**Annotated Bibliography**

Helen Casendino

Duda, J. J., M. S. Hoy, D. M. Chase, G. R. Pess, S. J. Brenkman, M. M. McHenry, and C. O. Ostberg. 2021. Environmental DNA is an effective tool to track recolonizing migratory fish following large‐scale dam removal. Environmental DNA 3:121–141.

Duda et al. (2021) assessed the efficacy of environmental DNA (eDNA) sampling as a measure of migratory fish abundance following the removal of the Elwha River dam. Using qPCR assays,  they targeted several fish species (including several salmonids) that would likely be found in the Elwha River watershed at various locations in the watershed. The authors compared the results yielded by eDNA methods to results yielded by other kinds of sampling (e.g., smolt traps), and found that eDNA methods are reliable in tracking migratory fish species. This study is useful to my project in that it provides primer sequences for coho salmon, which I will use to detect coho in streams in Bellingham.

Johnson, J. H., and N. H. Ringler. 1980. Diets of juvenile coho salmon ( *Oncorhynchus kisutch* ) and steelhead trout ( *Salmo gairdneri* ) relative to prey availability. Canadian Journal of Zoology 58:553–558.

Johnson and Ringler (1980) quantified benthic and surface prey types available to salmonids (juvenile coho salmon and steelhead trout) in a tributary of Lake Ontario, Canada. They compared available prey to the stomach contents of each species to see which taxa each preferred. The authors found that juvenile coho salmon tend to prefer terrestrial invertebrates over aquatic invertebrates, but of aquatic invertebrates, preferred orders trichoptera, diptera (chironomids), ephemeroptera, and plecoptera (in that order). This is useful to my project because if I know what prey types juvenile coho prefer, I can track how the abundance of those species is impacted by changes in coho abundance.

Logerwell, E. A., N. Mantua, P. W. Lawson, R. C. Francis, and V. N. Agostini. 2003. Tracking environmental processes in the coastal zone for understanding and predicting Oregon coho ( *Oncorhynchus kisutch* ) marine survival: *Oregon coho marine survival*. Fisheries Oceanography 12:554–568.

Logerwell et al. (2003) built a model to track variation in the abundance of coho salmon from Oregon to assess which environmental factors had the most impact on survival rates, and what survival rates we expect to see in the future. They projected that the survival rate of coho salmon entering the ocean in 2001 was 6-8%. Their model also supported that smolt migration occurred between April and June. This is important for my project, because I need to know when to expect juvenile coho in my study streams.

Institute for Watershed Studies, Huxley College of Environmental Studies, Western Washington University. 2006. *“Urban Streams Monitoring Project Final Report”*. Bellingham, Washington

The City of Bellingham commissioned scientists at Western Washington University to analyze samples of benthic macroinvertebrates in the watersheds of Padden Creek, Squalicum Creek, and Whatcom creek from 2001 to 2003. Their report provides high-resolution taxonomic data on invertebrates found at sites near my project’s sampling sites (especially near Padden and Squalicum Creek). This is beneficial to the development of my project because I need to know what species of aquatic invertebrate to design PCR primer assays for.

Chatila-Amos, K. 2021. Detecting Subarctic Caddisflies using eDNA and Measuring the Phylogenetic Signal of their Choice in Habitat. University of Guelph, Ontario, Canada

This master’s thesis assessed the efficacy of using a novel qPCR primer assay, compared to traditional sampling methods, to detect aquatic invertebrate *Philarctus bergrothi* from eDNA samples of creeks in Manitoba, Canada. The primer assay had to be highly specific to *P. bergrothi*, as there were ~43 sister taxa present in the habitats sampled. The author found that qPCR results (from eDNA samples) detected *P. bergrothi* at 96% of the sites it was detected via traditional sampling methods. This is informative for my project, as it shows that qPCR methods yield highly accurate detection of aquatic invertebrates.

Garlapati, D., B. Charankumar, K. Ramu, P. Madeswaran, and M. V. Ramana Murthy. 2019. A review on the applications and recent advances in environmental DNA (eDNA) metagenomics. Reviews in Environmental Science and Bio/Technology 18:389–411.

Garlapati et al. (2019) conducted a review of existing literature that uses eDNA methods to address several ecological questions and concerns (e.g., invasive species detection, predator-prey interactions, microbial diversity) in a variety of habitats, while offering suggestions for future undertakings in the field. This is useful to my project because it provides valuable references and synthesis of what methods have worked to detect predator-prey interactions using eDNA sampling, which my project is concerned with.

Shelton, A. O., R. P. Kelly, J. L. O’Donnell, L. Park, P. Schwenke, C. Greene, R. A. Henderson, and E. M. Beamer. 2019. Environmental DNA provides quantitative estimates of a threatened salmon species. Biological Conservation 237:383–391.

Shelton et al. (2019) modelled trends in out-migrating Chinook salmon by estimating abundance from beach seines and eDNA samples (qPCR methods) to measure the degree of agreement between the two sampling methods. The authors found that both sampling metrics yielded similar trends in abundance; results from the two sampling metrics at the population level were more correlated than results at the site-level. This study is informative to my project because it shows that current eDNA methods may still be better at tracking trends, rather than actual biomass, of salmonid populations. This is not an issue for my project, as I am most interested in how trends of coho salmon track with trends in aquatic insect prey species.

Masese, F., P. Raburu, and M. Muchiri. 2009. A preliminary benthic macroinvertebrate index of biotic integrity (B-IBI) for monitoring the Moiben River, Lake Victoria Basin, Kenya. African Journal of Aquatic Science 34:1–14.

Masese et al. (2009) created a benthic macroinvertebrate index of biotic integrity (B-IBI) to monitor the health of a river in Kenya, whose downstream area is heavily developed for agricultural purposes. They tested their B-IBI using known land-usage and benthic invertebrate assemblages, and found the latter to be significantly influenced by human activity. The study highlights the idea that aquatic invertebrates provide key insight into the health of a watershed, particularly in the context of different types and magnitudes of anthropogenic land-use. This is pertinent to my project, as I will be developing qPCR assays for various common aquatic invertebrates in the Bellingham area that may be useful for future B-IBI assessments.

Levi, T., J. M. Allen, D. Bell, J. Joyce, J. R. Russell, D. A. Tallmon, S. C. Vulstek, C. Yang, and D. W. Yu. 2019. Environmental DNA for the enumeration and management of Pacific salmon. Molecular Ecology Resources 19:597–608.

Levi et al. (2019) assessed the efficacy of eDNA sampling methods in tracking the abundance of salmonid species in Alaska, including sockeye and coho salmon. They found that eDNA methods were sufficient to track salmonid abundance; however, they emphasized that researchers must understand the life history of the species in question, as eDNA methods can’t distinguish between life stages. This is important to my study, because I only want to detect juvenile salmon (the life stage that would eat insects). Thus, I need to know the period of time in which juvenile salmon out-migrate to the ocean.

Soininen, E. M., A. Valentini, E. Coissac, C. Miquel, L. Gielly, C. Brochmann, A. K. Brysting, J. H. Sønstebø, R. A. Ims, N. G. Yoccoz, and P. Taberlet. 2009. Analysing diet of small herbivores: the efficiency of DNA barcoding coupled with high-throughput pyrosequencing for deciphering the composition of complex plant mixtures. Frontiers in Zoology 6:16.

Soininen et al. (2009) conducted both eDNA metabarcoding analysis and traditional diet analysis on the gut contents of two herbivorous vole species to assess the efficacy of eDNA metabarcoding in understanding herbivorous interactions, and found that the metabarcoding method yielded more taxonomically-specific results. This will be useful in the introduction of my study’s manuscript, as it provides an example of eDNA methods being used to look into population dynamics that are influenced by herbivory and predation.