition and predation near the infrastructure may encourage individuals to spread to surrounding areas.

Salmon farms in the Broughton Archipelago often seasonally employ artificial lights to illuminate their net-pens (Hay et al. 2004) and this has also been shown to attract wild fish and invertebrates in higher abundances (McConnell et al. 2010). The artificial lights are primarily used during winter and spring and therefore are unlikely to explain the aggregations seen in this study during the fall. The distance of the attractive effect from farm illumination is unknown but this is more likely to affect pelagic species near the surface and infrastructure rather than adjacent benthic populations quantified in this study.

4.7 Implications

Aquaculture sites alter the community characteristics of natural ecosystems and therefore may have negative consequences (Weir and Grant 2005). The asymmetrical population increases in high trophic level species may further alter the community dynamics. Predators exert top-down control of ecosystem structure; therefore, changes in predator abundances can lead to trophic cascades (Frank et al. 2005) and the subsequent inverse patterns of abundance or biomass across trophic levels (Pace et al. 1999). Increases in predatory fish populations associated with artificial reefs and marine protected areas often lead to decreased low trophic level populations (Bortone et al. 1998, Sosa-Lopez et al. 2005). This phenomenon could explain why increases in lower trophic level species were not observed near salmon farms. Farm subsidies may exert bottom-up control of the community by benefitting primary producer and consumer populations, but the attraction and increased abundance are masked by increased predation rates on lower trophic levels.

Asymmetry between the life spans of the aggregated fish species and the length of farm production cycles could result in further changes to the community characteristics. Copper, yellowtail, and quillback rockfish are long-lived species with life spans of 50, 64, and 95 years respectively (Love et al. 2002). The production cycles of salmon farms in the Broughton Archipelago are only 1.5 - 2 years and often include a fallow period between cycles. The cessation of production would remove the nutrient subsidies to the surrounding ecosystem, resulting in predator amplified communities with decreased forage opportunities. This cessation effect could further alter the community structure by increasing predation rates on lower trophic level species in order to compensate for the lack of farm subsidies.

Exposure of wild fish populations to farm effluent may have both positive and negative effects. Consumption of uneaten food pellets by wild fish may aid in dispersing the effluent over a larger area (Felsing et al. 2005). Nutrient enrichment of the surrounding ecosystem is a common problem associated with open net-pen aquaculture as a result of the input of commercial fish feed and waste (Sowles and Churchill 2004). Excess nutrients can lead to harmful algal blooms and changes in sediment chemistry (Handy and Poxton1993, Folke et al. 1994, Whyte et al. 2001). Wild fish are known to ingest farm feed pellets and could therefore decrease the concentration of nutrient loading in the local area (Oakes and Pondella 2009, Fernandez-Jover et al. 2006). Felsing et al. (2005) estimated that wild fish consume as much as 40-60% of cage-derived nutrients and can significantly decrease the impact of organic wastes on sediments. The increased abundance of wild fish seen in the Broughton Archipelago could increase the effectiveness of waste dispersal at these sites. Despite this phenomenon, nutrient loading and its associated effects are consistently seen at open net-pen aquaculture sites (Sowles and Churchill 2004).

The consumption of farm feed can expose wild fish to contaminants such as heavy metals, pesticides and antibiotics (Bustnes et al. 2010). Increased mercury content has been documented in commercial salmon feed and subsequently in wild rockfish populations associated with salmon farms in the Broughton Archipelago (deBruyn et al. 2006). The increased abundance of rockfish seen at farm sites increases the risk of contamination, as well as subsequent exposure to consumers if these populations are harvested. Antibiotics are commonly employed at commercial aquaculture sites to minimize the spread of disease (Cabello 2006) and antibiotic residues have been found in sediments and wild fish populations associated with aquaculture sites (Bjorkland et al. 1990). Antibiotic resistant bacteria have been quantified near salmon farms and the increased densities of wild fish near farms in the Broughton Archipelago could increase the rate of resistance development and the potential spread to other ecosystems (Cabello 2006). The potential migratory behaviour of yellowtail rockfish could facilitate this transfer and antibiotic exposure may adversely affect the natural parasite fauna of these populations.

Increased densities of fish associated with aquaculture sites could increase the likelihood of disease transfer between wild and farm fish, as well as within wild populations. Salmon farms have been shown to concentrate and transfer parasites such as sealice (*Lepeotheirus salmonis, Caligus clemensi*) to near-by wild fish populations (Krkosek et al. 2006, Morton et al. 2004, Morton et al. 2008). Increased prevalence of infection with sea lice has been linked to declines of wild salmonid populations in the Broughton Acrhipelago (Krkosek et al. 2007). *Caligus clemensi* and related species of *Lepeotheirus* copepods commonly infect rockfish in the Northeast Pacific (Love et al.

2002) therefore the increased abundance of rockfish associated with farms in the Broughton Archipelago could further increase the abundance and transfer of sea lice to wild salmonid populations. Increased host density of aggregated wild fish may also increase the parasite prevalence within these populations. Fernandez-Jover et al. (2010) found no effect of farms on the total parasite abundance in two species of wild fish; however, a farm-effect was correlated to decreases in some species of parasites and increases in others. These changes in host-parasite relationships may have negative effects on wild fish populations. Numerous disease outbreaks have been recorded at salmon farms, including netpen liver disease, bacterial kidney disease, infectious hematopoietic necrosis, infectious salmon anaemia and furunculousis (McVicar 1997, Sowles and Churchill 2004). Some of these have been shown to transfer from farm to wild populations and vice versa, therefore posing a significant threat to both (McVicar 1997). Higher densities of wild fish associated with salmon farms and the potential migratory behaviour of yellowtail rockfish may increase this risk. Diseases and parasites contracted at one farm site may be spread to other farms and wild populations through the migration of individuals to new sites. Rockfish associated with artificial reefs and less desirable habitat increase their home ranges and movement patterns considerably (Matthews 1990). The completion of a farm production cycle results in decreased nutrient inputs and therefore may increase the likelihood of migration to active farms near-by.

Larger aggregations of fish associated with aquaculture sites also have potential implications for fisheries. There is debate as to whether artificial structures result in greater production of biomass or simply concentrate near-by fish populations in a smaller area (Brickhill et al. 2005). Farm subsidies may increase the productivity of fish communities, resulting in an overall increase in the number of fish in the wider area. This could lead to increased catches near aquaculture sites. However, the inputs from the farm may simply attract and concentrate individuals from the surrounding area, resulting in an increased susceptibility of farm associated populations to over-fishing and subsequent population declines. In order to provide evidence for whether the aggregations of fish were the result of production or attraction, the length distributions of copper and quillback rockfish were compared between the two treatments. Assuming that all sizes of fish are equally attracted to farms, one would expect aggregations resulting from attraction to have the same distribution of lengths in farms and references. Higher production will result in increased recruitment of juveniles, therefore the length distributions should be significantly different and I would expect to see a larger proportion of smaller fish in the aggregated farm population. The length distributions of quillback rockfish did not differ significantly, suggesting that these populations are not experiencing increased production. The length distribution of copper rockfish was significantly different, with the farm populations having a significantly smaller mean length and a higher proportion of individuals below 15cm than reference populations (71% vs 27%). This result suggests that the copper populations near farms may experience increased recruitment and production.

4.8 Study limitations

Although the results show clear associations between salmon farms and wild fish populations, certain limitations were present in the study design, the most pertinent being the selection of suitable reference sites. Many factors can affect the characteristics of fish communities. While attempts were made to control for as many of these factors as possible, this is not always feasible in the field. Many habitat characteristics were quantified such as temperature, salinity, and visibility, whereas others such as substrate relief, and algal abundances were only qualified. Quantification of these variables would provide a stronger justification of the suitability of the reference sites.

The visual estimation of total lengths by divers often contains a significant level of error, leading to a bias towards over or underestimation (Edgar et al. 2004). Diver were trained in this study to reduce this bias using model fish of known size prior to collecting data. This technique has been shown to be effective in increasing the accuracy of length estimates (Bell et al. 1985). Often the bias of each individual observer is consistent in its direction and extent depending on the size of the fish and, therefore the data can be adjusted upon calculation of each diver's bias (Edgar et al. 2004). This technique could have been useful in increasing the accuracy of our size estimates. When we encountered large schools of fish, it was not possible to estimate the total length of each individual and an average length for the school was used. This may not accurately reflect the true sizes of individuals and results in a loss of the variability of total lengths within that school. Instead of estimating an exact length to the nearest cm, each individual could have been placed into broader size categories. Although this estimation could have decreased our level of accuracy, the precision may have increased.

Estimated trophic levels were only available for adults of each species. Many individuals quantified were sub-adults, which often have lower trophic levels as a result of differences in diet. More accurate estimates for each individual would be more appropriate for comparing relative changes in trophic levels within the community.

I attempted to address the question of whether the aggregating effects are a result of production or attraction by analyzing the size distributions of the copper and quillback rockfish populations. I was unable to use the data for yellowtail rockfish because most of the observations were of large schools and therefore I did not have true length estimates for most individuals. The data available for coppers and quillbacks were also limited and therefore had to be pooled. Although a significant difference was found in the length distributions of copper rockfish, the pooling of the data may have confounded the result. The difference in length distribution may be an artefact of the pooling of the data rather than a true ecological difference. The pooled data for both copper length distributions was normally distributed which should increase the reliability of these results

4.9 Future research

The results of this study provide insights into the magnitude and mechanisms of the attractive effects of open net-pen aquaculture sites, and future research should expand on both of these issues. Increased fish populations have been quantified up to hundreds of metres from the farm infrastructure, but the total distance of the effect is not known. Replacing the discrete treatment categories of farm and reference with a more continuous set of sample sites between these two categories could provide information about the total footprint of the attractive effects from aquaculture sites. This design could also estimate the rate of decline in the attractive effects with increasing distance from the source.

Repeating this study during different levels of farm production could also help tease apart the relative contributions of different inputs to the attractive effect. A before after control impact (BACI) study design could distinguish between the effects of increased habitat complexity from the input of infrastructure, and the effects of increased nutrient availability from the input of feed and fish waste. Data could be collected before the farm infrastructure is placed at a specific site, before the farm is stocked with fish, and after full production and feeding is underway. Differentiating between these mechanisms could be useful in determining the most effective means of mitigating the potential negative impacts associated with increased densities of fish populations near aquaculture sites.

The temporal variability of wild fish aggregations should also be determined. The community composition of farm-associated populations can change seasonally, with abundances of species increasing or decreasing at different times of the year (Bubic et al. 2011). A larger scale replication of this study would provide larger sample sizes and allow for a more robust analysis of the size distributions between the populations of each species. This could allow for a better estimation of whether the aggregations of fish are a result of attraction or production.

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